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(54) Title: **BAX-RESPONSIVE GENES FOR DRUG TARGET IDENTIFICATION IN YEAST AND FUNGI**

(57) Abstract: The invention describes the use of nucleic acids and polypeptides which are involved in a pathway eventually leading to programmed cell death of yeast or fungi for the preparation of a medicament for treating diseases associated with yeast or fungi or for the treatment of proliferative disorders or for preventing apoptosis in certain diseases. Methods are provided to identify compounds which selectively modulate the expression or functionality of said polypeptides in the same or a parallel pathway. Also provided are compounds as well as pharmaceutical compositions, medicaments and vaccines. The invention also comprises new nucleic acid sequences, probes and primers derived thereof, expression vectors and host cells transformed with said vectors, polypeptides and antibodies raised against said polypeptides.

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## BAX-RESPONSIVE GENES FOR DRUG TARGET IDENTIFICATION IN YEAST AND FUNGI

### Field of the invention

5 The present invention relates to the identification of genes and proteins encoded thereof from yeast and fungi whose expression is modulated upon programmed cell death and which genes, proteins or functional fragments and equivalents thereof may be used as selective targets for drugs to treat infections caused by or associated with yeast and fungi or for the treatment of proliferative disorders or for the prevention of apoptosis in certain diseases.

10

### Background to the invention

Invasive fungal infections (e.g. *Candida* spp., *Aspergillus* spp., *Fusarium* spp., *Zygomycetes* spp.) (Walsh, 1992) have emerged during the past two decades as important pathogens causing formidable morbidity and mortality in an increasingly diverse and progressively  
15 expanding population of immunocompromised patients. Those with the acquired immune deficiency syndrome (AIDS) constitute the most rapidly growing group of patients at risk for life-threatening mycosis. But fungal infections have also increased in frequency in several populations of other susceptible hosts, including very-low-birth-weight infants, cancer patients receiving chemotherapy, organ transplant recipients, burn patients and surgical patients with  
20 complications.

These fungal infections are not limited to humans and other mammals, but are also important in plants where they can cause diseases or cause the production of unwanted compounds (e.g. *Fusarium* spp., *Aspergillus* spp., *Botrytis* spp., *Cladosporium* spp.).

Although recent advances in antifungal chemotherapy have had an impact on these mycoses,  
25 expanding populations of immunocompromised patients will require newer approaches to antifungal therapy. The discovery of novel antifungal agents is thus an essential element of any new antifungal therapy.

Classical approaches for identifying antifungal compounds have relied almost exclusively on inhibition of fungal or yeast growth as an endpoint. Libraries of natural products, semi-synthetic,  
30 or synthetic chemicals are screened for their ability to kill or arrest growth of the target pathogen or a related nonpathogenic model organism. These tests are cumbersome and provide no information about a compound's mechanism of action. The promising lead compounds that emerge from such screens must then be tested for possible host-toxicity and detailed mechanism of action studies must subsequently be conducted to identify the affected molecular  
35 target.

Cells from multicellular organisms can commit suicide in response to specific signals or injury by an intrinsic program of cell death. Apoptosis is a form of programmed cell death which leads to elimination of unnecessary or damaged cells. Cells that are either unwanted or potentially harmful to the organism undergo the apoptotic process and show events like cell shrinkage, chromatin condensation, cytoplasmic condensation, digestion of nuclear DNA, loss of mitochondrial membrane potential, plasma membrane blebbing and phagocytosis of the cell debris (Schwartz, *et al.* 1993). The Bcl-2 family of proteins is centrally involved in the control of the programmed cell death process (PCD). Proteins of this group belong either to the inhibitors of cell death (Bcl-2, Bcl-X<sub>L</sub>) or to the group of proteins promoting apoptosis (Bax, Bak) (Oltvai and Korsmeyer 1994; Knudson and Korsmeyer 1997; Reed *et al.* 1998). The ability of the Bcl-2 family of proteins to regulate life and death of a cell is conserved across evolution. Finding of homologues of PCD regulatory genes in plants and animals suggests the possibility that some functions involved in this process may originally have evolved in unicellular organisms, before a divergent development between the plant and the animal kingdom had happened (Apte *et al.* 1995).

Expression of the pro-apoptotic human or mouse Bax protein in *Saccharomyces cerevisiae* did induce cell death in this budding yeast (Sato *et al.* 1994; Greenhalf *et al.* 1996; Zha *et al.* 1996). It was initially described as a process that resembled autophagy with dissolution of the internal organelles and vacuolisation. The apoptotic features characteristic for multicellular eucaryotic cells like morphological changes in nuclear shape and chromatin condensation, were not observed in this yeast (Zha *et al.* 1996). It was therefore suggested that Bax-induced cell death in *S. cerevisiae* is due to the toxicity of the Bax protein itself, mediated by a hypothetical pore-formation without any involvement of a death program (Muchmore *et al.* 1996).

Bax expression in the fission yeast *Schizosaccharomyces pombe* did in contrast show some of the typical apoptotic changes like DNA fragmentation, chromatin condensation, dissolution of the nuclear envelope and cytosolic vacuolisation, suggesting the presence of the evolutionary conserved PCD pathway in this unicellular eucaryote (Ink *et al.* 1997; Jurgensmeier *et al.* 1997). Since it is very unlikely that species dependent differences in the toxicity of the Bax protein are the reason for this observed difference between the two yeasts, a bona fide cell death pathway may well be present in *S. cerevisiae*.

Recent findings of a yeast mutant in the cell division cycle gene *CDC48* show a number of morphological and molecular features that are considered typical indicators of apoptosis markers in metazoan cells: exposure of phosphatidylserine on the outer leaflet of the cytoplasmic membrane, DNA breakage as well as chromatin condensation and fragmentation, supporting the existence of a basic PCD machinery in this unicellular yeast. This theory was

supported by the analysis of a wild type yeast cell expressing the human Bax protein. Comprehensive tests for morphological markers of apoptosis did show a series of changes, identical to morphological markers defining apoptosis (Ligr, Madeo *et al.* 1998). Recent findings from the same group (Madeo *et al.*, 1999) implicate oxygen stress as a general regulator of apoptosis in yeast but the actual mechanism of Bax lethality in *S. cerevisiae* remains unclear.

5 It is an aim of the present invention to provide new *bax* sequences for expression in yeast and fungi and tools for identifying yeast and candida functions in the pathways leading to programmed cell death.

10 It is an aim of the present invention to provide nucleic acids as well as polypeptides which represent potential molecular targets for the identification of new compounds which can be used in alleviating diseases or conditions associated with yeast or fungal infections.

It is a further aim of the present invention to provide uses of these nucleic acid and polypeptide molecules for treating diseases associated with yeast or fungi or for the preparation of (a) medicament(s) for treating said diseases.

15 It is also an aim of the invention to provide pharmaceutical compositions and vaccines comprising these nucleic acids or polypeptides.

It is also an aim of the present invention to provide vectors comprising these nucleic acids, as well as host cells transfected or transformed with said vectors.

20 It is also an aim of the invention to provide antibodies against these polypeptides, which can be used as such, or in a composition as a medicament for treating diseases associated with yeast and fungi.

It is another aim of the invention to provide methods to selectively identify compounds or polypeptides capable of inhibiting or activating expression of the polypeptides of the invention or capable of selectively modulating expression or functionality of such polypeptides. The nucleic acid and polypeptide molecules alternatively can be incorporated into an assay or kit to identify these compounds or polypeptides.

25 It is also an aim of the invention to provide methods for preventing infection with yeast or fungi.

It is a further aim of the invention to provide human homologues for the nucleic acids and polypeptides of the invention for use in treating proliferative disorders, such as cancer, or for the prevention of apoptosis in certain diseases, or for the preparation of a medicament for treating such disorders or diseases.

30 All the aims of the present invention have been met by the embodiments as set out below.



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All the aims of the present invention have been met by the embodiments as set out below.

### Summary of the invention

Since it has been discovered that the mammalian *bax* gene triggers apoptotic changes in yeast (Ligr *et al.*, 1998), this can be an indication that the molecular pathways eventually leading to programmed cell death may also be partially present in yeast cells and other unicellular eukaryotes. Identification of genes involved in this process could be important for the development of new antifungal therapeutics.

The present inventors overexpressed the Bax protein in the pathogenic yeast *Candida albicans* and found that this leads to a similar phenotype. However these results could only be received after having constructed a new synthetic *BAX* gene which could be adequately expressed in this pathogenic organism.

Furthermore, the present inventors identified a range of specific nucleic acids which are involved in the molecular pathways eventually leading to programmed cell death. The present inventors were able to identify via macro array screening a range of genes involved in a pathway eventually leading to programmed cell death in the yeast *Saccharomyces cerevisiae*. Genes which were differentially expressed (analysed using the Pathways™ software) at different time points after Bax expression are envisaged as candidate genes in the present invention.

Additionally, the invention also relates to *Candida spp.* homologues of the *S. cerevisiae* candidate genes and their uses in stimulating or preventing cell death in yeast and fungi, especially pathogenic yeast and fungi are herewith envisaged.

Furthermore, also part of the invention are the human homologues of these apoptosis-associated *S. cerevisiae* nucleic acids and polypeptides and their potential use in treating proliferative disorders in human and other mammals.

### Detailed description of the invention

The present invention relates to the use of a nucleic acid molecule encoding a polypeptide which is involved in a pathway eventually leading to programmed cell death of yeast or fungi and which nucleic acid sequence is selected from:

(a) a nucleic acid encoding a protein having an amino acid sequence as represented in any of

SEQ ID NOs 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248,

- 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 299, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 324, 326, 328, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 569, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 692, 694, 696, 698, 700, 702, 704, 706, 708, 710, 712, 714, 716, 718, 720, 722, 724, 726, 728, 730 and 732, or encoding a functional equivalent, derivative or bioprecursor of said protein,
- (b) a nucleic acid encoding a protein having an amino acid sequence which is more than 70% similar, preferably more than 75% or 80% similar, more preferably more than 85%, 90% or 95% similar and most preferably more than 97% similar to any of the amino acid sequences as represented by any of SEQ ID NOs 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 299, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 324, 326, 328, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 569, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614,

616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 692, 694, 696, 698, 700, 702, 704, 706, 708, 710, 712, 714, 716, 718, 720, 722, 724, 726, 728, 730 and 732,

(c) a nucleic acid encoding a protein having an amino acid sequence which is more than 70% identical, preferably more than 75% or 80% identical, more preferably more than 85%, 90% or 95% identical and most preferably more than 97% identical to any of the amino acid sequences as represented by any of SEQ ID NOs 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 299, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 324, 326, 328, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 569, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 692, 694, 696, 698, 700, 702, 704, 706, 708, 710, 712, 714, 716, 718, 720, 722, 724, 726, 728, 730 and 732,

(d) a nucleic acid comprising a sequence as represented in any of SEQ ID NOs 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295,

- 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481, 483, 485, 487, 489, 491, 493, 495, 497, 499, 501, 503, 505, 507, 509, 511, 513, 515, 517, 519, 521, 523, 525, 527, 529, 531, 533, 535, 537, 539, 541, 543, 545, 547, 549, 551, 553, 555, 557, 559, 561, 563, 565, 567, 569, 571, 573, 575, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, 627, 629, 631, 633, 635, 637, 639, 641, 643, 645, 647, 649, 651, 653, 655, 657, 659, 661, 663, 665, 667, 669, 671, 673, 687, 691, 693, 695, 697, 699, 701, 703, 705, 707, 709, 711, 713, 715, 717, 719, 721, 723, 725, 727, 729 and 731,
- (e) a nucleic acid which is more than 70% identical, preferably more than 75 or 80% identical, more preferably more than 85%, or 90% or 95% identical and most preferably more than 97% identical to any of the nucleic acid sequences as represented by any of SEQ ID NOs 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481, 483, 485, 487, 489, 491, 493, 495, 497, 499, 501, 503, 505, 507, 509, 511, 513, 515, 517, 519, 521, 523, 525, 527, 529, 531, 533, 535, 537, 539, 541, 543, 545, 547, 549, 551, 553, 555, 557, 559, 561, 563, 565, 567, 569, 571, 573, 575, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, 627, 629, 631, 633, 635, 637, 639, 641, 643, 645, 647, 649, 651, 653, 655, 657, 659, 661, 663, 665, 667, 669, 671, 673, 687, 691, 693, 695, 697, 699, 701, 703, 705, 707, 709, 711, 713, 715, 717, 719, 721, 723, 725, 727, 729 and 731,



(f) a nucleic acid encoding a functional fragment of any of the nucleic acids as specified in a) to e); and

(g) the complement of any of the nucleic acids as specified in a) to f),

for the preparation of a medicament for treating diseases associated with yeast or fungi.

5 Sequence similarity searches were performed using the BLAST software package version 2. Identity and similarity percentages were calculated using BLOSUM62 as a scoring matrix.

As known in the art, "similarity" between two polypeptides is determined by comparing the amino acid sequence and its conserved amino acid substitutes of one polypeptide to the sequence of a second polypeptide. Moreover, also known in the art is "identity" which means  
10 the degree of sequence relatedness between two polypeptide or two polynucleotide sequences as determined by the identity of the match between two strings of such sequences. Both identity and similarity can be readily calculated. While there exist a number of methods to measure identity and similarity between two polynucleotide or polypeptide sequences, the terms "identity" and "similarity" are well known to skilled artisans (Carillo and Lipton, 1988). Methods commonly  
15 employed to determine identity or similarity between two sequences include, but are not limited to, those disclosed in "Guide to Huge Computers (Bishop, 1994) and Carillo and Lipton (1988). Preferred methods to determine identity are designed to give the largest match between the two sequences tested. Methods to determine identity and similarity are codified in computer programs. Preferred computer program methods to determine identity and similarity between  
20 two sequences include, but are not limited to, GCG program package (Devereux *et al.*, 1984), BLASTP, BLASTN and FASTA (Altschul *et al.*, 1990).

The expression "functional fragment of a nucleic acid" as used herein means the minimal nucleic acid which is necessary to encode a functional protein (or polypeptide). For instance, in situations where a nucleic acid is provided comprising at the 5' end and at the 3' end more  
25 nucleotides than the actual open reading frame, the invention also relates to fragments of the nucleic acid which are smaller but which still contain the workable open reading frame. Also meant are parts of the open reading frame encoding a polypeptide having the same properties as the polypeptide encoded by the complete open reading frame.

The expression "a pathway eventually leading to programmed cell death" refers to a sequence  
30 of steps ultimately leading to cell death and which can be triggered at various steps in this pathway by various agents, such as Bax, Bak, CED4, hydrogen peroxide, diamide and farnesol. The nucleic acid sequences to be used according to this aspect of the invention from *Saccharomyces cerevisiae* are defined in SEQ ID NOs 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85,  
35 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125,

127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 5 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 691, 693, 695, 697, 699, 701, 703, 705, 707, 709, 711, 713 and 715; from *Candida albicans* are defined in SEQ ID NOs 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 10 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481, 483, 485, 487, 489, 491, 493, 495, 497, 499, 501, 503, 505, 507, 509, 511, 513, 515, 517, 519, 521, 523, 525, 527, 529, 531, 533, 535, 537, 539, 541, 543, 545, 547, 549, 551, 553, 555, 557, 559, 561, 563, 565, 567, 569, 571, 573, 575, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 15 609, 611, 613, 615, 617, 619, 621, 623, 625, 627, 629, 631, 633, 635, 637, 639, 641, 643, 645, 647, 649, 651, 653, 655, 657, 659, 661, 663, 665, 667, 669, 671, 673, 687, 718, 720, 722, 724, 726, 728, 730 and 732.

The yeast or fungi according to the invention may be, but are not restricted to, pathogenic yeast or fungi. As such, yeast or fungi may cause infections in healthy individuals as well as in 20 immunocompromised patients.

The expression "treating diseases associated with yeast and fungi" not only refers to diseases or infections caused by said organisms but also refers to allergic reactions caused by said organisms, such as the so-called "professional diseases" in, for instance, bakery and brewery and that are caused by yeast or fungi which are commonly known as "non-pathogenic". Some 25 examples of specific diseases associated with yeast or fungi are further exemplified.

The invention further relates to the use of nucleic acid sequence homologues of SEQ ID NOs 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 30 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 35 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377,

379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481, 483, 485, 487, 489, 491, 493, 495, 497, 499, 501, 503, 505, 507, 509, 511, 513, 515, 517, 519, 521, 523, 525, 527, 529, 531, 533, 535, 537, 539, 541, 543, 545, 547, 549, 551, 553, 555, 557, 559, 561, 563, 565, 567, 569, 571, 573, 575, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, 627, 629, 631, 633, 635, 637, 639, 641, 643, 645, 647, 649, 651, 653, 655, 657, 659, 661, 663, 665, 667, 669, 671, 673, 687, 691, 693, 695, 697, 699, 701, 703, 705, 707, 709, 711, 713, 715, 717, 719, 721, 723, 725, 727, 729 and 731 but isolated from other yeast and fungi strains which are also involved in a pathway eventually leading to programmed cell death. According to a more specific embodiment, these nucleic acid sequences are derived from *Aspergillus fumigatus*.

In a more specific embodiment the invention relates to a nucleic acid encoding a polypeptide which is involved in a pathway eventually leading to programmed cell death of yeast or fungi selected from:

(a) a nucleic acid encoding a protein having an amino acid sequence as represented in any of SEQ ID NOs 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 718, 720, 722, 724, 726, 728, 730 and 732, or encoding a functional equivalent, derivative or bioprecursor of said protein;

(b) a nucleic acid encoding a protein having an amino acid sequence which is more than 70% similar, preferably more than 75% or 80% similar, more preferably more than 85%, 90% or 95% similar and most preferably more than 97% similar to any of the amino acid sequences as represented by any of SEQ ID NOs 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586,

588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 718, 720, 722, 724, 726, 728, 730 and 732,

(c) a nucleic acid encoding a protein having an amino acid sequence which is more than 70% identical, preferably more than 75% or 80% identical, more preferably more than 85%, 90% or 95% identical and most preferably more than 97% identical to any of the amino acid sequences as represented by any of SEQ ID NOs 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 718, 720, 722, 724, 726, 728, 730 and 732,

(d) a nucleic acid comprising a sequence as represented in any of SEQ ID 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481, 483, 485, 487, 489, 491, 493, 495, 497, 499, 501, 503, 505, 507, 509, 511, 513, 515, 517, 519, 521, 523, 525, 527, 529, 531, 533, 535, 537, 539, 541, 543, 545, 547, 549, 551, 553, 555, 557, 559, 561, 563, 565, 567, 569, 571, 573, 575, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, 627, 629, 631, 633, 635, 637, 639, 641, 643, 645, 647, 649, 651, 653, 655, 657, 659, 661, 663, 665, 667, 669, 671, 673, 687, 717, 719, 721, 723, 725, 727, 729 and 731;

(e) a nucleic acid which is more than 70% identical, preferably more than 75% or 80% identical, more preferably more than 85%, 90% or 95% identical and most preferably more than 97% identical to any of the nucleic acid sequences as represented by any of SEQ ID NO 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481, 483, 485, 487, 489, 491, 493, 495, 497, 499, 501, 503, 505, 507, 509, 511, 513, 515, 517, 519, 521, 523, 525, 527, 529, 531, 533, 535, 537, 539, 541, 543, 545, 547, 549, 551, 553, 555, 557, 559, 561, 563, 565, 567, 569, 571, 573, 575, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613,

615, 617, 619, 621, 623, 625, 627, 629, 631, 633, 635, 637, 639, 641, 643, 645, 647, 649, 651, 653, 655, 657, 659, 661, 663, 665, 667, 669, 671, 673, 687, 717, 719, 721, 723, 725, 727, 729 and 731,

- 5 (f) a nucleic acid encoding a functional fragment of any of the nucleic acid sequences as specified in a) to e), and,  
(g) the complement of any of the nucleic acids as specified in a) to f).

In a preferred embodiment the invention relates to nucleic acids from *Candida albicans*, as represented by the SEQ ID NOs 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 10 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481, 483, 485, 487, 489, 491, 493, 495, 497, 499, 501, 503, 505, 507, 509, 511, 513, 515, 517, 519, 521, 523, 525, 527, 529, 531, 533, 535, 537, 539, 541, 543, 545, 547, 549, 551, 553, 555, 557, 559, 561, 563, 565, 567, 569, 571, 573, 575, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, 627, 629, 631, 633, 635, 637, 639, 641, 643, 645, 647, 15 649, 651, 653, 655, 657, 659, 661, 663, 665, 667, 669, 671, 673, 687, 717, 719, 721, 723, 725, 727, 729 and 731.

In an even more preferred embodiment the invention relates to an isolated nucleic acid from mammal or human origin which nucleic acid corresponds to a mammal or human homologue of at least one of the sequences represented in SEQ ID NOs 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 20 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 25 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 30 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481, 483, 485, 487, 489, 491, 493, 495, 497, 499, 501, 503, 505, 507, 509, 511, 513, 515, 517, 519, 521, 523, 525, 527, 529, 531, 533, 535, 537, 539, 541, 543, 545, 547, 549, 551, 553, 555, 557, 559, 561, 563, 565, 567, 569, 571, 573, 575, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 35 621, 623, 625, 627, 629, 631, 633, 635, 637, 639, 641, 643, 645, 647, 649, 651, 653, 655, 657,

659, 661, 663, 665, 667, 669, 671, 673, 687, 691, 693, 695, 697, 699, 701, 703, 705, 707, 709, 711, 713, 715, 717, 719, 721, 723, 725, 727, 729 and 731.

Therefore, according to a further preferred embodiment, the invention relates to an isolated nucleic acid from mammal or human origin which nucleic acid sequence is selected from:

- 5 (a) a nucleic acid encoding a protein having an amino acid sequence as represented in any of SEQ ID NOs 676, 678, 680, 682, 684 and 686, or encoding a functional equivalent, derivative or bioprecursor of said protein;
- (b) a nucleic acid encoding a protein having an amino acid sequence which is more than 70% similar, preferably more than 75% or 80% similar, more preferably more than 85%, 90% or  
10 95% similar and most preferably more than 97% similar to any of the amino acid sequences as represented by any of SEQ ID NOs 676, 678, 680, 682, 684 and 686;
- (c) a nucleic acid encoding a protein having an amino acid sequence which is more than 70% identical, preferably more than 75% or 80% identical, more preferably more than 85%, 90% or 95% identical and most preferably more than 97% identical to any of the amino acid  
15 sequences as represented by any of SEQ ID NOs 676, 678, 680, 682, 684 and 686;
- (d) a nucleic acid comprising a sequence as represented in any of SEQ ID NOs 675, 677, 679, 681, 683 and 685;
- (e) a nucleic acid which is more than 70% identical, preferably more than 75 or 80% identical, more preferably more than 85%, or 90% or 95% identical and most preferably more than  
20 97% identical to any of the nucleic acid sequences as represented by any of SEQ ID NOs 675, 677, 679, 681, 683 and 685;
- (f) a nucleic acid encoding a functional fragment of any of the nucleic acids as specified in a) to e); and
- (g) the complement of any of the nucleic acids as specified in a) to f),  
25 for the preparation of a medicament for treating diseases associated with yeast or fungi.

The invention also relates to the use of said nucleic acids for treating and/or preventing and/or alleviating proliferative disorders or for the prevention of apoptosis in certain disorders or diseases.

- 30 The expression "proliferative disorders" or "proliferative diseases" refers to an abnormality within a patient or animal such as cancer. Normal cells start to proliferate due to a change in the coding or non-coding sequence of the DNA resulting in a swollen or distended tissue. Mutation may arise without obvious cause. An abnormal benign or malignant mass of tissue is formed that is not inflammatory. Cells of pre-existent tissue start to divide unexpectedly and resulting cell mass possesses no physiologic function.

The expression "apoptosis" or "apoptosis-related diseases" includes diseases such as autoimmunity diseases, ischemia, diseases related with viral infections or neurodegenerations.

It should be clear that the invention also relates to all nucleic acids according to the invention and which are specifically described above, and which can be DNA, cDNA, genomic DNA, synthetic DNA, or RNA wherein T is replaced by U. A nucleic acid according to the invention may also comprise any modified nucleotide known in the art.

The term "nucleic acid sequence" also includes the complementary sequence to any single stranded sequence given.

According to the invention, these sequences and their homologues in other yeast and fungi or in human or other mammals as well as the polypeptides which they encode represent novel molecular targets which can be incorporated into an assay to selectively identify compounds capable of inhibiting or activating expression of such polypeptides. Furthermore, the invention also relates to the potential use of said sequences in alleviating diseases or conditions associated with yeast or fungi infections, such as diseases caused by *Candida* spp., *Aspergillus* spp., *Microsporum* spp., *Trichophyton* spp., *Fusarium* spp., *Zygomycetes* spp., *Botritis* spp., *Cladosporium* spp., *Malassezia* spp., *Epidermophyton floccosum*, *Blastomyces dermatitidis*, *Coccidioides immitis*, *Histoplasma capsulatum*, *Paracoccidioides brasiliensis*, *Cryptococcus neoformans*, and *Sporothrix schenckii*, such as, but not limited to:

- Candidiasis, caused by *C. albicans* and other members of the genus *Candida*, which are primary or secondary mycotic infections, also named candidosis, moniliasis and thrush;
- Aspergilliosis, caused by members of the genus *Aspergillus*, form a spectrum of diseases;
- Histoplasmosis, caused by *Histoplasma capsulatum*, which is a pulmonary disease always seen in HIV positive or other immunocompromised individuals;
- Paracoccidioidomycosis, caused by *Paracoccidioides brasiliensis*, which is a granulomatous disease that originates as a pulmonary disease;
- Blastomycosis, caused by *Blastomyces dermatitidis*, which may be a benign and self-limiting infection or a chronic granulomatous and suppurative mycosis, also named Chicago disease or Gilchrist's disease;
- Coccidioidomycosis, caused by *Coccidioides immitis*, and which is a respiratory infection that typically resolves rapidly, but the mycosis can become acute, chronic, severe or fatal; also named San Joaquin Valley fever or Valley fever;
- Cryptococcosis, caused by *Cryptococcus neoformans*, which is a chronic, subacute to acute pulmonary, systemic or meningitic disease, also named Torulosis;

- Sporotrichosis, caused by *Sporothrix schenckii*, which is a chronic infection characterized by nodular lesions of cutaneous or subcutaneous tissues and adjacent lymphatics that suppurate, ulcerate and drain.

Some of the pathways leading to apoptosis are conserved between mammalian cells and yeast  
5 or fungi. Therefore the invention also relates to the potential use of homologous sequences from human or mammalian origin for preventing and/or alleviating diseases or conditions where apoptosis or non-apoptosis of cells is impaired, for instance in proliferative disorders. In this respect also cancer can be seen as a proliferative disorder. Furthermore, targets which are part of such a conserved pathway may be used to stimulate or inhibit the apoptosis in mammalian  
10 cells. E.g. stimulation of apoptosis is desirable in the treatment of tumor cells/tissues.

Human homologues according to the invention can be obtained by selective hybridisation of the yeast and candida nucleic acid molecules of the invention against human genome or cDNA libraries according to methods well known in the art (Sambrook *et al.*, 1989). Human polypeptide homologues are obtained from the corresponding human nucleic acid homologous  
15 nucleotide sequences.

The present invention further relates to a nucleic acid capable of selectively hybridising to at least one of the nucleic acid molecules according to the invention, or the complement thereof.

The term "selectively hybridising" or "specifically hybridising" means hybridising under conditions wherein sequences can be detected which are homologues of the sequences of the  
20 invention, but which are for instance derived from heterologous cells or organisms, and wherein said sequences do not hybridize with known sequences. In a preferred embodiment, mammalian homologues can be detected. It is well known to the person skilled in the art which methods for hybridisation can be used and which conditions are necessary for selectively or specifically hybridising. Preferably, hybridization under high stringency conditions can be  
25 applied (Sambrook *et al.*, 1989).

As such, the present invention also relates to the use of the nucleic acid sequences of the invention for detecting homologues in heterologous organisms including but not limited to mammalian organisms.

The invention also relates to an isolated nucleic acid comprising a human homologue of at least  
30 one of the yeast or candida nucleic acids described earlier. The invention also relates to a polypeptide encodable by said human homologue of said nucleic acid.

In a further embodiment the invention also relates to an expression vector comprising a human homologue of at least one of the yeast or candida nucleic acids described herein. Said expression vector according can be an expression vector wherein said nucleic acid sequence is  
35 operably linked to one or more control sequences allowing the expression in prokaryotic and/or



eukaryotic host cells. According to a further embodiment, the expression vector comprises an inducible promoter and/or a reporter molecule.

The invention also relates to a host cell transformed, transfected or infected with any of the above described vectors.

- 5 According to a preferred embodiment, the invention relates to an antisense version of any of the nucleic acids of the invention and described above.

The present invention more particularly relates to an antisense molecule comprising a nucleic acid capable of selectively hybridising to at least one of the nucleic acids of the invention. In an interesting embodiment the invention relates to a nucleic acid capable of selectively hybridising  
10 to a human homologue of at least one yeast or candida nucleic acid described herein.

Polynucleotides according to the invention may be inserted into vectors in an antisense orientation in order to provide for the production of antisense RNA. Antisense RNA or other antisense nucleic acids may also be produced by synthetic means.

The present invention also advantageously provides nucleic acid molecules of at least  
15 approximately 10 contiguous nucleotides of a nucleic acid according to the invention and preferably from 10 to 50 nucleotides. These sequences may, advantageously be used as probes or primers to initiate replication, or the like. Such nucleic acid sequences may be produced according to techniques well known in the art, such as by recombinant or synthetic means. The probes will hybridise specifically with any of the nucleic acid molecules of the  
20 invention. The primers will specifically amplify any of the nucleic acid molecules of the invention. The probes or primers according to the invention may also be used in diagnostic kits or the like for detecting the presence of a nucleic acid according to the invention. These tests generally comprise contacting the probe with the sample under hybridising conditions and detecting the presence of any duplex or triplex formation between the probe and any nucleic acid in the  
25 sample.

According to the present invention these probes may be anchored to a solid support. Preferably, they are present on an array so that multiple probes can simultaneously hybridize to a single biological sample. The probes can be spotted onto the array or synthesized *in situ* on the array. (Lockhart *et al.*, 1996). A single array can contain more than 100, 500 or even 1,000 different  
30 probes in discrete locations. Such arrays can be used to screen for compounds interacting with said probes.

Advantageously, the nucleic acid sequences, according to the invention may be produced using recombinant or synthetic means, such as for example using PCR cloning mechanisms which generally involve making a pair of primers, which may be from approximately 10 to 50  
35 nucleotides to a region of the gene which is desired to be cloned, bringing the primers into

contact with mRNA, cDNA, or genomic DNA from the yeast or fungal cell, performing a polymerase chain reaction under conditions which bring about amplification of the desired region, isolating the amplified region or fragment and recovering the amplified DNA. Generally, such techniques as defined herein are well known in the art, such as described in Sambrook *et al.* (1989). These techniques can be used to clone homologues of the nucleic acid sequences of the invention in other organisms.

The nucleic acids or oligonucleotides according to the invention may carry a revealing label. Suitable labels include radioisotopes such as  $^{32}\text{P}$ ,  $^{33}\text{P}$  or  $^{35}\text{S}$ , enzyme labels or other protein labels such as biotin or fluorescent markers. Such labels may be added to the nucleic acids or oligonucleotides of the invention and may be detected using techniques known in the art.

According to another embodiment of the invention, the nucleic acid sequences according to the invention as defined above may, advantageously, be included in a suitable vector, preferably an expression vector which may be transformed, transfected or infected into a host cell. In such an expression vector the nucleic acid is operably linked to one or more control sequences allowing the expression in host cells, such as a suitable promoter, or the like, to ensure expression of the proteins according to the invention in a suitable prokaryotic or eukaryotic host cell. Said promoter may be either constitutive, inducible or cell- or tissue- or organ-specific. The expression vector may advantageously be a plasmid, cosmid, virus or other suitable vector which is known to those skilled in the art. The expression vector and the host cell defined herein also form part of the present invention. Said host cell can be from bacterial, yeast, fungal, insect, mammal or human origin, or any other host wherein said vector can be introduced by at least one of the methods known in the art. However, preferred host cells are lower eukaryotic cells such as a yeast cell or a fungal cell. Yeast and fungal cells are particularly advantageous because they provide the necessary post-translational modifications to the expressed proteins of the invention, similar to those of the natural proteins from which they are derived. These modifications confer optimal conformation of said proteins, which when isolated may advantageously be used in kits, methods or the like.

In a further embodiment, the expression vector may further comprise an inducible promoter, and/or further a reporter molecule.

The invention further relates to any one of the nucleic acids as defined above for use as a medicament.

Nucleotide sequences according to the invention are particularly advantageous for providing selective therapeutic targets for treating yeast or fungi-associated infections. For example, an antisense nucleic acid capable of binding to the nucleic acid sequences according to the invention may be used to selectively inhibit expression of the corresponding polypeptides,

leading to impaired growth or death of yeast and fungi with reductions of associated illnesses or diseases.

Also envisaged in the present invention are promoter or other control sequences that are comprised within the nucleic acids of the invention, said nucleic acid control sequences can also  
5 serve as a target for the identification of compounds or proteins which interfere with the control of expression of downstream encoded polypeptides.

Furthermore, also the human homologues of the yeast and candida nucleic acids may be useful in diseases where apoptosis of cells plays a substantial role, both in situations where apoptosis of (particular) cells is wanted or unwanted.

10 The invention thus also relates to the use of any of the nucleic acids of the invention or to a human homologue thereof for treating proliferative disorders or for the prevention of apoptosis in certain disorders or diseases. As described above, the invention also relates to the use of antisense molecules of the nucleic acids of the invention or to an antisense of any of the human homologues for treating proliferative disorders or for the prevention of apoptosis in certain  
15 disorders or diseases.

Said nucleic acids, human homologues and antisense molecules can also be used for the preparation of a medicament for treating or preventing the above-mentioned diseases.

According to yet another embodiment, the invention relates to at least one polypeptide encodable by a nucleic acid of the invention.

20 The invention also relates to the use of a polypeptide which is involved in a pathway eventually leading to programmed cell death of yeast or fungi, said polypeptide being selected from:

(a) a protein having an amino acid sequence as represented in any of SEQ ID NOs 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112,  
25 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292,  
30 294, 296, 298, 299, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 324, 326, 328, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462,  
35 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498,

- 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 692, 694, 696, 698, 700, 702, 704, 706, 708, 710, 712, 714, 716, 718, 720, 722, 724, 726, 728, 730 and 732, or encoding a functional equivalent, derivative or bioprecursor of said protein;
- (b) a protein having an amino acid sequence which is more than 70% similar, preferably more than 75% or 80% similar, more preferably more than 85%, 90% or 95% similar and most preferably more than 97% similar to any of the amino acid sequences as represented by any of SEQ ID NOs 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 324, 326, 328, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 692, 694, 696, 698, 700, 702, 704, 706, 708, 710, 712, 714, 716, 718, 720, 722, 724, 726, 728, 730 and 732,
- (c) a protein having an amino acid sequence which is more than 70% identical, preferably more than 75% or 80% identical, more preferably more than 85%, 90% or 95% identical and most preferably more than 97% identical to any of the amino acid sequences as represented by any of SEQ ID NOs 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54,

56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 299, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 324, 326, 328, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 569, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 692, 694, 696, 698, 700, 702, 704, 706, 708, 710, 712, 714, 716, 718, 720, 722, 724, 726, 728, 730 and 732, and,

(d) a functional fragment of any of said proteins as defined in a) to c),  
for the preparation of a medicament for treating diseases associated with yeast or fungi.

The term "functional fragment" of a protein means a truncated version of the original protein or polypeptide referred to. The truncated protein sequence can vary widely in length; the minimum size being a sequence of sufficient size to provide a sequence with at least a comparable function and/or activity of the original sequence referred to, while the maximum size is not critical. In some applications, the maximum size usually is not substantially greater than that required to provide the desired activity and/or function(s) of the original sequence. A functional fragment can also relate to a subunit with similar function as said protein. Typically, the truncated amino acid sequence will range from about 5 to about 60 amino acids in length. More typically, however, the sequence will be a maximum of about 50 amino acids in length, preferably a maximum of about 60 amino acids. It is usually desirable to select sequences of at least about 10, 12 or 15 amino acids.

Functional fragments include those comprising an epitope which is specific or unique for the proteins according to the invention. Epitopes may be determined using, for example, peptide

scanning techniques as described in Geysen *et al.* (1986). Preferred functional fragments have a length of at least, for example, 5, 10, 25, 50, 75, 100, 125, 150, 175 or 200 amino acids.

The polypeptides to be used according to the invention from *Saccharomyces cerevisiae*, are represented by SEQ ID NOs 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50,

5 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 10 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 299, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 324, 326, 328, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 692, 694, 696, 698, 700, 702, 704, 706, 708, 710, 712, 714 and 716. Also according to the 15 invention is the use of the polypeptides from *Candida albicans* as represented by the SEQ ID NOs 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 20 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 569, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 718, 720, 722, 724, 726, 728, 730 and 732, and the use of human polypeptides as represented by SEQ ID NOs 676, 678, 25 680, 682, 684 and 686.

Thus, according to a preferred embodiment, the present invention relates to an isolated polypeptide which is involved in a pathway for programmed cell death of yeast or fungi, for instance a *Candida* spp., selected from:

(a) a polypeptide having an amino acid sequence as represented in any of SEQ ID NOs 30 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 35 568, 569, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590,

592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 718, 720, 722, 724, 726, 728, 730 and 732, or encoding a functional equivalent, derivative or bioprecursor of said protein;

- 5 (b) a polypeptide having an amino acid sequence which is more than 70% similar, preferably more than 75% or 80% similar, more preferably more than 85%, 90% or 95% similar and most preferably more than 97% similar to any of the amino acid sequences as represented by any of SEQ ID NOs 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 718, 720, 722, 724, 726, 728, 730 and 732,
- 10 (c) a polypeptide having an amino acid sequence which is more than 70% identical, preferably more than 75% or 80% identical, more preferably more than 85%, 90% or 95% identical and most preferably more than 97% identical to any of the amino acid sequences as represented by any of SEQ ID NOs 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 718, 720, 722, 724, 726, 728, 730 and 732, and
- 15 (d) a functional fragment of any of said polypeptides as defined in a) to c).
- 20
- 25
- 30

According to a further preferred embodiment, the present invention relates to an isolated polypeptide which is involved in a pathway for programmed cell death of mammalian cells selected from:

- (a) a polypeptide having an amino acid sequence as represented in any of SEQ ID NOs 676, 678, 680, 682, 684 and 686, or encoding a functional equivalent, derivative or bioprecursor of said protein;
- 5 (b) a polypeptide having an amino acid sequence which is more than 70% similar, preferably more than 75% or 80% similar, more preferably more than 85%, 90% or 95% similar and most preferably more than 97% similar to any of the amino acid sequences as represented by any of SEQ ID NOs human 676, 678, 680, 682, 684 and 686;
- 10 (c) a polypeptide having an amino acid sequence which is more than 70% identical, preferably more than 75% or 80% identical, more preferably more than 85%, 90% or 95% identical and most preferably more than 97% identical to any of the amino acid sequences as represented by any of SEQ ID NOs 676, 678, 680, 682, 684 and 686; and,
- (d) a functional fragment of any of said polypeptides as defined in a) to c).

The invention also relates to the polypeptides of the invention and described above for use as a  
15 medicament.

Pharmaceutical or fungicidal compositions comprising at least one of the nucleic acids, antisense molecules, polypeptides of the invention optionally together with a pharmaceutically acceptable carrier, diluent or excipient therefor, are also part of the invention.

The polypeptides described above or the human or mammal homologues thereof can also be  
20 used for treating proliferative disorders or for the prevention of apoptosis in certain diseases.

The invention furthermore relates to a pharmaceutical composition for use as a medicament for treating proliferative disorders or for the prevention of apoptosis in certain diseases comprising a nucleic acid molecule of the invention or a human homologue thereof, an antisense molecule to at least one of the nucleic acids of the invention or an antisense molecule to a mammalian  
25 homologue of said nucleic acid or a polypeptide of the invention or a human homologue thereof together with a pharmaceutically acceptable carrier, diluent or excipient therefor.

The polypeptide or protein according to the invention may also include variants of any of the polypeptides of the invention as specified above having conservative amino acid changes.

The present invention also relates to a vaccine for immunizing a mammal comprising at least  
30 one (recombinant) nucleic acid molecule or at least one (recombinant) polypeptide of the invention in a pharmaceutically acceptable carrier. Preferred vaccines are those that can be used for immunization against infections caused by yeast and fungi. Other preferred vaccines can be used for immunizing mammals against proliferative disorders or for preventing apoptosis in certain diseases.



Pharmaceutically acceptable carriers include any carrier that does not itself induce the production of antibodies harmful to the individual receiving the composition. Suitable carriers are typically large, slowly metabolizing macromolecules such as proteins, polysaccharides, polylactic acids, polyglycolic acids, polymeric amino acids, amino acid copolymers; and inactive virus particles. Such carriers are well known to those of ordinary skill in the art.

A "vaccine" is an immunogenic composition capable of eliciting protection against infections caused by yeast or fungi, whether partial or complete.

Said vaccine compositions may include prophylactic as well as therapeutic vaccine compositions. When a vaccine is used for protecting individuals against certain infections or diseases, it is called a prophylactic vaccine. A vaccine may also be useful for treatment of an individual, in which case it is called a therapeutic vaccine.

The term "therapeutic" refers to a composition capable of treating infections caused by yeast or fungi or capable of treating proliferative disorders.

Also encompassed within the present invention are antibodies, monoclonal or polyclonal, capable of specifically binding to one or more epitopes of the polypeptides or proteins of the invention. The polypeptides of the invention are represented in SEQ ID NOs 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 299, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 324, 326, 328, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 676, 678, 680, 682, 684, 686, 688, 692, 694, 696, 698, 700, 702, 704, 706, 708, 710, 712, 714, 716, 718, 720, 722, 724, 726, 728, 730 and 732.

The term "specific binding" implies that there is substantially no cross-reaction of the antibody with other proteins.

The antibodies according to the invention may be produced according to techniques which are known to those skilled in the art. Monoclonal antibodies may be prepared using conventional  
5 hybridoma technology as described by Kohler and Milstein (1979). Polyclonal antibodies may also be prepared using conventional technology well known to those skilled in the art, and which comprises inoculating a host animal, such as a mouse, with a protein or epitope according to the invention and recovering the immune serum. The present invention also includes fragments of whole antibodies which maintain their binding activity, such as for example, Fv, F(ab') and  
10 F(ab')<sub>2</sub> fragments as well as single chain antibodies.

The antibodies of the invention are capable of specifically binding to at least one of the yeast or candida polypeptides as defined earlier or to a human homologue thereof or to a specific epitope of said polypeptide or said human homologue. The invention also relates to the use of said antibodies in treating and/or preventing and/or alleviating proliferative disorders or for the  
15 prevention of apoptosis in certain diseases. Said antibodies may also be used for the preparation of a medicament for and/or preventing and/or alleviating proliferative disorders or for the prevention of apoptosis in certain diseases.

Antibodies according to the invention may also be used in a method of detecting the presence of a polypeptide according to the invention, which method comprises reacting the antibody with  
20 a sample and identifying any protein bound to said antibody. A kit may also be provided for performing said method which comprises an antibody according to the invention and means for reacting the antibody with said sample.

The antibodies according to the invention may be used as a medicament or may be comprised in a pharmaceutical composition. According to a more specific embodiment, the antibodies may  
25 be used in the preparation of a medicament for treating diseases associated with yeast and fungi where the yeast or fungus is chosen from, but not restricted to *Candida* spp., *Aspergillus* spp., *Microsporum* spp., *Trichophyton* spp., *Fusarium* spp., *Zygomycetes* spp., *Botritis* spp., *Cladosporium* spp., *Malassezia* spp., *Epidermophyton floccosum*, *Blastomyces dermatitidis*, *Coccidioides immitis*, *Histoplasma capsulatum*, *Paracoccidioides brasiliensis*, *Cryptococcus neoformans*, and *Sporothrix schenckii*.  
30

The invention also relates to a method of preventing infection with yeast or fungi, comprising administering a composition containing at least one polypeptide of the invention to a mammal in effective amount to stimulate the production of protective antibody or protective T-cell response. According to another embodiment, the present invention provides a method of identifying  
35 compounds or polypeptides which selectively inhibit, induce or interfere with the

expression/production of the polypeptides encoded by the nucleotide sequences of the invention, or compounds which selectively inhibit, activate or interfere with the functionality of polypeptides expressed from the nucleotide sequences according to the invention, or which selectively inhibit, induce or interfere with the metabolic pathways in which these polypeptides are involved. Compounds (or polypeptides) may carry agonistic or antagonistic properties. The compounds (and polypeptides) to be screened may be of extracellular, intracellular, biologic or chemical origin.

Different alternative methods for identification of said compounds or polypeptides form part of the present invention.

10 According to a specific embodiment the invention relates to a method of identifying compounds which selectively modulate expression or functionality of polypeptides involved in a pathway eventually leading to programmed cell death of yeast and fungi or in metabolic pathways in which said polypeptides are involved, which method comprises (a) contacting a compound to be tested with yeast or fungal cells transformed, transfected or infected with an expression vector  
15 comprising an antisense sequence of at least one of the nucleic acid sequences of the invention, which expression results in underexpression of said polypeptide, in addition to contacting one or more wild type cells with said compound, (b) monitoring the growth and/or death rate or activity of said transformed, transfected or infected cells compared to said wild type cells; wherein differential growth or activity of said transformed, transfected or infected yeast or fungal cells is indicative of selective action of said compound on a polypeptide in the same or a parallel pathway, (c) alternatively monitoring the growth and/or death rate and/or activity of said transformed, transfected or infected cells compared to transformed, transfected or infected cells which were not contacted with the compound to be tested, wherein differential growth or activity of said mutated yeast or fungi cells is indicative of selective action of said  
20 compound on a polypeptide in the same or a parallel pathway, (d) alternatively monitoring changes in morphologic and/or functional properties of components in said transformed, transfected or infected cells caused by the addition of the compound to be tested, and (e) optionally identifying the compound .

Alternative methods for identifying compounds which selectively modulate expression or  
30 functionality of polypeptides involved in a pathway eventually leading to programmed cell death of yeast or fungi or in metabolic pathways in which said compounds are involved, may comprise the use of any other method known in the art resulting in gene activation, gene inactivation, gene modulation or gene silencing.

Another alternative to the above described method comprises (a) contacting a compound to be  
35 tested with a genetically modified yeast or fungus in which modification results in the

overexpression or underexpression of at least one of the nucleic acids or the polypeptides of the invention, which overexpression or underexpression of said nucleic acid or polypeptide prevents, delays or sensitizes for apoptosis of said genetically modified yeast or fungus, in addition to contacting wild type cells with said compound, (b) monitoring the growth and/or death rate and/or activity of said genetically modified yeast or fungi cells compared to said wild type cells wherein differential growth or activity of said genetically modified yeast or fungi cells is indicative of selective action of said compound on a polypeptide in the same or a parallel pathway, (c) alternatively monitoring the growth and/or death rate and/or activity of said genetically modified cells compared to genetically modified cells which were not contacted with the compound to be tested, wherein differential growth or activity of said genetically modified yeast or fungi cells is indicative of selective action of said compound on a polypeptide in the same or a parallel pathway, (d) alternatively monitoring changes in morphologic and/or functional properties of components in said genetically modified cells caused by the addition of the compound to be tested, and, (e) optionally identifying the compound.

The invention also relates to a method of identifying compounds which selectively modulate expression of polypeptides which are involved in a pathway eventually leading to programmed cell death of yeast or fungi which method comprises (a) contacting host cells transformed, transfected or infected with an expression vector comprising a promoter sequence of a nucleic acid molecule of the invention joined in frame with a reporter gene and (b) monitoring increased or decreased expression of said reporter gene caused by the addition of the compound being tested. This enables to analyse the influence of the compound onto all/most aspects of transcriptional activation. Alternatively additional tests can routinely be performed to test the influence of the compound onto mRNA stability, translation and protein stability. All these aspects influence the concentration of corresponding proteins and consequently influence the effect of these on the metabolism of the cell.

The invention further relates to a method of identifying compounds or polypeptides which bind to or modulate the properties of polypeptides which are involved in a pathway eventually leading to programmed cell death of yeast or fungi, which method comprises (a) contacting a compound or polypeptide to be tested with at least one of the polypeptides of the invention, (b) detecting the complex formed between the compound or polypeptide to be tested and said polypeptide, (c) alternatively, examining the diminution/increase of complex formation between said polypeptide and a receptor/binding partner, caused by the addition of the compound or polypeptide being tested, (c) alternatively, examining the alteration in the functional activity of the polypeptide, caused by the addition of the compound or polypeptide being tested, and (d) optionally identifying the compound or polypeptide.

The invention also relates to a method for identifying compounds interacting with a polypeptide involved in a pathway eventually leading to programmed cell death of yeast and fungi comprising the steps of (a) providing a two-hybrid screening system wherein a polypeptide of the invention and a protein interacting with said polypeptide or an interacting polypeptide obtainable by a method as described above, are expressed, (b) interacting said compound with the complex formed by the expressed proteins as defined in a), (c) detecting a second complex, wherein the presence of said second complex identifies a compound which specifically binds to one of said polypeptide or to said second complex, and optionally (d) identifying the compound. According to another embodiment the invention relates to a method for identifying compounds which selectively modulate expression of polypeptides which are involved in a pathway eventually leading to programmed cell death of yeast or fungi which method comprises: (a) contacting host cells transformed, transfected or infected with an expression vector comprising a promoter sequence of a nucleic acid of the invention joined in frame with a reporter gene, (b) monitoring increased or decreased expression of said reporter gene caused by the addition of the compound being tested, and, optionally (c) identifying the compound.

Yet another embodiment of the invention is a method for identifying polypeptides involved in a pathway eventually leading to programmed cell death comprising the steps of: (a) providing a two hybrid system wherein a polypeptide encoded by a nucleic acid or by any of the vectors of the invention as a bait and a *S. cerevisiae* cDNA library as a prey are used, (b) detecting an interaction between said polypeptide and a *S. cerevisiae* polypeptide encoded by said cDNA library, and, optionally (c) identifying said *S. cerevisiae* polypeptide.

The term "cells" as used in the above methods relates to any type of cells such as, but not limited to bacterial, yeast, fungal, plant or human cells.

Compounds found using this approach may additionally be tested on their efficiency in killing or inhibiting the growth of wild type cells in order to confirm their utility as medicament for treating wild type pathogenic strains/tumor cells.

According to the invention, the term "mutation" includes point mutations, deletions, insertions, duplications or any modification in the nucleic acid encoding said polypeptide, or at a different location in the genome of said cells, influencing the expression of said nucleic acid or polypeptide. In case point mutations occur, the number of nucleotides will be identical compared to the original sequence; only a change in nucleotide sequence can be observed. This stands in contrast with the other listed mutations where the number of the nucleotides will be different from the number observed in the wild type sequence and consequently will also reflect in a change of the nucleotide sequence.

Changes in morphologic and/or functional properties of cell components which can be monitored include for example morphological and molecular changes such as abnormal cell morphology, nuclear fragmentation, DNA breakage or changes in the expression of certain enzymes such as caspases, as well as monitoring changes in membrane potential or activity of mitochondria and release of cytochrome c from mitochondria. All these changes can be monitored on the whole cell which is contacted to the compound to be tested.

Detection of the complex formation can be performed using several approaches. First, binding of a compound onto a polypeptide can be studied using classical binding tests: one of the binding partners, compound or polypeptide is labeled and interaction of both is measured. Most of these tests comprise following steps: incubating both binding partners in conditions where binding is allowed, separation of free label from bound label present in the complex formed between both partners, and measuring the number of labeled complexes formed. Separation of free and bound label can be performed via filtration, centrifugation or other means as known by the person skilled in the art. Other techniques allow visualisation of complex formation without the need of such a separating step. For example, test systems using SPA (scintillation proximity assay) beads are based on the principle that radioactive  $^3\text{H}$  can only be measured when present in scintillation fluid. SPA beads contain scintillation fluid and can be coated with one of the binding partners. When this bead is approached and binds the other binding partner which is radioactively labeled, a signal will be detected allowing the complex to be visualised. Binding of the radioactive compound onto the scintillation bead is needed in order to result in a detectable signal; non-bound radioactive partners that stay free into the solution will not result in a detectable signal.

The protein or peptide fragments according to the invention employed in such a method may be for example in solution or coated on suspended beads as described above. Alternatively, these can be affixed to a solid support, borne on a cell or phage surface or located intracellularly.

When protein or peptide fragments are coated on solid supports, they can be tested for their binding affinity for large numbers of compounds. These can be used in different kinds of high throughput screenings in order to identify compounds having suitable binding affinity to the polypeptides according to the invention. Platform technologies or technologies based on SPR (see below) can be applied.

One may measure for example, the formation of complexes between the proteins of the invention and the compound being tested. Alternatively, one may examine the diminution or increase of complex formation between the protein according to the invention and a receptor/binding partner caused by the compound being tested.

Proteins which interact with the polypeptide of the invention may be identified by investigating protein-protein interactions using the two-hybrid vector system first proposed by Chien *et al.* (1991).

This technique is based on functional reconstitution *in vivo* of a transcription factor which  
5 activates a reporter gene. More particularly the technique comprises providing an appropriate host cell with a DNA construct comprising a reporter gene under the control of a promoter regulated by a transcription factor having a DNA binding domain and an activating domain, expressing in the host cell a first hybrid DNA sequence encoding a first fusion of a fragment or  
10 all of a nucleic acid sequence according to the invention and either said DNA binding domain or said activating domain of the transcription factor, expressing in the host at least one second hybrid DNA sequence, such as a library or the like, encoding putative binding proteins to be investigated together with the DNA binding or activating domain of the transcription factor which is not incorporated in the first fusion; detecting any binding of the proteins to be investigated with a protein according to the invention by detecting for the presence of any reporter gene  
15 product in the host cell; optionally isolating second hybrid DNA sequences encoding the binding protein.

An example of such a technique utilizes the GAL4 protein in yeast. Gal4 is a transcriptional activator of galactose metabolism in yeast and has a separate domain for binding to activators upstream of the galactose metabolising genes as well as a protein-binding domain. Nucleotide  
20 vectors may be constructed, one of which comprises the nucleotide residues encoding the DNA binding domain of Gal4. These binding domain residues may be fused to a known protein encoding sequence, such as for example the nucleic acids according to the invention. The other vector comprises the residues encoding the protein-binding domain of Gal4. These residues are fused to residues encoding a test protein. Any interaction between polypeptides encoded by the  
25 nucleic acid according to the invention and the protein to be tested leads to transcriptional activation of a reporter molecule in a GAL4 transcription deficient yeast cell into which the vectors have been transformed. Preferably, a reporter molecule such as  $\beta$ -galactosidase is activated upon restoration of transcription of the yeast galactose metabolism genes. Alternatively, other reporter proteins can be used such as EGFP (enhanced green fluorescent  
30 protein), or hEGFP. This latter has a decreased lifetime enabling the system to screen for compounds improving the interaction of studied binding partners.

The two-hybrid approach was first developed for yeast, and is an ideal screening system when looking for compounds active in killing yeast or fungi. Indeed, proteins expressed in this system will most probably carry the correct modifications as found in the pathogenic yeast strains. In  
35 addition, compounds active in this test system allow to screen and select compounds which are

able to enter the cell, this selection is not possible when using *in vitro* test systems. When compounds are needed to target mammalian cells, modification of the studied proteins can be different, changing the structure of corresponding proteins. Moreover working with yeast might block certain compounds to enter the cell, which are normally able to traverse the mammalian cell membrane. Consequently, working with mammalian two-hybrid system for this purpose will give already an immediate selection of the compounds that may enter mammalian cells.

Alternative *in vitro* methods can be used to investigate protein - protein interactions. Protein interaction analysis *in vitro* can shed light on their role in the intact cell by providing valuable information on specificity, affinity, and structure-function relation ship. Significant progress in this respect has become with the advent, in the last few years, of commercially available biosensor technology. This allows to study macromolecular interactions in real-time, providing a wealth of high-quality data that can be used for kinetic analysis, affinity measurements, competition studies, etc. A major advantage of biosensor analysis is that there is no requirement for labeling one of the interacting components and then separating bound from free molecules- a fact that simplifies experimental procedures and provides more accurate measurements. The principle of surface plasmon resonance (SPR) is based on the detection of a change of the refractive index of the medium when a compound or protein binds to an immobilised partner molecule. For the SPR technology, one needs to load one of the interacting partners to the chip surface, followed by the superfusion of the second binding partner or more molecules. The second partner can be available as purified product, but alternatively a complex suspension containing this partner can also be used. Interaction of two or more compounds can be analysed, alternatively, compounds can be identified interfering or increasing this binding affinity towards each other.

SPR is not restricted to protein-protein interactions; any macromolecule with a suitable size will change the refractive index of the medium in contact with the biosensor surface and therefore give a signal. Studies have been done with protein-DNA interactions, as well as protein-lipid interactions. Moreover intact viruses, and even cells, can also be injected over the biosensor surface, in order to analyse their binding to receptors, lectins, and so on.

Alternatively, NMR is also an excellent tool for a detailed study of protein-protein or DNA-protein interactions. Isotope edited or isotope filtered experiments whereby one compound is isotopically labeled with  $^{15}\text{N}$  or  $^{13}\text{C}$  are an ideal way to study these complexes. This method does not allow high throughput analysis of compounds interfering or enhancing molecular interactions. Nevertheless, medium or low throughput systems can be used to confirm results obtained by the high throughout assays or in cases where none of the binding partners are labeled. Other techniques which can be used to study interactions are: overlay, ligand blotting,



band-shift, co-immuno-precipitation, size exclusion chromatography and microcalorimetry (In. "Protein targeting Protocols" Ed. Clegg R.A. Humana Press, Totowa, New Jersey).

Compounds modulating pathways leading to apoptosis may change the activity of the polypeptide of the invention. Therefore screening tests may be setup looking for altered protein activity of the polypeptide of the invention. Based on the amino acid sequence a possible function of the polypeptide might be envisaged; activities can be confirmed and corresponding activity test can be started.

Alternatively additional tests can be performed to test the influence of the compound onto protein stability, post-translational modification, precursor processing and protein translocation.

All these aspects influence the concentration and/or activity of corresponding proteins and consequently influence the effect of these onto the metabolism of the cell. Also here, medium or low throughput systems can be used to confirm results obtained by the high throughput assays. In cases compounds need to be found to target tumor cells, screening assays will have to be used focused on the stimulation of the apoptotic pathway. This invention therefore also relates to *in vitro* and *in vivo* model systems comprising tumor tissue or cells expressing the polypeptides according to the invention which can be used to screen for therapeutic agents. *In vivo* modelsystems allow to test for compound efficacy but also the toxicity of these compounds can be tested. The compounds identified using any of the methods described in the invention not only include compounds which exert their effect in promoting cell death of yeast and fungi, but also include compounds which prevent or delay cell death. The latter compounds can be used to prevent or delay apoptosis of endogenic yeast or fungi in humans and other mammals which may be caused by pathogens or toxic environmental components.

According to a preferred aspect of the invention, the yeast or fungi according to any of the methods described, are chosen from *Candida* spp., *Aspergillus* spp., *Microsporum* spp., *Trichophyton* spp., *Fusarium* spp., *Zygomycetes* spp., *Botritis*, spp., *Cladosporium* spp., *Malassezia* spp., *Epidermophyton floccosum*, *Blastomyces dermatitidis*, *Coccidioides immitis*, *Histoplasma capsulatum*, *Paracoccidioides brasiliensis*, *Cryptococcus neoformans*, and *Sporothrix schenckii*.

The invention also relates to a compound identified using any of the methods of the invention. Compounds identifiable or identified using a method according to the invention, may advantageously be used as a medicament. The invention also relates to a method for treating diseases associated with yeast or fungi comprising admixing a compound obtainable by a method of the invention with a suitable pharmaceutically acceptable carrier.

The invention further relates to a method for preparing pharmaceutical composition for treating diseases associated with yeast or fungi comprising admixing a compound as identified above

with a suitable pharmaceutically acceptable carrier. The invention also relates to said pharmaceutical composition.

The compounds or pharmaceutical compositions of the invention can be used for the preparation of a medicament to treat diseases or conditions associated with yeast and fungi infections, more preferably where the yeast or fungus is chosen from *Candida* spp., *Aspergillus* spp., *Microsporum* spp., *Trichophyton* spp., *Fusarium* spp., *Zygomycetes* spp., *Botritis*, spp., *Cladosporium* spp., *Malassezia* spp., *Epidermophyton floccosum*, *Blastomyces dermatitidis*, *Coccidioides immitis*, *Histoplasma capsulatum*, *Paracoccidioides brasiliensis*, *Cryptococcus neoformans*, and *Sporothrix schenckii*.

These compounds may also advantageously be included in a pharmaceutical composition together with a pharmaceutically acceptable carrier, diluent or excipient therefor.

A medicament according to the invention not only relates to fungicidal and fungistatic compounds for treating humans or mammals but also relates to fungicides for treating plants.

According to yet another embodiment, the invention relates to a genetically modified yeast or fungus in which modification results in the overexpression or underexpression of at least one of the nucleic acids or the polypeptides of the invention, which overexpression or underexpression of said nucleic acid or polypeptide prevents, delays or sensitizes for apoptosis of said genetically modified yeast or fungus. These genetically modified organisms may have a positive effect on the endogenic flora of humans and other mammals. The genetically modified yeast or fungi can be included in a pharmaceutical composition or can be used for the preparation of a medicament for prophylactic or therapeutic use.

Also according to the invention is the use of a compound obtainable by a method of the invention, a pharmaceutical composition or a genetically modified organism as described above for the preparation of a medicament for modifying the endogenic flora of humans and other mammals.

According to another embodiment, the invention relates to a genetically modified mammalian cell or non-human organism in which modification results in the overexpression or underexpression of at least one of the nucleic acids of the invention or a human homologue thereof or at least one of the polypeptides of the invention or a human homologue thereof, which overexpression or underexpression of said nucleic acid or polypeptide prevents or delays apoptosis of said genetically modified mammalian cell or in said genetically modified non-human organism.

According to a preferred embodiment, the invention relates to a genetically modified mammalian cell or non-human organism as described above wherein said modification comprises the

expression of an antisense molecule to at least one of the nucleic acids of the invention or an antisense molecule to a mammalian homologue of said nucleic acid.

The invention also relates to a method for identifying compounds for stimulating or inhibiting apoptosis comprising the use of at least one of the nucleic acid sequences of the invention or a  
5 human homologue thereof and/or at least one of the polypeptides of the invention or a human homologue thereof and/or a genetically modified mammalian cell or non-human organism as described in the invention.

Some examples of preferred human homologues of yeast and/or *Candida* spp. sequences which can be used in the above methods are represented in SEQ ID NOs 675 to 686.

10 The invention further relates to the compounds identifiable according to the above-described method and their use as a medicament.

The invention further relates to a method for preparing a pharmaceutical composition for treating proliferative disorders or for preventing apoptosis in certain diseases comprising admixing a compound identifiable according to the above-described methods with a suitable  
15 pharmaceutically acceptable carrier.

The invention also relates to the use of compounds obtainable by the above described methods for the preparation of a medicament for treating proliferative disorders or for preventing apoptosis in certain disorders.

Furthermore, the present inventors overexpressed the Bax protein in the pathogenic yeast  
20 *Candida albicans* and found that this leads to a similar phenotype. However these results could only be received after having constructed a new synthetic *bax* gene which could be adequately expressed in this pathogenic organism.

Therefore, the present invention relates to an isolated nucleic acid representing a synthetic BAX-gene for expression in *Candida* spp. selected from the group of:

- 25     a) a nucleic acid comprising a sequence as represented by SEQ ID NO 1,  
      b) a nucleic acid comprising a fragment of a sequence of SEQ ID NO 1 and encoding a functional fragment of the sequence represented by SEQ ID NO 2,  
      c) a nucleic acid comprising a sequence as represented in any of SEQ ID NOs 3 to 10,  
      d) a nucleic acid which is more than 75 % identical, preferably more than 80%, 85%, 90%  
30     or 95% identical, most preferably more than 97% identical to the nucleic acid as represented by SEQ ID NO 1, or to a nucleic acid according to the nucleic acid as defined in b) or c), and  
      e) a nucleic acid as defined in any one of (a) to (i) interrupted by intervening DNA sequences,

or a nucleic acid representing the complement of any of said nucleic acids as defined in (a) to (d).

The synthetic *BAX* gene shows 73.7% identity with the gene coding for Bax- $\alpha$ . It should be clear that the present invention also relates to nucleic acids wherein other, also frequently used  
5 *Candida* spp. codons, are used instead of the choice made for the sequence represented in SEQ ID NO 1. (Table 8)

It should be clear that all nucleic acids according to the invention and which are specifically described above, can be DNA, cDNA, genomic DNA, synthetic DNA, or RNA wherein T is replaced by U.

10 According to another embodiment of the invention, the nucleic acid sequences according to the invention as defined above may, advantageously, be included in a suitable vector, preferably an expression vector which may be transformed, transfected or infected into a host cell. In such an expression vector the nucleic acid is operably linked to one or more control sequences allowing the expression in host cells, such as a suitable promotor, or the like, to ensure expression of the  
15 proteins according to the invention in a suitable prokaryotic or eukaryotic host cell. In this respect, a constitutive or an inducible promoter can be used.

As described in the examples, the invention also relates to nucleic acids and constructs comprising the synthetic *BAX*, or parts thereof, as a fusion with a carrier gene, such as, but not restricted to the yeast *GFP* gene. It is not necessary to include the complete gene of the fusion  
20 partner in the expression construct, so the invention relates to various fusion products which can result from the synthetic *BAX* gene and its fusion partner.

The expression vectors comprising the synthetic construct or fusion protein and the host cell defined herein also form part of the present invention. Said host cell can be from bacterial, yeast, fungal, insect, mammal or human origin. An interesting host cell according to the  
25 invention is a *Candida* spp. cell.

In another embodiment, the expression vector may further comprise an inducible promoter, and/or further a reporter molecule.

The invention also relates to a vector as described above for inducing programmed cell death in *Candida* spp.

30 The invention further also relates a genetically modified yeast or fungal cell as described above wherein said modification results in the onset of at least one pathway eventually leading to programmed cell death.

The invention also relates to a genetically modified *Candida* spp. cell wherein said modification results in the onset of at least one pathway eventually leading to programmed cell death

According to a further embodiment, the invention relates to a method for identifying genes in *Candida* spp. which are differentially expressed in a pathway eventually leading to programmed cell death using a synthetic *BAX* gene, as described above, or a vector comprising said gene as described herein, or a genetically modified yeast or fungal cell as described above.

- 5 In this respect different model systems are envisaged. It has been shown in the present invention that expression of the synthetic *BAX* gene as a fusion protein more rapidly kills the host cells than when expressed without a fusion partner. Accordingly there will be a difference in which *Candida* spp. genes will be differentially expressed in each system. The invention thus relates to methods for identifying genes in *Candida* spp. which are differentially expressed in a  
10 pathway eventually leading to programmed cell death, wherein in said methods the host cells will need a longer or shorter time period for starving. Said time period is dependent on the expression construct or system used.

The invention further relates to a method for obtaining and identifying *Candida* spp. sequences (genes or polypeptides) involved in a pathway eventually leading to programmed cell death  
15 comprising the steps of:

- a) providing a two hybrid system wherein a polypeptide encoded by a nucleic acid as described above or a vector as described above as a bait and a *Candida* spp. cDNA library as a prey are expressed,
- b) detecting an interaction between said polypeptide and a *Candida* spp. polypeptide  
20 encoded by said cDNA library, and,
- c) identifying said *Candida* spp. polypeptide.

The invention also relates to a method for identifying inhibitors (or inhibitor sequences) of Bax-induced cell death comprising the steps of:

- a) providing a genetically modified organism as described above,
- 25 b) expressing a cDNA library in said genetically modified organism, and,
- c) identifying a polypeptide or a cDNA which expression has a beneficial effect on the survival and/or growth of said genetically modified organism.

The invention further relates to a method for identifying Bax-resistant yeast or fungi comprising the steps of:

- 30 a) providing (a) genetically modified yeast or fungi as described above,
- b) treating said genetically modified yeast or fungi with a mutagen,
- c) isolating resistant yeast or fungal cells, and,
- d) optionally identifying and/or characterizing mutated genes in said resistant yeast or fungal cells.

The invention further relates to any of the methods described above wherein said genetically modified organism is a *Candida* spp.

The invention also relates to an isolated *Candida* spp. nucleic acid identifiable by any of the methods described above.

5

The invention, now being generally described, may be more clearly understood by reference to the following examples, which are included merely for purposes of illustration of certain aspects and embodiments of the present invention and are not intended to limit the invention. The contents of all references referred to in this text are hereby incorporated by reference.

## FIGURE AND TABLE LEGENDS

**Figure 1.** *Saccharomyces cerevisiae* sequences based on information obtained from the Saccharomyces Genome Database (SGD) (SEQ ID NOs 17 to 396 and SEQ ID NOs 691 to 716)

**Figure 2.** *Candida albicans* (SEQ ID NOs 397 to 674, 687, 688 and 717 to 732) and human homologues (SEQ ID NOs 675 to 686).

Human homologues were confirmed via forward and reverse BLAST using BLOSUM62 as a scoring matrix.

**YGL080W** (SEQ ID NO 161) codes for a yeast protein with an unknown cellular role and an unknown biochemical function. The human homologue (330 bp (SEQ ID NO 675), 109 aa (SEQ ID NO 676)) LOC51660/g7706369 has no reported cellular role or biochemical function.

**YGR243W** (SEQ ID NO 189) codes for a yeast protein with an unknown cellular role and an unknown biochemical function. The human homologue (384 bp (SEQ ID NO 677), 127 aa (SEQ ID NO 678)) DKFZP564B167/g5817257 has no reported cellular role or biochemical function.

**YGR183C (QCR9)** (Table 3) codes for a yeast protein with a known cellular role and a known biochemical function. QCR9 codes for subunit 9 of ubiquinol cytochrome-c reductase (7.3 kDa protein) which is a component of the ubiquinol cytochrome-c reductase complex. Cellular role: energy generation. Biochemical function: oxidoreductase and active transporter. The human homologue (132aa (SEQ ID NO 679), 399bp (SEQ ID NO 680)) AF161536 was predicted to have an analogous cellular role and biochemical function.

**YBR009C** (SEQ ID NO 37), **YGR209C** (SEQ ID NO 187) and **YPR028W** (SEQ ID NO 393) correspond to known yeast ORFs. Their human homologues have a reported cellular role or biochemical function.

**Figure 3.** Yeast genome macroarray containing a total of 6144 gene ORFs spotted on 2 nylon membrane filters (I and II). Each filter contains 2 fields and each field is divided into 8 grids, organised in 24 rows and 8 columns.

The spots represent the genome wide expression profile without (Minus BAX) and with (Plus BAX) induction of Bax expression for 30 min, 1 hour, 2 hours, 3 hours and 6 hours.

**Figure 4** Yeast cells with a disrupted **YGR183C** gene are fully resistant to Bax-induced cell death. Resistance is observed in both the low-copy (A) and the high-copy (B) Bax

expression system. Clonogenic survival was determined by recovering cells at various times from galactose-containing medium and plating of 1000 cells on glucose-based semisolid medium. Data are representative of three experiments (mean  $\pm$  SD, n=3). SD bars are obscured by symbols.

- 5 **Figure 5.** Scheme for the synthesis of the synthetic *BAX* gene using *C. albicans* optimal codons.
- Figure 6.** DNA (SEQ ID NO 1) and protein (SEQ ID NO 2) sequence of the synthetic *C. albicans BAX* gene.
- Figure 7.** Representation of the expression constructs of the synthetic *CaBAX* gene (A) and the *yEGFP-synth CaBAX* fusion (B).
- 10 **Figure 8.** Growth of the *Candida Albicans* transformants: the individual transformants of pGAL1P:synth*CaBAX* and pGAL1P:*GFP-synthCaBAX* were streaked onto plates containing either 2% glucose or 2% galactose as sole carbon source. Growth was monitored 4 days later.
- 15 **Figure 9.** Growth kinetics of GAL1P:synth*CaBAX* (A) and GAL1P:*GFP-synthCaBAX* (B) on galactose containing minimal medium.
- Figure 10.** Immunoblot analysis of two independent transformants of GAL1P:synth*CaBAX* after 15 hours *Bax* induction on minimal galactose containing media. The arrow at 20kDa indicates the position of the *Bax* protein. The band seen at 50kDa probably represents a cell wall mannan. Not all of the contamination of the polyclonal *Bax* antibody could be removed by the treatment with *S. cerevisiae* mannan.
- 20 **Figure 11.** Immunoblot analysis of the GAL1P:*GFP-synthCaBAX* strain on galactose containing minimal medium. The band appearing at 45kDa represents the *Gfp-Bax* fusion protein, while the band at 20kDa represents the *Gfp* protein alone.
- 25 **Figure 12.** FACS analysis of two independent GAL1P:*GFP-synthCaBAX* transformants grown on galactose containing media: the light grey peak indicates the autofluorescence of the wt strain, the *GFP-fluorescence* peak is not shaded.
- Figure 13.** Viability test synth*CaBAX* (A) and *GFP-synthCaBAX* transformants (B): Cells were pregrown in minimal dextrose medium and then switched to fresh minimal medium containing galactose. At the time points indicated, samples were taken and equal cell amounts were spread on minimal dextrose plates. The appearing colonies represented the viable fraction of the total pool.
- 30 **Tabl 1.** Oligonucleotides used for construction of the synthetic *CaBAXx* gene: start and stop codon are in bold, restriction sites used for cloning are in bold and italic.
- 35



**Tables 2- 6.** Genes modulated by Bax expression in *S. cerevisiae*.

This list includes the genes for which mRNA levels changed significantly after a 30 min (Table 2), 1 hour (Table 3), 2 hours (Table 4), 3 hours (Table 5) or 6 hours (Table 6) induction of Bax protein expression. The Qt values were calculated using the Pathways<sup>TM</sup> software (Research Genetics).

5

**Table 7.** Genes modulated by *Bax* expression in *S. cerevisiae*. This list includes all the genes for which mRNA levels changed significantly after induction of Bax protein expression. The Qt values were calculated using the Pathways software (Research Genetics). Positive values correspond with upregulated genes. Negative values correspond with downregulated genes. (Comparable with ↑ and ↓ respectively in Tables 2-6).

10

**Table 8.** Codon usage for the synthetic *BAX* gene.

**Table 9.** Regulation of 23 selected "Bax-specific" functions.

## EXAMPLES

### **Example 1. Differential gene expression analysis upon Bax-induced cell death**

#### **Materials and media**

5 Bacterial strain *Escherichia coli* MC1061 (Casadaban and Cohen, 1980) was used for the construction and the amplification of plasmids. Yeast strains were grown under normal conditions on standard media (Sherman *et al.*, 1979). The *Saccharomyces cerevisiae* strain INVSc1 (Invitrogen®, San Diego, CA, USA) was transformed by means of the lithium acetate method (Schiestl and Gietz, 1989) with YIpUTyL or YIpUTyLMuBax, after linearisation in the Ty  
10  $\delta$  element (Zhu, 1986).

#### **Cloning of mouse BAX cDNA**

Mouse *bax* cDNA, encoding the mouse Bax- $\alpha$  protein, was cloned by Pfu DNA polymerase (Stratagene®, Lo Jolla, CA, USA) chain reaction amplification (PCR) from an EL4/13.18  
15 thymoma cDNA library (BCCM™/LMBP-LIB15) by making use of the primers:

5'-ATGGACGGGTCCGGGAGCAG-3' (SEQ ID NO 689) and

5'-TCAGCCCATCTTCTTCCAGATGGTGAG-3' (SEQ ID NO 690).

The resulting PCR product was cloned in a *HincII*-openend pUC19 according to standard procedures (Sambrook J. *et al.*, 1989).

20

#### **Plasmid constructions**

The 2 $\mu$  ori and the *URA3* marker gene were removed from pUT332 (Gatignol *et al.*, 1990) by successive digestions with *Clal* and *BglII*. A *BamHI-HindIII GAL1* promoter fragment was ligated into the *BglII-HindIII*-opened plasmid. A *XbaI-Fspl FLP* terminator fragment was inserted into  
25 this *XbaI-HindIII*(blunted)-opened plasmid so that the plasmid YIpUT was obtained. Insertion of a blunted *EcoRI-BsaAI* Ty  $\delta$  element in the *KpnI-AatII*-opened and blunted YIpUT resulted in the plasmid YIpUTy. Subsequent insertion of the *LEU2* marker gene, as a blunted *BsaAI-BsrGI* fragment, in the *BamHI*-openend and blunted YIpUTy resulted in the plasmid YIpUTyL.

Mouse *bax* cDNA was excised from pUC19 by digestion with *XbaI* and *HindIII* and subcloned  
30 into the *XbaI-HindIII*-opened plasmid YIpUTyL, obtaining the final expression plasmid YIpUTyLMuBax.

The plasmid YIpUTyLMuBax has been deposited in the BCCM™/LMBP culture collection as pSCTyGALmBax with accession number 3871 under restricted use.

**GeneFilters**

The Yeast GeneFilters™ were purchased from Research Genetics Inc. (Huntsville, AL, USA).

The Yeast GeneFilters™ are hybridization ready nylon membranes containing a total of 6144 gene ORFs (Open Reading Frames) individually amplified by PCR and spotted on 2 nylon  
5 membrane filters (Filter I and II). The filters are cut in the upper right corner and the DNA is on the labeled side of the filter.

Filter I contains 3072 ORFs organized into two fields (fields 1 and 2). Each field contains 1536 ORFs divided into 8 grids (A, B, C, D, E, F, G and H). The grids are organized in 24 rows and 8  
columns.

10 Filter II contains 3072 ORFs organized in two fields (field 3 and 4). Fields 3 and 4 are organized in the same way as fields 1 and 2.

**The Yeast ORF target**

The yeast filters consist of over 6144 PCR products corresponding to 6144 yeast ORFs derived  
15 from the SGD. The PCR reactions used ORF specific primer pairs designed to amplify the entire open reading frame. The primers were generated from unique sequences containing the start codon ATG and termination codon (kindly provided by M. Cherry at Stanford Genome Center). Thus the PCR product contains the complete open reading frame including the start and stop  
codons. These products were purified and resuspended at 50 nanograms per microliter in a  
20 colored solution to allow the printing to be monitored. A robotic device was used to spot approximately 1/10 of a microliter of the denatured PCR product solution on a positively charged nylon membrane. The DNA was then UV cross-linked to the membrane.

**Results****25 Induction of Bax-expression in yeast cells**

A preculture of yeast strain INVSc1 containing YlpUTyLMuBax, wherein 5 Bax cassettes under the control of the *GAL1* promoter are integrated in the genome near Ty  $\delta$  elements, was grown overnight in minimal glucose-containing medium in parallel with the yeast strain INVSc1 containing YlpUTyL as a control. The precultures were diluted in 100-ml minimal glucose-  
30 containing medium and grown until an OD<sub>600</sub> of 1 was reached. Subsequently, the yeast cells were transferred into 100-ml galactose-containing medium and incubated for an additional period of 30 min, 1 hour, 2 hours, 3 hours or 6 hours.

**RNA isolation**

Total RNA was isolated using RNApure™ Reagent (Genhunter Corporation Nashville, TN, USA) according to the GenHunter protocol. 1.5 10<sup>9</sup> cells were concentrated in a microcentrifuge tube and 1ml RNApure™ Reagent was added together with 1 g of glass pearls. The yeast cells  
5 were broken by thorough mixing during five 2-minutes periods, and placed on ice in-between to avoid RNA degradation. Chloroform (150 µl) was added to the lysate and centrifuged for 10 min at 4°C and at 15000 rpm. The supernatant was transferred to a new tube and the RNA was precipitated with an equal volume of isopropanol. After 10 min incubation on ice, the RNA was pelleted by centrifugation and the pellet was washed with 70% ice-cold ethanol. The dried RNA  
10 pellet was resuspended in 50 µl RNase free dH<sub>2</sub>O.

**First strand cDNA synthesis in the presence of  $\alpha$ -<sup>33</sup>P dCTP**

Probes with high specific activity were prepared by first strand cDNA synthesis using total RNA isolated from INVSc1 YIpUTyLMuBax or INVSc1 YIpUTyL yeast cells and incorporation of  $\alpha$ -<sup>33</sup>P  
15 dCTP as follows: 2 µl (1 µg/ml) of Oligo dT was added to 20 µg of total RNA in a maximal volume of 8 µl RNase-free dH<sub>2</sub>O and incubated at 70°C for 10 min. After cooling down on ice for 1 min, the following components were added:

6 µl 5x concentrated First Strand Buffer (GIBCO-BRL, Paisley, UK)  
1 µl 0,1 M DTT  
20 1 µl RNase Block (40 units/µl) (Stratagene)  
1,5 µl 20 mM dXTP-solution (X = A, G and T) (Amersham Pharmacia biotech Uppsala, Sweden)  
1,5 µl SuperScript™ Reverse Transcriptase (200 units/µl) (GIBCO-BRL)  
10 µl  $\alpha$ -<sup>33</sup>P dCTP (10mCi/ml, 3000 Ci/mmol) (Amersham Pharmacia biotech Uppsala,  
25 Sweden),

and incubated for 2 h at 37°C during which first strand cDNA synthesis took place.

Unincorporated label was separated from the probe on a Sephadex G-50 column (Amersham Pharmacia biotech Uppsala, Sweden). The radioactivity incorporated in the probe was measured by liquid scintillation. The specific activity of the probes was 5.10<sup>8</sup> cpm/µg for both  
30 the INVSc1YIpUTyL and the INVSc1 YIpUTyLMuBax probes.

Additionally, the length of first strand cDNA probes was controlled on an alkaline 2% agarose gel using standard electrophoresis techniques, and resulted in the detection, via stimulated phosphorescence autoradiography, of the bulk of the fragments around 500 bp.

**Hybridisation with the *S. cerevisiae* Yeast GeneFilters™ and signal detection**

The Yeast GeneFilters™ were successively hybridised with the  $\alpha$ -<sup>33</sup>P dCTP labelled cDNA probes using the MicroHyb™ solution provided by the manufacturer (Research Genetics Inc., Huntsville, AL, USA). This solution was applied as well in the prehybridisation step as during  
5 hybridisation. The MicroHyb™ solution contains formamide to allow hybridisation to occur at lower temperatures.

The hybridisation experiment was performed essentially as follows: during prehybridisation, the Yeast GeneFilters™ were placed in a hybridisation flask (35x250 mm) filled with 5 ml MicroHyb™ solution (42°C) containing 5  $\mu$ l polydA (1  $\mu$ g/ml) and incubated for 24 hours at 42°C  
10 whilst rotating (10 rpm). After disposal of the prehybridisation solution, the denatured (3 min at 100°C) cDNA was added in 5 ml prewarmed MicroHyb solution and again incubated overnight at 42°C whilst rotating. Following two wash steps of 20 min in wash buffer (2x SSC, 1% SDS) at 50°C, a third wash step was performed in a second wash buffer (0,5x SSC, 1% SDS) for an additional 15 min at room temperature. The Yeast GeneFilters™ were placed in a  
15 PhosphorImager™ cassette (Molecular Dynamics, Sunnyvale, CA, USA) with storage phosphor screen. After 4 days of development the screen was scanned at a resolution of 50  $\mu$ m using the (BioRad, Richmond, CA, USA) Personal FX. The results of these can be seen in Figure 3.

**Example 2. Quantification of Hybridisation Signals**

20 Quantification of the hybridisation signals was done using the Pathways™ software (Research Genetics, Huntsville, AL, USA) and these signals were normalised against all data points. Comparison of these normalised data revealed differentially expressed candidate genes. Visual inspection of the hybridisation spots confirmed their selection. The genes as well as the factors with which they are up- or down- regulated are listed in the Tables 2 to 6 for each individual time  
25 point. An overview of the up and down regulated genes modulated in function of induction of Bax expression for several time points is shown in Table 7. The sequences of these genes and amino acid sequences that they encode are shown in Figure 1.

**Example 3. Comparative gene expression analysis upon Bax-induced cell death and H<sub>2</sub>O<sub>2</sub>-induced cell death****The oxidative H<sub>2</sub>O<sub>2</sub>-challenge**

A preculture of yeast strain INVSc1 containing YlpUTyL was grown overnight in minimal glucose-containing medium. The preculture was diluted in 100-ml minimal glucose-containing medium and grown until an OD<sub>600</sub> of 1 was reached. Subsequently, the yeast cells were  
35 transferred into 100-ml galactose-containing medium supplemented with 0.1 mM H<sub>2</sub>O<sub>2</sub>, and

incubated for an additional period of 1 hour. This oxidative challenge resulted in the same final toxicity as a 1-hour induction of Bax expression in the same growth conditions.

***First strand cDNA synthesis in the presence of  $\alpha$ -<sup>32</sup>P dCTP***

- 5 RNA was isolated as mentioned in Example 1. Probes with high specific activity were prepared (detailed in Example 1) by first strand cDNA synthesis using total RNA isolated from INVSc1 YlpUTyLMuBax or INVSc1 YlpUTyL (growth conditions as described in Example 1) or oxidatively stressed INVSc1 YlpUTyL yeast cells.

The specific activity of all probes was  $5 \cdot 10^8$  cpm/ $\mu$ g.

10

***Quantification of Hybridisation Signals***

Hybridisation and signal detection as described in Example 1. Conversion of the digital images to a 16 bit TIFF format using the Quantity One program (BioRad, Hercules, CA, USA) preserved image data and was necessary for file import into the Pathways® software (Research Genetics,

- 15 Huntsville, AL, USA). Pathways® was used for the quantification of hybridisation signals and these signals were normalised against all data points.

***Identification of Bax-responsive genes***

Pairwise comparisons of the normalised data obtained from INVSc1 YlpUTyLMuBax (B) and INVSc1 YlpUTyL (C) revealed differentially expressed genes. To determine the -fold induction or repression, the normalised signal intensity after Bax induction (B) was divided by that before the shock (C). Visual inspection of the hybridisation spots confirmed their selection (*replacement*).

25 ***Identification of Bax-specific genes within the Bax-responsive pool***

Pairwise comparisons of the normalised data obtained from INVSc1 YlpUTyLMuBax (B) and INVSc1 YlpUTyL (C) at the 1-hour time point revealed differentially expressed genes. Linear ratios (B vs C) were estimated significant when changes were at least two-fold and the normalised signal intensity of one spot was at least tenfold above the average background value. The normalised data of the Bax-responsive genes were compared with data obtained from the H<sub>2</sub>O<sub>2</sub>-stressed INVSc1 YlpUTyL (H). A Bax-responsive (up-regulated/down-regulated) gene was considered to be Bax-specific when the normalised signal intensity after Bax induction was at least twice as high/low as the corresponding intensity after oxidative stress. Visual inspection of the hybridisation spots confirmed their selection. An overview of the Bax-

30

specific genes for the 1-hour time point is shown in Table 9. The sequences of these genes and amino acid sequences that they encode are shown in Figure 2.

**Example 4. Search for homologues in *Candida albicans* and human**

- 5 Sequence similarity searches against public and commercial sequence databases were performed with the BLAST software package (Altschul *et al.*, 1990) version 2. Both the original nucleotide sequence and the six-frame conceptual translations were used as query sequences. The used public databases were the EMBL nucleotide sequence database (Stoesser *et al.*, 1998), the SWISS-PROT protein sequence database and its supplement TrEMBL (Bairoch and
- 10 Apweiler, 1998), and the ALCES *Candida albicans* sequence database (Stanford University, University of Minesota). The commercial sequence database used was the PathoSeq™ microbial genomic database (Incyte Pharmaceuticals Inc., Palo Alto, CA, USA).
- Sequence similarity searches were performed using the BLAST software package version 2. The identity between 2 sequences was calculated as percentage identical residues, the
- 15 similarity percentage between two sequences was calculated using BLOSUM62 as a scoring matrix.
- The sequences of homologues *Candida* spp. and human genes and the corresponding amino acid sequences are shown in Figure 2.

20 **Example 5. Screening for compounds modulating expression of polypeptides involved in induction of cell death of *C. albicans***

- The method proposed is based on observations (Sandbaken *et al.*, 1990; Hinnebusch and Liebman 1991; Ribogene PCT WO 95/11969, 1995) suggesting that underexpression or overexpression of any component of a process (e.g. translation) could lead to altered sensitivity
- 25 to an inhibitor of a relevant step in that process. Such an inhibitor should be more potent against a cell limited by a deficiency in the macromolecule catalyzing that step and/or less potent macromolecule, as compared to the wild type (WT) cell.
- Mutant yeast strains, for example, have shown that some steps of translation are sensitive to the stoichiometry of macromolecules involved. (Sandbaken *et al.*, 1990). Such strains are more
- 30 sensitive to compounds which specifically perturb translation (by acting on a component that participates in translation) but are equally sensitive to compounds with other mechanisms of action.
- This method thus not only provides a means to identify whether a test compound perturbs a certain process but also an indication of the site at which it exerts its effect. The component

which is present in altered form or amount in a cell whose growth is affected by a test compound is potentially the site of action of the test compound.

The assay to be set up involves measurement of growth and/or death rate of an isogenic strain which has been modified only in a certain specific allele, relative to a wild type (WT) *Candida albicans* strain, in the presence of R-compounds. Strains can be ones in which the expression of a specific protein is impaired upon induction of anti-sense or strains which carry disruptions in an essential gene. An *in silico* approach to find novel genes in *Candida albicans* will be performed. A number of essential genes identified in this way will be disrupted (in one allele) and the resulting strains can be used for comparative growth and/or death rate screening.

#### **Example 6. Assay for High Throughput screening for drugs**

35 µl minimal medium (S medium + 2% galactose + 2% maltose) is transferred in a transparent flat-bottomed 96 well plate (MW96) using an automated pipetting system (Multidrop, Labsystems, Helsinki, Finland). A 96-channel pipettor transfers 2.5 µl of R-compound at  $10^{-3}$  M in DMSO from a stock plate into the assay plate.

The selected *Candida albicans* strains (mutant and parent (CAI-4) strain) are stored as glycerol stocks (15%) at  $-70^{\circ}\text{C}$ . The strains are streaked out on selective plates (SD medium) and incubated for two days at  $30^{\circ}\text{C}$ . For the parent strain, CAI-4, the medium is always supplemented with 20 µg/ml uridine. A single colony is scooped up and resuspended in 1 ml minimal medium (S medium + 2% galactose + 2% maltose). Cells are incubated at  $30^{\circ}\text{C}$  for 8 hours while shaking at 250 rpm. A 10 ml culture is inoculated at 250.000 cells/ml. Cultures are incubated at  $30^{\circ}\text{C}$  for 24 hours while shaking at 250 rpm. Cells are counted in Coulter counter and the final culture (S medium + 2% galactose + 2% maltose) is inoculated at 20.000 to 50.000 cells/ml. Cultures are grown at  $30^{\circ}\text{C}$  while shaking at 250 rpm until a final  $\text{OD}_{600}$  of 0.24 (+/- 0.04) is reached.

200 µl of this yeast suspension is added to all wells of MW96 plates containing R-compounds in a 450 µl total volume. MW96 plates are incubated (static) at  $30^{\circ}\text{C}$  for 48 hours.

Optical densities are measured after 48 hours.

Test growth is expressed as a percentage of positive control growth for both mutant (x) and wild type (y) strains. The ratio (x/y) of these derived variables is calculated.

#### **Example 7. Yeast cell viability assay upon induction of Bax expression**

**Materials and media**



Yeast strains were grown under normal conditions on standard media (Sherman *et al.*, 1979). The *Saccharomyces cerevisiae* BY4742 wild type strain and BY4742 with the *YGR183C* gene disruption (EUROSCARF collection) were transformed by means of the lithium acetate method (Schiestl and Gietz, 1989) with the low-copy centromeric pRS415Bax plasmid or pRS415 as a control, or with the high-copy episomal pRS425Bax plasmid or pRS425 as a control.

### Plasmid constructions

The Bax expression cassette, a *BsgI*(blunted)-*SapI*(blunted) fragment excised from YlpUTyLMuBax containing the *GAL1* promoter, the *bax* cDNA and the *FLP* terminator, was ligated into the *Eco*136II-opened pRS415 (ATCC 87520) and pRS425 (ATCC 77106) plasmids, obtaining the low-copy centromeric pRS415Bax and the high-copy episomal pRS425Bax expression plasmids.

### Results

Single colonies of yeast cells transformed with pRS415 or pRS415Bax or pRS425 or pRS425Bax were grown in 10 ml minimal glucose-containing medium with vigorous aeration at 30°C to an optical density of 1 OD<sub>600</sub>. Cells were pelleted by centrifugation and washed two times with sterile dH<sub>2</sub>O before resuspending in 10 ml minimal galactose-containing medium. After culturing for various times at 30°C, the total cell density of the cultures was determined, and 1000 cells were spread on minimal glucose-based semisolid medium, followed by incubation at 30°C for 3 days. The number of colonies on plates from the 0 hr cultures was designated as 100% (Fig. 4).

### Example 8. Bax Expression in *Candida* cells

#### Strains

The *Candida albicans* strain CAI4 (*ura3 $\Delta$* ) was used to perform the experiments (Fonzi and Irwin 1993).

*E. coli* transformations were done using the Top10 strain from Invitrogen (San Diego, CA, USA) (F' *mcrA*  $\Delta$ (*mrr-hsdRMS-mcrBC*)  $\Delta$ 80/*lacZ*  $\Delta$ M15  $\Delta$ *lacX74 deoR recA1 araD139*  $\Delta$ (*ara-leu*)7697 *galU galK rpsL* (Str<sup>R</sup>) *endA1 nupG*).

#### Media

Synthetic dextrose media (SD), containing 2% glucose, 1.34% Yeast Nitrogen Base without amino acids and 0.77g/l CSM-ura (Bio 101, Vista, CA, USA) was used to grow the *Candida albicans* transformants. In case of the wild type (CAI4), the media was supplemented with

50µg/ml uridine. To prepare plates the media was solidified with 2% agar. Expression of the synthetic *BAX* gene was performed using 2% galactose as carbon source.

#### Construction of the codon-optimised *BAX* gene

- 5 Construction of the synthetic *BAX* gene followed the nomenclature described for *Candida albicans* (Lloyd and Sharp 1992; Brown, *et al.* 1991; <http://alces.med.umn.edu/candida/codons.html>; <http://www.kazusa.or.jp/codon>). To ensure a high expression of the synthetic gene, the subset of 'optimal' codons of highly expressed genes was used to design the synthetic *BAX* gene.
- 10 The synthCa*BAX* gene was constructed in three parts using eight oligonucleotides (Fig. 5). The sequences of the oligonucleotides are given in Table 7. Primer A1 introduced upstream of the ATG codon a *Pst* I site and a *Bgl* II site. The *Pst* I site was used later on for direct cloning into the *Candida albicans* expression vector, while the *Bgl* II site served as a linker for a *yEGFP* fusion. Primer C2 introduced a *Sma* I site, suitable for cloning into the expression vector.
- 15 Fragment A and B were synthesised in two steps: in a first PCR round primer X1 and X2 (X represents A or B, respectively) were used together. The resulting fragment served as a template in a second PCR round together with primers X1 and X3. Fragment C was synthesised in a single PCR round using the primers C1 and C2. Fragment A and B were cloned into the pCR-BluntII-TOPO vector (Stratagene), while fragment C was cloned into the pCR2.1-TOPO
- 20 vector (Stratagene). All three fragments were sequenced to ensure that no mutation was introduced by the PCR.
- Subsequently, fragment A was digested with *Pst* I and *Taq* I, fragment B with *Taq* I and *Bam* HI and fragment C with *Bam* HI and *Sma* I. The three products were cloned in a quadruple ligation into pUC21 digested with *Pst* I and *Sma* I resulting in the plasmid pUC21:synthCandidaBAX.
- 25 The sequence of the synthetic *BAX* gene is shown in Figure 6.

#### Construction of synthetic *BAX*- and *GFP*-synthetic *BAX* expression plasmids

- A *Pst* I-*Sma* I fragment containing the ORF of the synthetic *BAX* gene was cloned into the *Pst* I-*Stu* I digested vector pGAL1ACT1LUC (W. Martinet, EP application nr 99204557.5) resulting in
- 30 the expression construct pGAL1P:synthCa*BAX* (Fig. 7A). To facilitate recognition of the AUG codon during formation of initiation complexes a purine base (A) was introduced at position -3 from the AUG codon (Kozak 1981) using the Quick change site directed mutagenesis kit from Stratagene.
- The yeast enhanced *GFP* gene *yEGFP*; (Cormack *et al.* 1997) was amplified by PCR using
- 35 primer 5'-AACTGCAGATGTCTAAAGGTGAAGAATTATTC-3' (SEQ ID NO 11) as upstream primer and primer 5'-GGAAGATCTTCCTTTGTACAATTCATCC ATACC-3' (SEQ ID NO 12) as

downstream primer. The sense primer introduced a *Pst* I site (shown in bold and italic), while the anti-sense primer contained a *Bgl* II linker (shown in bold and italic) for fusion with the synthetic *BAX* gene. After cloning of the *yEGFP* gene into the pCR2.1-TOPO vector (Stratagene), the gene was sequenced to ensure that no mutation was introduced by PCR.

- 5 The *yEGFP*-synth *Candida BAX* fusion was created by cloning a *Pst*I-*Bgl*II *yEGFP* fragment together with a *Bgl* II-*Sma* I synthetic *Candida BAX* fragment into the *Pst* I-*Stu* I digested expression vector pGAL1ACT1LUC. The obtained pGAL1P:*yEGFP*-synthCa*BAX* fusion construct (Fig.7B) was sequenced to ensure that no frameshift had occurred.

#### 10 **Creation of the synthetic *BAX* expression strains**

- Transformation of the expression plasmids was performed using a modified procedure (Logghe, unpublished) of the spheroblasting protocol (Herreros *et al.* 1992). The plasmids were linearised with *Bpu*1102 I to allow directed integration into the genome at the GAL1 promoter site. Correct integration was analysed by Southern blotting. Therefore genomic DNA from different
- 15 transformants was prepared using the Nucleon<sup>®</sup> extraction and purification kit (Amersham Pharmacia Biotech) and digested with *Xba* I. The *BAX* probe used in the Southern blot was prepared by PCR. The PCR was performed using the pGAL1P:synthCa*BAX* plasmid as template, together with the sense primer 5'-ATGGATGGTTCTGGTGAAC-3' (SEQ ID NO 13) and the anti-sense primer 5'-TTAACCCATTTTTTCCAGATG-3' (SEQ ID NO 14). Standard
- 20 PCR conditions were used. For detection of the *yEGFP* a probe was synthesised by PCR using primer 5'-AGAGATCTCGAGGGATCC-3' (SEQ ID NO 15) as sense primer and primer 5'-GCATTATTTGTACAATTCATCC-3' (SEQ ID NO 16) as anti-sense primer. Southern blot hybridisation and detection were performed using the AlkPhos DIRECT labelling and detection system (Amersham Pharmacia Biotech) following the instructions of the manufacturer.

25

#### **Western blot analysis**

- For Western blot analysis cells were pre-grown over night in SD-ura media till late log phase. The cells were harvested by centrifugation, washed twice with water and inoculated in SG-ura to induce *Bax* expression. Induction was performed for 15 hours. Yeast crude extracts were
- 30 prepared as described before (Sambook, Fritsch *et al.* 1989). Detection of the *Bax* protein was performed using a polyclonal rabbit anti-mouse /rat *Bax* antibody (Pharmingen). Due to contamination of this antibody with yeast cell wall mannan antibodies, a very high background occurred. This problem could be avoided by pre-incubation of the antibody with 0.5mg/ml purified yeast mannan (Rossanese *et al.* 1999). Detection of the *Gfp* protein was done using an
- 35 anti-*Gfp* monoclonal antibody (Molecular Probes, Eugene, OR, USA).

### Growth curves

For growth curves, yeast cells were grown for 24 h in SD-ura medium (supplemented with uridine for the wild type). These cultures were harvested, washed twice with water and inoculated to an OD<sub>600</sub> of 0.1 into fresh SD-ura or SG-ura media. Growth was monitored in  
5 microtitre plates using the Bioscreen C system (Labsystems).

### Viability tests

Cells were pregrown in minimal dextrose medium to an OD<sub>600</sub> of 1. After washing the cells twice with water they were switched to minimal medium containing galactose as carbon source. At the  
10 time points indicated, samples were taken and equal cell amounts were spread on minimal dextrose plates. The appearing colonies represent the viable fraction of the pool.

### Results : Conditional expression of the synthetic *BAX* gene in *Candida albicans*

A cDNA encoding the full-length mouse Bax protein was placed under control of the *Candida albicans* GAL1 promoter allowing for conditional expression when cells are grown in galactose  
15 containing media. Initial experiments were performed using the wild type mouse *bax* gene. Expression of this gene did not result in any detectable phenotype, no difference in growth compared to the wild type was observed when cells were grown on galactose containing media (data not shown). This could be due to the non-traditional codon strategy adopted by *Candida*  
20 *albicans* and related species. Analysis of the codons used in the mouse *BAX* gene revealed a for *Candida albicans* not optimal codon usage as found for highly expressed genes in this yeast. To ensure a high expression of the *BAX* gene a codon-adapted, synthetic version of the gene was created using the strategy described above. The synthetic *BAX* gene was fused to the *yEGFP* to allow screening for transformants with a high *yEGFP-synthCaBAX* expression level  
25 using FACS technology. The newly obtained plasmids pGAL1P:synthCaBAX and pGAL1:*GFP-synthCaBAX* were transformed into the *C. albicans* CAI4 strain. Transformants were selected on uridine-free minimal medium. About 25 transformants of each expression construct were chosen and streaked onto minimal dextrose medium (non-inducing conditions) as well as on minimal galactose medium (inducing conditions). After two days incubation at 30°C all  
30 transformants did grow on the glucose containing media. When galactose was used as a sole carbon source, most of the transformants did not grow (Fig. 8). Southern blot analysis of the galactose negative transformants revealed that a copy of the synthCaBAX gene had been integrated into the endogenous copy of the GAL1 promoter. To study differences in growth, the transformants were grown over night in synthetic glucose containing medium. Subsequently,  
35 cells were washed with water and switched to fresh medium containing galactose as carbon source. While the wild type strain did grow well on galactose containing media no growth was

observed for the Bax expressing transformants (Fig. 9A and B). Western blot analysis of the synthCaBAX transformants showed accumulation of the Bax protein (15 hours Bax induction, Fig. 10). A similar result was observed when immunoblotting was performed with the GFP-synthCaBAX expressing strains. Here the fusion protein was detected at the expected  
5 molecular weight of about 45K under inducing conditions (galactose as carbon source). In addition to the fusion protein a band appeared at the molecular weight of about 20K. This corresponds to the molecular weight of the Gfp protein alone. Addition of a Gfp-expressing strain as a positive control to the western blot did confirm these results. Here the Gfp protein was detected at the same molecular weight as the unexpected band in the GFP-synthCaBAX  
10 expressing strain (Fig. 11). This is most probably due to a partly proteolytic degradation of the fusion protein. Analysis of the Gfp-fluorescence using FACS technology showed a high Gfp-fluorescence signal for the transformants expressing the fusion protein (Fig. 12). When cell viability was analysed, different results were obtained for the synthCaBAX strain and the GFP-synthCaBAX strain. The synthCaBAX strain showed quite a rapid decrease in the amount of colony forming units during the first 6 hours of incubation on galactose containing media.  
15 Afterwards the process slowed down significantly. This is in contrast to the results obtained for the strain expressing the gfp-synthCabax fusion protein. Here almost all the cells died at a very rapid rate during the first 3 hours of incubation in media containing galactose as sole carbon source. It is possible that the Bax trigger in the synthCabax expressing cells is not strong  
20 enough to kill all cells. The cell has enough time to activate a sort of defence mechanism, possibly by proteolytic degradation of the Bax protein. The situation is different for the fusion protein. Gfp is a very stable protein itself. Fusion of the Gfp to another protein could result in a stabilisation of this protein. It would be more resistant to proteolytic degradation. This would explain the situation for the Gfp-Bax fusion. The Gfp-Bax protein is more protected from  
25 proteolytic degradation. Like that it is for a longer period present in the cell. The death trigger is herewith stronger, so the cells die faster. The time that the cells have to activate the proteolytic machinery is not sufficient for them to survive.

Table 1:

Oligo	Sequence 5' → 3'
A1	AACTGCGAGGAAGATCTCCATGGATGGTCTGGTGAACAATGGGTTCTGGTGG TCCAACCTCTTCTGAACAAATCATGAAACCGGTGCTTCTTGTTG (SEQ ID NO 3) TAGAAGCATCTTGTGGTGGTTCGAAGGTCAATTCTGGGTTTCACCCAGCC ATTCTACCAGCTCTATCTTGGATGAACCTTGCAACAAGAAAGCACC (SEQ ID NO 4) GGAATTCTCGACATCAGCGATCATCTTTGCAATTCATGTAGAAATCCAATTC ATCACCGATTCTTCTCAAAACATTCAGACAATTTTGGTAGAGCATCTTGTG (SEQ ID NO 5) GGAATTCGCTGATGTCGATACCGATTCTCCAAGAGAAGTCTTCTCAGAGTCG CTGCTGATATGTCGCTGATGGTAACCTCAACTG (SEQ ID NO 6) AATCTGGGACTTTGGTACACAAAGCTTTCAGACCCTTTCAGAAAGCGAAGTA GAACAAGCGACGACTCTACCCAGTTGAAGTTACCA (SEQ ID NO 7) CCACCTTGATCTTGGATCCAGACCAACAATCTTCTCTCAAGAAATCCAAGGTC CAACCCATGATGGTTCGATCAATCTGGGACTTTG (SEQ ID NO 8) ATTGTTGGTCTGGATCCAAGATCAAGGTGGTGGGAGGTTGTGTCTTACTT CGGTACCCCAACCTGGCAACCGTCA (SEQ ID NO 9) TCCCCCGGGGATTAAACCCATTTTTCAGATGGTCAAAAGACGGTCAAGAC ACCAGCGACGAAGATGGTGACGGTTTGCCAGGTGGG (SEQ ID NO 10)
A2	
A3	
B1	
B2	
B3	
C1	
C2	

**Table 2: Overview of the differentially expressed genes after 30 min Bax expression****Comparison: INVSc1 YlpUTL versus INVSc1 YlpUTyLB**

ORF	Gene	Normalised intensities		Up/down	Cr value
		L	YEB		
<i>Cellular role : Cell cycle control</i>					
YBR133C	HSL7	18932.54	37877.20	↑	2.00
<i>Cellular role : Polymerase II transcription</i>					
YDR253C	MET32	17661.13	45567.17	↑	2.58
YBR112C	SSN6	26698.87	65315.83	↑	2.45
YDR145W	TAF61	38697.96	73117.62	↑	1.89
YBR289W	SNF5	33111.77	72328.70	↑	2.18
YDR216W	ADR1	30127.45	8815.87	↓	3.42
YEL009C	GCN4	16533.76	3030.44	↓	5.46
YBR089C-A	NHP6B	22698.63	6297.49	↓	3.60
YMR043W	MCM1	39141.64	84180.45	↑	2.15
YKR092C	SRP40	5965.63	16105.82	↑	2.70
YMR273C	ZDS1	14699.61	35508.04	↑	2.42
YPL089C	RLM1	34922.91	67856.88	↑	1.94
YOR372C	NDD1	20285.12	44445.20	↑	2.19
YPL037C	EGD1	30633.33	5250.70	↓	5.83
<i>Cellular role : Cell polarity</i>					
YBL085W	BOI1	7693.29	18614.99	↑	2.42
<i>Cellular role : Chromatine structure</i>					
YBR009C	HHF1	16668.00	4178.80	↓	3.99
YNL030W	HHF2	49878.04	12566.96	↓	3.97
YDR224C	HTB1	67355.40	23156.82	↓	2.91
YBL002W	HTB2	25269.02	5383.97	↓	4.69
<i>Cellular role: RNA processing</i>					
YER112W	USS1	12776.74	31470.70	↑	2.46
YPL190C	NAB3	6381.36	17892.11	↑	2.80
YNL112W	DBP2	9956.84	28036.48	↑	2.82
<i>Cellular role: Energy generation</i>					
YPL078C	ATP4	26902.69	5980.38	↓	4.50
YDL004W	ATP16	36525.08	3004.34	↓	12.16
YDR377W	ATP17	14419.41	756.86	↓	19.05
YDR529C	QCR7	35346.95	5394.65	↓	6.55
YGR008C	STF2	13275.51	2276.27	↓	5.83
YEL039C	CYC7	13604.38	2689.66	↓	5.06
YKL150W	MCR1	105337.67	30743.75	↓	3.43
YLR038C	COX12	52687.73	5455.83	↓	9.66
YLR327C		113.966.77	54.014.65	↓	2.11
<i>Cellular role: Carbohydrate metabolism</i>					
YBR149W	ARA1	15149.55	4095.17	↓	3.70
YHR094C	HXT1	12526.90	785.73	↓	15.94
YDR345C	HXT3	36643.13	1632.48	↓	22.45
YDR343C	HXT6	77064.71	32060.05	↓	2.40
YDR342C	HXT7	76349.13	27615.15	↓	2.76
<i>Cellular role: Signal transduction</i>					
YER177W	BMH1	22856.29	44771.71	↑	1.96
YDR099W	BMH2	40127.38	74572.38	↑	1.86

YGR070W	ROM1	12055.28	28169.57	↑	2.34
YGR023W	MTL1	7354.78	19648.06	↑	2.67
<i>Cellular role: Protein synthesis</i>					
YGR034W	RPL26B	71942.48	74625.22	↑	1.04
<i>Cellular role: Protein folding</i>					
YLR216C	CPR6	9616.80	31126.02	↑	3.24
<i>Cellular role: Protein modification/degradation</i>					
YFR052W	RPN12	5583.57	14855.67	↑	2.66
YDL147W	RPN5	31932.20	52939.11	↑	1.66
YGR132C	PHB1	15429.56	5591.19	↓	2.76
YGR135W	PRE9	39921.63	5517.17	↓	7.24
YFR010W	UBP6	1892.76	828.94	↓	2.28
<i>Cellular role: Cell stress</i>					
YIR037W	GPX3	7869.22	21789.00	↑	2.77
YDR513W	TTR1	55986.32	33263.12	↓	1.68
YCL035C	GRX1	70248.30	10969.97	↓	6.40
YFL014W	HSP12	41689.29	18658.48	↓	2.23
YHR053C	CUP1A	72852.07	43488.52	↓	1.68
YHR055C	CUP1B	71934.03	56799.80	↓	2.77
YMR173W	DDR48	16870.70	5022.40	↓	3.32
YMR251W-A	HOR7	26879.95	417.36	↓	64.41
YLR043C	TRX1	58251.39	4435.79	↓	13.13
YBL064C	PRX1	21525.00	40969.00	↑	1.90
YOL151W	GRE2	2624.55	24152.03	↑	9.20
<i>Cellular role: Unknown</i>					
YBL081W		73834.11	74612.35	↑	1.01
YDR366C		39998.46	57428.80	↑	1.44
YCR004C	YCP4	6869.06	28115.73	↑	4.09
YCR013C		3988.55	15144.34	↑	3.80
YBR050C	REG2	4687.91	14408.20	↑	3.07
YBL109W		18744.60	35440.24	↑	1.89
YDR154C		19565.23	69428.03	↑	3.55
YEL071W	DLD3	22235.73	68790.83	↑	3.09
YHR095W		14426.76	34896.68	↑	2.42
YGR069W		43413.57	72420.39	↑	1.67
YDR544C		13587.00	27004.37	↑	1.99
YGR236C		24927.59	8032.35	↓	3.10
YIL057C		24246.39	773.56	↓	31.34
YGL080W		23425.00	3217.81	↓	7.28
YGL072C		16437.52	2652.80	↓	6.20
YHR056C	RSC30	72072.88	57446.85	↓	1.25
YKL054C	VID31	17990.49	38258.80	↑	2.13
YLR311C		7992.40	24164.87	↑	3.02
YJR115W		64690.69	102066.34	↑	1.58
YJL188C	BUD19	7580.28	22325.70	↑	2.95
YKR040C		50934.78	100733.41	↑	1.98
YLR053C		8117.66	20317.34	↑	2.50
YOR121C		59950.94	92470.43	↑	1.54
YNL143C		98911.28	110534.34	↑	1.12
YOR131C		7941.55	22353.72	↑	2.81
YNL338W		21800.45	38777.28	↑	1.78
YNL179C		13729.36	39516.53	↑	2.88
YOL150C		3408.74	60298.39	↑	17.69



YMR107W		65118.70	10042.46	↓	6.48
YKL065C	YET1	69556.19	12804.88	↓	5.43
YJR096W		21780.37	10655.13	↓	2.04
YJL161W		16468.73	2618.26	↓	6.29
YML128C	MSC1	80130.20	13795.84	↓	5.81
YMR251W		26879.95	417.36	↓	64.41
YMR173W-A		110104.98	61951.23	↓	1.78
YPL201C		17913.32	5018.97	↓	3.57
YOR285W		64074.73	29749.43	↓	2.15
YOR286W		13458.08	733.06	↓	18.36
<i>Cellular role: Cell wall maintenance</i>					
YKR076W	ECM4	2674.15	13040.04	↑	4.88
YLR390W	ECM19	5472.05	15145.85	↑	2.77
<i>Cellular role: Membrane fusion</i>					
YHR138C		19921.35	3707.57	↓	5.37
<i>Cellular role: Vesicular transport</i>					
YHR161C	YAP180A	13086.35	30160.90	↑	2.30
YPL085W	SEC16	6668.57	15206.49	↑	2.28
YKL196C	YKT6	18933.84	2890.07	↓	6.55
YPR028W	YIP2	25434.34	2049.47	↓	12.41
<i>Cellular role: DNA repair/recombination</i>					
YDL059C	RAD59	1948.61	13089.13	↑	6.72
<i>Cellular role: DNA synthesis</i>					
YEL032W	MCM3	23422.85	44327.48	↑	1.89
<i>Cellular role: Amino acid metabolism</i>					
YIL074C	SER33	3978.42	16702.66	↑	4.20
YGR155W	CYS4	4184.59	19270.89	↑	4.61
<i>Cellular role: Fatty acid metabolism</i>					
YHR179W	OYE2	2291.36	40274.02	↑	17.58
<i>Cellular role: Protein translocation</i>					
YNL131W	TOM22	16287.21	1679.78	↓	9.70
<i>Cellular role: Small molecule transport</i>					
YDR276C	SNA1	21148.46	1580.68	↓	13.38
YOR267C	HRK1	62689.30	110516.24	↑	1.76
YHR039-C	VMA10	60107.90	8490.93	↓	7.08
YOR382W	FIT2	6780.82	27236.15	↑	4.02

**Table 3: Overview of the differentially expressed genes after 1h Bax expression****Comparison: INVSc1 YlpUTL versus INVSc1 YlpUTyLB**

DRF	Gene	Normalised intensities		Up/down	Q-value
		UTL	UTyLB		
Cellular role : Polymerase II transcription					
YDR145W	TAF61	20729.58	57376.27	↑	2.77
YDR216W	ADR1	5925.91	18459.00	↑	3.11
YBR112C	CYC8	50186.77	64511.50	↑	1.29
YMR043W	MCM1	21011.54	53700.49	↑	2.56
YPL089C	RLM1	23440.54	64284.32	↑	2.74
YOR372C	NDD1	26412.58	50804.99	↑	1.92
Cellular role : Cell cycle control					
YBR133C	HSL7	18761.64	53238.86	↑	2.84
Cellular role : Cell polarity					
YBL085W	BOI1	37895.40	57761.52	↑	1.52
Cellular role : Chromatine structure					
YDR224C	HTB1	13661.40	55656.34	↑	4.07
Cellular role: Energy generation					
YGR183C	QCR9	23181.54	81865.40	↑	3.53
YLR294C		5054.57	28994.72	↑	5.74
YKL150W	MCR1	43663.07	60593.16	↑	1.39
YMR256C	COX7	7606.58	28801.54	↑	3.79
YOL126C	MDH2	34144.61	65326.97	↑	1.91
YLR327C		97415.94	101651.17	↑	1.04
Cellular role: Vesicular transport					
YHR161C	YAP180A	11602.81	34695.20	↑	2.99
YLR206W	ENT2	14439.24	34621.70	↑	2.40
Cellular role: Carbohydrate metabolism					
YDR342C	HXT7	65273.56	22231.06	↓	2.94
YDR343C	HXT6	43572.28	6075.38	↓	7.17
YDR345C	HXT3	76352.52	40296.00	↓	1.89
YGR192C	TDH3	38472.30	14145.84	↓	2.72
YKR097W	PCK1	22919.81	38225.98	↑	1.67
YOR374W	ALD4	33711.37	2607.43	↓	12.93
Cellular role: Signal transduction					
YER177W	BMH1	16298.14	31748.91	↑	1.95
YDR099W	BMH2	50572.45	65123.58	↑	1.29
Cellular role: Cell wall maintenance					
YLR110C	CCW12	102525.29	11230.41	↓	9.13
Cellular role: Protein modification/degradation					
YOR261C	RPN8	12575.49	32568.47	↑	2.59
Cellular role: Cell stress					
YHR053C	CUP1A	32531.53	63579.94	↑	1.95
YHR055C	CUP1B	27939.92	65142.82	↑	2.33
YMR173W	DDR48	38338.83	60514.70	↑	1.58
YOR031W	CRS5	2922.32	23848.60	↑	8.16

YLR109W	AHP1	43067.08	6302.46	↓	6.83
Cellular role: Unknown					
YBL081W		82476.13	44279.86	↑	1.86
YBL109W		22998.63	63428.23	↑	2.76
YDR366C		14599.17	46494.73	↑	3.18
YDR154C		21296.57	56534.93	↑	2.65
YGR236C	SPG1	17717.80	64439.96	↑	3.64
YHR056C	RSC30	27020.16	65110.42	↑	2.41
YGR182C		8171.02	34669.96	↑	4.24
YDR544C		14797.70	37704.91	↑	2.55
YHR162W		13836.79	33381.64	↑	2.41
YGR243W		30829.66	59765.39	↑	1.94
YBR050C	REG2	14008.24	29603.16	↑	2.11
YEL071W	DLD3	19487.41	35273.39	↑	1.81
YDR133C		83074.54	62986.96	↓	1.32
YDR134C		83111.03	16839.53	↓	4.94
YHL021C		46028.06	8577.00	↓	5.37
YKL054C	VID31	28018.46	66537.91	↑	2.37
YLR311C		7803.52	31160.73	↑	3.99
YMR107W		13453.15	78850.98	↑	5.86
YKL066W		8751.84	24129.32	↑	2.76
YMR173W-A		38338.83	60514.70	↑	1.58
YML053C		23670.86	66254.48	↑	2.80
YOR121C		17039.58	58016.58	↑	3.40
YOL106W		19917.67	69853.66	↑	3.51
YNL338W		17864.90	49911.08	↑	2.79
YJR115W		84858.02	98161.71	↑	1.16
Cellular role: Small molecule transport					
YOR267C	HRK1	90123.84	96824.51	↑	1.07

**Table 4: Overview of the differentially expressed genes after 2h Bax expression****Comparison: INVSc1 YlpUTL versus INVSc1 YlpUTyLB**

ORF	Gene	Normalised Intensities		Up/Down	Q <sub>1</sub> value
		YLB	YLB		
<b>Cellular role: Protein modification/degradation</b>					
YCL052C	PBN1	5264.22	8175.70	↑	1.55
YDL147W	RPN5	22386.40	47857.67	↑	2.14
YOR261C	RPN8	27349.25	42198.05	↑	1.54
YGR132C	PHB1	5252.03	8459.53	↑	1.61
YBR139W		9458.26	3611.21	↓	2.62
<b>Cellular role : Unknown</b>					
YDR202C	RAV2	7483.71	10089.19	↑	1.35
YBR062C		4893.97	9894.82	↑	2.02
YDR366C		25468.2	59682.92	↑	2.34
YBL109W		24803.62	37444.64	↑	1.51
YDR154C		21166.26	33434.35	↑	1.58
YEL071W	DLD3	34153.85	44083.39	↑	1.29
YGR236C	SPG1	16978.52	31419.12	↑	1.85
YGR182C		30569.31	58805.05	↑	1.92
YDR544C		15937.14	24421.99	↑	1.53
YHR162W		26610.34	33794.73	↑	1.27
YHR056C	RSC30	33372.66	68425.24	↑	2.05
YDR133C		75520.99	62984.59	↓	1.20
YCR010C	ADY2	17240.59	11835.82	↓	1.46
YDR134C		72723.66	9776.23	↓	7.44
YGR069W		65418.73	53767.35	↓	1.22
YIL057C		16510.16	2198.04	↓	7.51
YGL072C		12209.68	6509.91	↓	1.88
YGL080W		22550.76	11525.24	↓	1.96
YLR311C		11095.31	24660.47	↑	2.22
YJR115W		74757.79	103422.48	↑	1.38
YMR099C		7057.15	11477.42	↑	1.63
YMR173W-A		31901.05	48886.91	↑	1.47
YML132W	COS3	24648.97	34895.33	↑	1.42
YKL066W		13581.94	25433.97	↑	1.87
YJL142C		7205.86	11920.21	↑	1.65
YLR346C		6447.57	11569.63	↑	1.79
YLR053C		41161.10	78636.82	↑	1.91
YMR110C		19410.64	29661.23	↑	1.53
YKR075C		19104.57	29948.72	↑	1.57
YOR121C		36492.56	59452.09	↑	1.63

Cellular role : Unknown					
YOL108W		31382.10	76664.72	↑	2.44
YNL338W		24117.93	38981.22	↑	1.62
YNL134C		9617.33	14613.60	↑	1.52
YKL065C	YET1	52422.65	33794.03	↓	1.55
YMR009W		20666.22	9519.29	↓	2.17
YJL144W		10316.92	3122.77	↓	3.30
YML128C	MSC1	584128.13	25434.11	↓	2.29
YNL179C		21938.96	10883.98	↓	2.02
YOL109W	ZEO1	22711.98	6581.11	↓	3.45
YNR002C	FUN34	18241.25	9752.25	↓	1.87
Cellular role: Chromatine structure					
YDR224C	HTB1	25356.73	30827.54	↑	1.22
YBL002W	HTB2	9241.68	14261.54	↑	1.54
YBL003C	HTA2	3453.55	6553.49	↑	1.90
YNL031C	HHT2	13376.02	2348.84	↓	5.69
Cellular role: Polymerase II transcription					
YBR289W	SNF5	59542.27	65885.13	↑	1.11
YDR073W	SNF11	12190.01	23088.03	↑	1.89
YMR043W	MCM1	66457.16	77022.05	↑	1.16
YPL089C	RLM1	49844.99	60624.28	↑	1.22
Cellular role : Signal transduction					
YDR099W	BMH2	55902.13	73874.51	↑	1.32
Cellular role: Cell stress					
YBL064C	PRX1	11203.87	14815.42	↑	1.32
YBR101C		25016.27	35781.64	↑	1.43
YLR043C	TRX1	10864.53	3912.03	↓	2.78
YGR209C	TRX2	30492.33	37829.20	↑	1.24
YER103W	SSA4	8763.38	15799.18	↑	1.80
YHR055C	CUP1B	18824.43	77613.05	↑	4.12
YHR053C	CUP1A	32726.62	63536.72	↑	1.94
YDR256C	CTA1	9614.29	4232.17	↓	2.27
YCR021C	HSP30	8090.05	3604.78	↓	2.24
YCL035C	GRX1	28437.57	12843.99	↓	2.21
YGR086C		36796.12	24272.57	↓	1.52
YFL014W	HSP12	61868.64	23288.19	↓	2.66
YOR031W	CRS5	6015.69	14519.12	↑	2.41
YMR251W-A	HOR7	17731.14	4231.39	↓	4.19
YOR120W	GCY1	114252.98	78052.05	↓	1.46
Cellular role: Protein synthesis					
YAL003W	EFB1	3044.80	5772.68	↑	1.90
YOL127W	RPL25	6266.96	12055.41	↑	1.92
YHR010W	RPL27	4057.16	10856.34	↑	2.68
YLR325C	RPL38	5401.85	12955.89	↑	2.40
YJL189W	RPL39	2044.64	8010.67	↑	3.92
YIL148W	RPL40A	5052.35	11595.54	↑	2.30
YKR094C	RPL40B	3994.57	10011.13	↑	2.54
YOL139C	CDC33	4132.18	8956.14	↑	2.17

Cellular role : Protein folding					
YLR216C	CPR6	20353.43	32713.37	↑	1.61
YKL117W	SBA1	11144.25	1500.56	↓	7.43
Cellular role: Vesicular transport					
YCR009C	RVS161	5350.32	9780.92	↑	1.83
YHR161C	YAP180A	25136.63	32461.67	↑	1.29
YBL078C	AUT7	16528.91	9843.25	↓	1.68
Cellular role : Carbohydrate metabolism					
YBL058W	SHP1	4626.50	8179.94	↑	1.77
YBR149W	ARA1	30706.41	9637.76	↓	3.19
YDR178W	SDH4	14880.91	6237.35	↓	2.39
YHR094C	HXT1	30389.99	18383.00	↓	1.65
YMR011W	HXT2	39524.90	21221.96	↓	1.86
YDR345C	HXT3	77025.40	56749.40	↓	1.36
YDR343C	HXT6	73149.70	8676.17	↓	8.43
YDR342C	HXT7	75331.76	27052.43	↓	2.78
YKL060C	FBA1	16273.54	21323.23	↑	1.31
Cellular role : Cell cycle control					
YBR133C	HSL7	32903	41964.32	↑	1.28
Cellular role : Energy generation					
YMR256C	COX7	18558.01	40422.91	↑	2.18
YML129C	COX14	11418.54	21798.88	↑	1.91
YFR033C	QCR6	9159.48	13398.67	↑	1.46
YDR529C	QCR7	24821.75	16556.87	↓	1.50
YJL166W	QCR8	15554.30	24509.26	↑	1.58
YHR001W-A	QCR10	12416.35	23465.31	↑	1.89
YBR039W	ATP3	11709.79	3088.19	↓	3.79
YPL078C	ATP4	11325.64	13769.72	↑	1.22
YPL271W	ATP15	3261.75	7839.05	↑	2.40
YLR327C		51742.90	128511.27	↑	2.48
YLR294C		15832.61	38544.44	↑	2.43
YAL060W	FUN49	11792.72	5778.91	↓	2.04
Cellular role: Small molecule transport					
YDR276C	SNA1	19337.39	12392.29	↓	1.56
YGR197C	SNG1	4766.18	10484.09	↑	2.20
YHR039C-B	VMA10	21190.93	10592.98	↓	2.00
YOR267C	HRK1	111849.17	101339.10	↓	1.10
Cellular role: RNA processing					
YGR250C		8709.92	17358.43	↑	1.99
Cellular role : Cell wall maintenance					
YER150W	SPI1	55592.73	22403.59	↓	2.48
YLR110C	CCW12	35147.41	5786.88	↓	6.07
Cellular role : Cell polarity					
YOR122C	PFY1	14459.45	20176.41	↑	1.40
Cellular role : Amino acid metabolism					
YPR035W	GLN1	20894.14	7522.05	↓	2.78

**Table 5:** Overview of the differentially expressed genes after 3h Bax expression**Comparison: INVSc1 YlpUTL versus INVSc1 YlpUTyLB**

ORF	Gene	Normalised intensities YTL	Normalised intensities YLB	Up/down	Q-value
<i>Cellular role : Cell cycle control</i>					
YBR133C	HSL7	63562.10	43191.28	↓	1.47
<i>Cellular role : Cell polarity</i>					
YBL085W	BOI1	32734.79	23497.41	↓	1.39
<i>Cellular role : Chromatine structure</i>					
YDR545W	YRF1-1	20111.51	11479.67	↓	1.75
<i>Cellular role: Energy generation</i>					
YCR005C	CIT2	11882.42	25632.94	↑	2.16
YGR183C	QCR9	74474.20	11510.99	↓	6.47
YOL126C	MDH2	55984.88	17978.10	↓	3.11
<i>Cellular role: Carbohydrate metabolism</i>					
YBR019C	GAL10	3092.50	15697.54	↑	5.08
YDR345C	HXT3	14086.41	25657.66	↑	1.82
YKR097W	PCK1	50736.44	20858.02	↓	2.43
<i>Cellular role: Signal transduction</i>					
YDR099W	BMH2	63285.16	56028.91	↓	1.13
<i>Cellular role: Protein synthesis</i>					
YHR010W	RPL27A	23254.90	7217.14	↓	3.22
YLR325C	RPL38	26725.96	9121.29	↓	2.93
<i>Cellular role: Cell stress</i>					
YFL014W	HSP12	40848.44	69781.91	↑	1.71
YHR053C	CUP1A	20399.10	65037.14	↑	3.19
YHR055C	CUP1B	21763.09	64594.58	↑	2.97
YMR173W	DDR48	75407.16	36354.37	↓	2.07
YOL052C-A	DDR2	20479.72	33702.23	↑	1.65
<i>Cellular role: Unknown</i>					
YIL057C		7602.78	24104.02	↑	3.17
YHR056C	RSC30	41473.41	64809.08	↑	1.56
YDR544C		55075.67	29731.72	↓	1.85
YKR040C		48049.71	59649.47	↑	1.24
YNL338W		86107.91	30045.62	↓	2.87
YJR115W		74889.58	81238.98	↓	1.08
YBL109W		64754.79	57185.99	↓	1.13
YMR173W-A		75407.16	36354.37	↓	2.07

**Table 6: Overview of the differentially expressed genes after 6h Bax expression****Comparison: INVSc1 YlpUTL versus INVSc1 YlpUTyLB**

OFF	Gene	Normalised intensities		Up/down	Q value
		INVSc1 YlpUTL	INVSc1 YlpUTyLB		
<i>Cellular role: Cell stress</i>					
YDR171W	HSP42	13484.04	27183.07	↑	2.02
YFL014W	HSP12	41197.12	29081.08	↓	1.42
YDR513W	TTR1	19985.22	12935.62	↓	1.54
YCL035C	GRX1	31735.39	12930.71	↓	2.45
YGR209C	TRX2	54455.65	47569.21	↓	1.14
YHR053C	CUP1A	81488.84	15289.39	↓	5.33
YHR055C	CUP1B	81278.95	20031.69	↓	4.06
YMR251W-A	HOR7	18824.54	5914.28	↓	3.18
<i>Cellular role: Signal transduction</i>					
YDR099W	BMH2	29412.99	58598.42	↑	1.99
<i>Cellular role: Protein synthesis</i>					
YGL147C	RPL9A	13655.66	1585.97	↓	8.61
YGR085C	RPL11B	27465.15	3791.35	↓	7.24
YDR418W	RPL12B	14417.77	1555.24	↓	9.27
YLR029C	RPL15A	37122.11	9321.81	↓	3.98
YOR312C	RPL20B	50334.94	5706.59	↓	8.82
YBR191W	RPL21A	21740.90	2571.30	↓	8.46
YPL079W	RPL21B	31059.43	5023.61	↓	6.18
YOL127W	RPL25	75971.72	11749.17	↓	6.47
YHR010W	RPL27A	45716.64	8096.40	↓	5.65
YDR471W	RPL27B	14636.79	2613.40	↓	5.60
YDL075W	RPL31A	11969.47	2611.53	↓	4.58
YBL092W	RPL32	7872.80	857.85	↓	9.18
YDL191W	RPL35A	28582.59	6046.25	↓	4.73
YDL136W	RPL35B	25433.49	5064.51	↓	5.02
YLR325C	RPL38	48051.23	8217.18	↓	5.85
YIL148W	RPL40A	47028.95	9543.85	↓	4.93
YKR094C	RPL40B	39900.50	5957.78	↓	6.70
YHR141C	RPL42B	10163.88	937.21	↓	10.84
YML063W	RPS1B	15916.48	1144.54	↓	13.91
YGL123W	RPS2	12505.56	2243.26	↓	5.57
YOR096W	RPS7A	24164.37	3223.60	↓	7.50
YBL072C	RPS8A	17198.50	3233.30	↓	5.32
YER102W	RPS8B	16234.83	1791.18	↓	9.06
YBR189W	RPS9B	10075.22	2150.89	↓	4.68
YOR293W	RPS10A	51787.23	12110.74	↓	4.28
YDR064W	RPS13	9736.57	1587.67	↓	6.13
YDR450W	RPS18A	37913.71	5674.60	↓	6.68
YML026C	RPS18B	14458.01	2027.28	↓	7.13
YKL156W	RPS27A	23725.18	11117.26	↓	2.13
YLR167W	RPS31	38648.54	2611.97	↓	14.80
YJL138C	TIF2	20154.61	7264.66	↓	2.77
<i>Cellular role: Energy metabolism</i>					
YGR183C	QCR9	57357.59	80447.53	↑	1.40
YDL004W	ATP16	25047.95	10988.85	↓	2.28
YKL150W	MCR1	50931.46	37076.83	↓	1.37



YLR038C	COX12	39506.06	29534.70	↓	1.34
Cellular role: Unknown					
YDR442W		14654.61	2242.42	↓	6.54
YDR134C		17025.59	10561.72	↓	1.61
YHR056C	RSC30	81350.52	31447.10	↓	2.59
YKR040C		48390.21	90125.88	↑	1.86
YLR414C		13463.40	8085.92	↓	1.67
YLR312C		25589.67	16184.57	↓	1.58
YJL188C	BUD19	22074.09	4526.39	↓	4.88
YOR285W		75099.98	61896.00	↓	1.21
YOL109W	ZEO1	66287.15	35502.43	↓	1.87
Cellular role: Chromatine structure					
YBR009C	HHF1	11173.15	5416.74	↓	2.06
YNL030W	HHF2	31366.74	20132.23	↓	1.56
Cellular role: Nucleotide metabolism					
YDR399W	HPT1	13339.03	5333.81	↓	2.50
Cellular role: Polymerase II transcription					
YEL009C	GCN4	34617.98	20798.63	↓	1.66
YPL037C	EGD1	17862.37	8229.01	↓	2.17
Cellular role: Vesicular transport					
YBL078C	AUT7	42661.70	32333.01	↓	1.32
YOR327C	SNC2	22716.56	13704.48	↓	1.66
Cellular role : Small molecule transport					
YHR039C-B	VMA10	44429.30	23826.51	↓	1.86
Cellular role : Cell wall maintenance					
YKL097W-A	CWP2	13529.93	1617.20	↓	8.37
Cellular role: Carbohydrate metabolism					
YKL060C	FBA1	33329.74	10367.82	↓	3.21

**Table 7:**

Sequence ID NO	ORF	GENE	30 min	1h	2h	3h	6h
SEQ ID NO 17	YAL003W	EFB1			1.90		
SEQ ID NO 19	YAL060W	FUN49			-2.00		
SEQ ID NO 21	YBL002W	HTB2	-4.69		1.54		
SEQ ID NO 23	YBL058W	SHF1			1.77		
SEQ ID NO 25	YBL064C	PRX1	1.90		1.32		
SEQ ID NO 27	YBL072C	RPS8A					-5.32
SEQ ID NO 29	YBL081W		1.01	1.86			
SEQ ID NO 31	YBL085W	BOI1	2.42	1.52		-1.39	
SEQ ID NO 33	YBL092W	RPL32			2.76		-9.18
SEQ ID NO 35	YBL109W		1.89	2.76	1.51	-1.13	
SEQ ID NO 37	YBR009C	HHF1	-3.99				-2.06
SEQ ID NO 39	YBR019C	GAL10				5.08	
SEQ ID NO 41	YBR039W	ATP3			-3.70		
SEQ ID NO 43	YBR050C	REG2	3.07	2.11			
SEQ ID NO 45	YBR062C				2.02		
SEQ ID NO 47	YBR089C-A	NHP6B	-3.60				
SEQ ID NO 49	YBR101C				1.43		
SEQ ID NO 51	YBR112C	SSN6	2.45	1.29			
SEQ ID NO 53	YBR133C	HSL7	2.00	2.84	1.28	-1.47	
SEQ ID NO 55	YBR139W				-2.60		
SEQ ID NO 57	YBR149W	ARA1	-3.70		-3.11		
SEQ ID NO 59	YBR189W	RPS9B					-4.68
SEQ ID NO 61	YBR191W	RPL21A					-8.46
SEQ ID NO 63	YBR289W	SNF5	2.18		1.11		
SEQ ID NO 65	YCL035C	GRX1	-6.40		-2.20		-2.45
SEQ ID NO 67	YCL052C	PBN1			1.55		
SEQ ID NO 69	YCR004C	YCP4	4.09				
SEQ ID NO 71	YCR005C	CIT2				2.16	
SEQ ID NO 73	YCR009C	RVS161			1.83		
SEQ ID NO 75	YCR010C				-1.40		
SEQ ID NO 77	YCR013C		3.80				
SEQ ID NO 79	YCR021C	HSP30			-2.20		
SEQ ID NO 81	YDL004W	ATP16	-12.16				-2.28
SEQ ID NO 83	YDL059C	RAD59	6.72				
SEQ ID NO 85	YDL075W	RPL31A					-4.58
SEQ ID NO 87	YDL147W	RPN5	1.66		2.14		
SEQ ID NO 89	YDR064W	RPS13					-6.13
SEQ ID NO 91	YDR073W	SNF11			1.89		
SEQ ID NO 93	YDR099W	BMH2	1.86	1.29	1.32	-1.13	1.99
SEQ ID NO 95	YDR133C			-1.32	-1.20		
SEQ ID NO 97	YDR134C			-4.94	-7.40		-1.61
SEQ ID NO 99	YDR145W	TAF61	1.89	2.77			
SEQ ID NO 101	YDR154C		3.55	2.65	1.58		
SEQ ID NO 103	YDR171W	HSP42					2.02
SEQ ID NO 105	YDR178W	SDH4			-2.30		
SEQ ID NO 107	YDR202C	RAV2			1.35		
SEQ ID NO 109	YDR216W	ADR1	-3.42	3.11			
SEQ ID NO 111	YDR224C	HTB1	-2.91	4.07	1.22		
SEQ ID NO 113	YDR253C	MET32	2.58				
SEQ ID NO 115	YDR256C	CTA1			-2.20		
SEQ ID NO 117	YDR276C	SNA1	-13.38		-1.50		

Sequence ID NO	ORF	GENE	30 min	1h	2h	3h	6h
SEQ ID NO 119	YDR342C	HXT7	-2.76	-2.94	-2.70		
SEQ ID NO 121	YDR343C	HXT6	-2.40	-7.17	-8.40		
SEQ ID NO 123	YDR345C	HXT3	-22.45	-1.89	-1.30	1.82	
SEQ ID NO 125	YDR366C		1.44	3.18	2.34		
SEQ ID NO 127	YDR377W	ATP17	-19.05				
SEQ ID NO 129	YDR399W	HPT1					-2.50
SEQ ID NO 131	YDR418W	RPL12B					-9.27
SEQ ID NO 133	YDR513W	TTR1	-1.68				-1.54
SEQ ID NO 135	YDR544C		1.99	2.55	1.53	-1.85	
SEQ ID NO 137	YDR545W	YRF1-1				-1.75	
SEQ ID NO 139	YEL009C	GCN4	-5.46				-1.66
SEQ ID NO 697	YEL032W	MCM3	1.89				
SEQ ID NO 141	YEL039C	CYC7	-5.06				
SEQ ID NO 143	YEL071W	DLD3	3.09	1.81	1.29		
SEQ ID NO 145	YER103W	SSA4			1.80		
SEQ ID NO 147	YER112W	USS1	2.46				
SEQ ID NO 149	YER150W	SPI1			-2.40		
SEQ ID NO 151	YER177W	BMH1	1.96	1.95			
SEQ ID NO 153	YFR010W	UBP6	-2.28				
SEQ ID NO 155	YFR033C	QCR6			1.46		
SEQ ID NO 157	YFR052W	RPN12	2.66				
SEQ ID NO 159	YGL072C		-6.20		-1.80		
SEQ ID NO 161	YGL080W		-7.28		-1.90		
SEQ ID NO 163	YGL123W	RPS2					-5.57
SEQ ID NO 165	YGR008C	STF2	-5.83				
SEQ ID NO 167	YGR023W	MTL1	2.67				
SEQ ID NO 169	YGR034W	RPL26B	1.04				
SEQ ID NO 171	YGR069W		1.67		-1.20		
SEQ ID NO 173	YGR070W	ROM1	-2.34				
SEQ ID NO 175	YGR086C				-1.50		
SEQ ID NO 177	YGR132C	PHB1	-2.76		1.61		
SEQ ID NO 179	YGR135W	PRE9	-7.24				
SEQ ID NO 181	YGR155W	CYS4	4.61				
SEQ ID NO 183	YGR192C	TDH3		-2.72			
SEQ ID NO 185	YGR197C	SNG1			2.20		
SEQ ID NO 187	YGR209C	TRX2			1.24		-1.14
SEQ ID NO 189	YGR243W			1.94			
SEQ ID NO 191	YGR250C				1.99		
SEQ ID NO 193	YHL021C			-5.37			
SEQ ID NO 195	YHR001W-A	QCR10			1.89		
SEQ ID NO 197	YHR039C-B	VMA10	-7.08		-2.00		-1.86
SEQ ID NO 199	YHR053C	CUP1A	-1.68	1.95	1.94	3.19	-5.33
SEQ ID NO 201	YHR055C	CUP1B	-2.77	2.33	4.12	2.97	-4.06
SEQ ID NO 203	YHR056C		-1.25	2.41	2.05	1.56	-2.59
SEQ ID NO 205	YHR094C	HXT1	-15.94		-1.60		
SEQ ID NO 207	YHR095W		2.42				
SEQ ID NO 209	YHR138C		-5.37				
SEQ ID NO 211	YHR161C	YAP180A	2.30	2.99	1.29		
SEQ ID NO 213	YHR162W			2.41	1.27		
SEQ ID NO 215	YHR179W	OYE2	17.58				
SEQ ID NO 217	YIL057C		-31.34		-7.50	3.17	
SEQ ID NO 219	YIL074C	SER33	4.20				
SEQ ID NO 221	YIR037W	GPX3	2.77				

Sequence ID NO	ORF	GENE	30 min	1h	2h	3h	6h
SEQ ID NO 223	YJL138C	TIF2					-2.77
SEQ ID NO 225	YJL142C				1.65		
SEQ ID NO 227	YJL144W				-3.30		
SEQ ID NO 229	YJL161W		-6.29				
SEQ ID NO 231	YJL166W	QCR8			1.58		
SEQ ID NO 233	YJR096W		-2.04				
SEQ ID NO 235	YJR115W		1.58	1.16	1.38	-1.08	
SEQ ID NO 237	YKL054C	VID31	2.13	2.37			
SEQ ID NO 239	YKL060C	FBA1			1.31		-3.21
SEQ ID NO 241	YKL065C	YET1	-5.43		-1.55		
SEQ ID NO 243	YKL066W			2.76	1.87		
SEQ ID NO 245	YKL097W-A	CWP2					-8.37
SEQ ID NO 247	YKL117W	SBA1			-7.43		
SEQ ID NO 249	YKL150W	MCR1	-3.43	1.39			-1.37
SEQ ID NO 251	YKL156W	RPS27A					-2.13
SEQ ID NO 253	YKL196C	YKT6	-6.55				
SEQ ID NO 255	YKR040C		1.98			1.24	1.86
SEQ ID NO 257	YKR075C				1.57		
SEQ ID NO 259	YKR076W	ECM4	4.88				
SEQ ID NO 261	YKR092C	SRP40	2.70				
SEQ ID NO 263	YKR097W	PCK1		1.67		-2.43	
SEQ ID NO 265	YLR029C	RPL15A					-3.98
SEQ ID NO 267	YLR038C	COX12	-9.66				-1.34
SEQ ID NO 269	YLR043C	TRX1	-13.13		-2.78		
SEQ ID NO 271	YLR053C		2.50		1.91		
SEQ ID NO 273	YLR109W	AHP1		-6.83			
SEQ ID NO 275	YLR110C			-9.13	-6.07		
SEQ ID NO 277	YLR206W	ENT2		2.40			
SEQ ID NO 279	YLR216C	CPR6	3.24		1.61		
SEQ ID NO 281	YLR294C			5.74	2.43		
SEQ ID NO 283	YLR311C		3.02	3.99	2.22		
SEQ ID NO 285	YLR312C						-1.58
SEQ ID NO 287	YLR327C		-2.10	1.04	2.48		
SEQ ID NO 289	YLR346C				1.79		
SEQ ID NO 291	YLR390W	ECM19	2.77				
SEQ ID NO 293	YLR414C						-1.67
SEQ ID NO 295	YML053C			2.80			
SEQ ID NO 297	YML129C	COX14			1.91		
SEQ ID NO 299	YML132W	COS3			1.42		
SEQ ID NO 301	YMR009W				-2.17		
SEQ ID NO 303	YMR011W	HXT2			-1.86		
SEQ ID NO 305	YMR043W	MCM1	2.15	2.56	1.16		
SEQ ID NO 307	YMR099C				1.63		
SEQ ID NO 309	YMR107W		-6.48	5.86			
SEQ ID NO 311	YMR110C				1.53		
SEQ ID NO 313	YMR173W	DDR48	-3.32	1.58		-2.07	
SEQ ID NO 691	YMR173W-A		-1.78	1.58	1.47	-2.07	
SEQ ID NO 315	YMR251W		-64.41				
SEQ ID NO 317	YMR251W-A	HOR7	-64.41		-4.19		-3.18
SEQ ID NO 319	YMR256C	COX7		3.79	2.18		
SEQ ID NO 321	YMR273C	ZDS1	2.42				
SEQ ID NO 323	YNL030W	HHF2	-3.97				-1.56
SEQ ID NO 325	YNL031C	HHT2			-5.69		

Sequence ID NO	ORF	GENE	30 min	1h	2h	3h	6h
SEQ ID NO 327	YNL112W	DBP2	2.82				
SEQ ID NO 329	YNL131W	TOM22	-9.70				
SEQ ID NO 331	YNL134C				1.52		
SEQ ID NO 333	YNL143C		1.12				
SEQ ID NO 335	YNL179C		2.88		-2.02		
SEQ ID NO 337	YNL338W		1.78	2.79	1.62	-2.87	
SEQ ID NO 339	YNR002C	FUN34			-1.87		
SEQ ID NO 709	YOL052C-A	DDR2				1.65	
SEQ ID NO 341	YOL106W			3.51	2.44		
SEQ ID NO 343	YOL109W	ZEO1			-3.45		-1.87
SEQ ID NO 345	YOL126C	MDH2		1.91		-3.11	
SEQ ID NO 347	YOL139C	CDC33			2.17		
SEQ ID NO 349	YOL150C		17.69				
SEQ ID NO 351	YOL151W	GRE2	9.20				
SEQ ID NO 353	YOR120W	GCY1			-1.46		
SEQ ID NO 355	YOR121C		1.54	3.40	1.63		
SEQ ID NO 357	YOR122C	PFY1			1.40		
SEQ ID NO 359	YOR131C		2.81				
SEQ ID NO 361	YOR261C	RPN8		2.59	1.54		
SEQ ID NO 363	YOR267C		1.76	1.07	-1.10		
SEQ ID NO 365	YOR285W		-2.15				-1.21
SEQ ID NO 367	YOR286W		-18.36				
SEQ ID NO 369	YOR327C	SNC2					-1.66
SEQ ID NO 371	YOR372C	NDD1	2.19	1.92			
SEQ ID NO 373	YOR374W	ALD4		-12.93			
SEQ ID NO 375	YOR382W		4.02				
SEQ ID NO 377	YPL037C	EGD1	-5.83				-2.17
SEQ ID NO 379	YPL078C	ATP4	-4.50		1.22		
SEQ ID NO 381	YPL079W	RPL21B					-6.18
SEQ ID NO 383	YPL085W	SEC16	2.28				
SEQ ID NO 385	YPL089C	RLM1	1.94	2.74	1.22		
SEQ ID NO 387	YPL190C	NAB3	2.80				
SEQ ID NO 389	YPL201C		-3.57				
SEQ ID NO 391	YPL271W	ATP15			2.40		
SEQ ID NO 393	YPR028W	YIP2	-12.41				
SEQ ID NO 395	YPR035W	GLN1			-2.78		

TABLE 8

C. albicans 522 CDS's										S. cerevisiae 11645 CDS's		
aa	codons	frequency: per thousand	total number	codon chosen for		codons used in		frequency: per thousand	total number			
				synthCaBAX gene		wt muBAX gene						
Ala	GCU	30.7	8686	x		6		21.1	118595			
	GCC	12.7	3582			4		12.6	70785			
	GCA	15.4	4357			2		16.2	91018			
	GCG	2	578			1		6.1	34546			
Arg	CGU	5.9	1682			1		6.5	36518			
	CGC	0.7	204			1		2.6	14571			
	CGA	3.5	989			3		3	16957			
	CGG	0.8	220			3		1.7	9801			
	AGA	23.6	6673	x		1		21.3	119672			
	AGG	2.7	769			2		9.3	52057			
Asn	AAU	37.9	10731	x		1		36	202351			
	AAC	18.7	5293			2		24.9	140194			
Asp	GAU	43.6	12323	x		5		37.8	212658			
	GAC	14.7	4152			7		20.4	114451			
Cys	UGU	9.7	2757	x		1		8	44797			
	UGC	1.7	493			1		4.7	26357			
Gln	CAA	35.2	9964	x		1		27.5	154529			
	CAG	6.9	1948			8		12.2	68463			
Glu	GAA	49.5	14001	x		3		45.9	257930			
	GAG	11.5	3252			10		19.1	107568			

TABLE 8 - continued

aa	codons	C. albicans 522 CDS's				S. cerevisiae 11645 CDS's		
		frequency: per thousand	total number	codon chosen for synthCaBAX gene	codons used in wt muBAX gene	frequency: per thousand	total number	
Gly	GGU	33.5	9492	x	2	23.9	134515	
	GGC	4.5	1281		7	9.7	54629	
	GGA	13.7	3874		2	10.9	61481	
His	GGG	7.7	2182		8	6	33627	
	CAU	14	3964			13.7	77260	
	CAC	5.8	1642			7.8	43878	
Ile	AUU	39.9	11281	x	3	30.2	169795	
	AUC	14.2	4005		7	17.1	96126	
	AUA	12.3	3478			17.8	100027	
Leu	UUA	1	295	x		26.3	148133	
	UUG	36.1	10204			27.1	152590	
	CUU	9.8	2777			12.2	68479	
	CUC	2.5	694			5.4	30218	
	CUA	4	1133			13.4	75414	
Lys	AAA	48.6	13760	x	2	42.1	236746	
	AAG	19.4	5477		6	30.8	173174	
Met	AUG	18.4	5219	x	8	20.9	117410	
Phe	UUU	28.6	8100	x	4	26	146355	
	UUC	15.9	4486		7	18.2	102389	

TABLE 8 - continued

C. albicans 522 CDS's					S. cerevisiae 11645 CDS's		
aa	codons	frequency: per thousand	total number	codon chosen for synthCaBAX gene	codons used in wt muBAX gene	frequency: per thousand	total number
Pro	CCU	13.2	3722		1	13.6	76366
	CCC	3.6	1027		5	6.8	38247
	CCA	26.6	7531	x		18.2	102277
	CCG	2.4	686		1	5.3	29758
Ser	CUG	3.1	875		9	10.4	58583
	UCU	23.3	6595	x	1	23.6	132608
	UCC	10.3	2928		4	14.2	79928
	UCA	24.6	6955			18.8	105570
	UCG	6.5	1836		1	8.6	48186
	AGU	23.6	6673			14.2	79649
	AGC	4.5	1269		5	9.7	54330
Thr	ACU	30.7	8689		1	20.2	113634
	ACC	13.9	3928	x	8	12.6	70777
	ACA	17.4	4928		5	17.7	99759
	ACG	3.6	1019		1	8	44817
Trp	UGG	11	3115	x	6	10.3	58092
Tyr	UAU	24	6782			18.8	105489
	UAC	11.6	3280	x	2	14.7	82483
Val	GUU	33.2	9391		1	22	123726
	GUC	10.3	2927	x	3	11.6	65203
	GUA	8	2265			11.8	66100
	GUG	10	2842		7	10.7	60033



**TABLE 9: Regulation of 23 selected "Bax-specific" functions**

<i>Cellular role: Amino-acid metabolism</i>					
ORF	Gene	Control	Bax	H2O2	B vs C
YOR302W	YOR302W	11541.92	26806.35	8895.74	2.32
<i>Cellular role: Cell stress</i>					
ORF	Gene	Control	Bax	H2O2	B vs C
YML028W	TSA1	12889.91	2166.45	11327.36	0.17
<i>Cellular role: Chromatin/chromosome structure</i>					
ORF	Gene	Control	Bax	H2O2	B vs C
YBR009C	HHF1	2149.69	8655.43	2909.14	4.03
YDR224C	HTB1	13661.40	55656.34	18829.27	4.07
YNL030W	HHF2	8676.99	19603.93	4732.39	2.26
<i>Cellular role: Energy generation</i>					
ORF	Gene	Control	Bax	H2O2	B vs C
YBL099W	ATP1	2728.21	8786.71	1644.48	3.22
YGR183C	QCR9	23181.54	81865.40	24053.00	3.53
YJL166W	QCR8	5296.71	18093.93	5001.65	3.42
YLR038C	COX12	7336.65	19935.69	5118.43	2.72
<i>Cellular role: Signal transduction</i>					
ORF	Gene	Control	Bax	H2O2	B vs C
YHR135C	YCK1	3939.64	8358.11	3707.17	2.12
YOL100W	PKH2	2218.45	6088.96	2619.31	2.74
<i>Cellular role: Transcription factor</i>					
ORF	Gene	Control	Bax	H2O2	B vs C
YDR216W	ADR1	5925.91	18459.00	6434.43	3.11
<i>Cellular role: Unknown</i>					
ORF	Gene	Control	Bax	H2O2	B vs C
YDR504C	YDR504C	2741.47	6908.49	2839.62	2.52
YGR146C	YGR146C	2099.74	5616.94	1303.89	2.68
YGR236C	SPG1	17717.80	64439.96	24134.29	3.64
YHR138C	YHR138C	6218.30	14817.41	5220.50	2.38
YJL142C	YJL142C	6988.27	16006.02	6740.46	2.29
YKL123W	YKL123W	2826.82	5952.34	2766.04	2.11
YLR414C	YLR414C	4510.80	11867.69	3531.27	2.63
YMR107W	YMR107W	13453.15	78850.98	17417.00	5.86
YOL099C	YOL099C	3690.45	11604.72	5454.15	3.14
YPL201C	YPL201C	15960.14	33633.74	7449.66	2.11
YJL060W	YJL060W	8798.50	2406.39	6356.11	0.27

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**CLAIMS**

1. An isolated nucleic acid representing a synthetic *BAX*-gene selected from the group consisting of:
  - 5 a) a nucleic acid comprising a sequence as represented by SEQ ID NO 1,
  - b) a nucleic acid comprising a fragment of a sequence of SEQ ID NO 1 and encoding a functional fragment of the sequence represented by SEQ ID NO 2,
  - c) a nucleic acid comprising a sequence as represented in any of SEQ ID NOs 3 to 10,
  - d) a nucleic acid which is more than 75 % identical to the nucleic acid as represented by  
10 SEQ ID NO 1, or to a nucleic acid according to the nucleic acid as defined in b) or c),  
and,
  - e) a nucleic acid as defined in any one of (a) to (i) interrupted by intervening DNA sequences,  
or a nucleic acid representing the complement of any of said nucleic acids as defined in (a)  
15 to (d).
2. An isolated nucleic acid according to claim 1 which is DNA, cDNA, genomic DNA, synthetic DNA, or RNA wherein T is replaced by U.
3. A vector comprising a nucleic acid as defined in claim 1 or 2.
4. A vector according to claim 3 which is an expression vector wherein said nucleic acid  
20 sequence is operably linked to one or more control sequences allowing the expression in prokaryotic and/or eukaryotic host cells.
5. An expression vector according to claim 4 which comprises an inducible promoter
6. An expression vector according to claim 4 or 5 which comprises a sequence encoding a reporter molecule.
- 25 7. A vector according to any of claims 3 to 6 for inducing programmed cell death in *Candida* spp.
8. A host cell transformed, transfected or infected with a vector according to any of claims 3 to 7.
9. A host cell of claim 8 which is a bacterial, yeast or fungal cell.
- 30 10. A host cell according to claim 8 or 9 wherein said cell is a *Candida* spp. cell.
11. A genetically modified yeast or fungal cell according to claim 9 wherein said modification results in the onset of at least one pathway eventually leading to programmed cell death.

12. A genetically modified *Candida* spp. cell according to claim 10 wherein said modification results in the onset of at least one pathway eventually leading to programmed cell death.
13. A method for identifying Bax-resistant yeast or fungi comprising the steps of:
- a) providing (a) genetically modified yeast or fungi according to claim 11,
  - 5 b) treating said genetically modified yeast or fungi with a mutagen,
  - c) isolating resistant yeast or fungal cells, and,
  - d) optionally identifying and/or characterizing mutated genes in said resistant yeast or fungal cells.
14. A method for identifying *Candida* spp. sequences which are differentially expressed in a pathway eventually leading to programmed cell death using a nucleic acid as defined in claim 1 or 2, a vector according to any of claims 3 to 7 or a genetically modified host cell according to claim 10.
15. A method for obtaining and identifying *Candida* spp. sequences involved in a pathway eventually leading to programmed cell death comprising the steps of:
- 15 a) providing a two hybrid system wherein a polypeptide encoded by a nucleic acid according to claim 1 or a vector according to any of claims 3 to 7 as a bait and a *Candida* spp. cDNA library as a prey are expressed,
  - b) detecting an interaction between said polypeptide and a *Candida* spp. polypeptide encoded by said cDNA library, and,
  - 20 c) identifying said *Candida* spp. polypeptide or cDNA.
16. A method for identifying inhibitors (or inhibitor sequences) of Bax-induced cell death comprising the steps of:
- a) providing a genetically modified organism according to claim 10,
  - b) expressing a cDNA library in said genetically modified organism, and,
  - 25 c) identifying a polypeptide or a cDNA which expression has a beneficial effect on the survival and/or growth of said genetically modified organism.
17. A method according to claim 16 wherein said genetically modified organism is a *Candida* spp.
- 30 18. An isolated *Candida* spp. nucleic acid identifiable by any of the methods of any of claims 12 to 17.
19. An isolated *Candida* spp. nucleic acid according to claim 18 selected from:

- (a) a nucleic acid encoding a protein having an amino acid sequence as represented in any of SEQ ID NOs 434, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 718, 720, 722, 724, 726, 728, 730 and 732, or encoding a functional equivalent, derivative or bioprecursor of said protein,
- b) a nucleic acid encoding a protein having an amino acid sequence which is more than 70 % similar to any of the amino acid sequences represented in SEQ ID NOs 434, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 718, 720, 722, 724, 726, 728, 730 and 732,
- c) a nucleic acid encoding a protein having an amino acid sequence which is more than 70 % identical to any of the amino acid sequences represented in SEQ ID NOs 434, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 718, 720, 722, 724, 726, 728, 730 and 732,

- 5 d) a nucleic acid comprising a sequence as represented in any of SEQ ID NOs 433, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481, 483, 485, 487, 489, 491, 493, 495, 497, 499, 501, 503, 505, 507, 509, 511, 513, 515, 517, 519, 521, 523, 525, 527, 529, 531, 533, 535, 537, 539, 541, 543, 545, 547, 549, 551, 553, 555, 557, 559, 561, 563, 565, 567, 569, 571, 573, 575, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, 627, 629, 631, 633, 635, 637, 639, 641, 643, 645, 647, 649, 651, 653, 655, 657, 659, 661, 663, 665, 667, 669, 671, 673, 687, 717, 719, 721, 723, 725, 727, 729 and 731,
- 10 e) a nucleic acid which is more than 70 % identical to any of the nucleic acid sequences as represented by any of SEQ ID NOs 433, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481, 483, 485, 487, 489, 491, 493, 495, 497, 499, 501, 503, 505, 507, 509, 511, 513, 515, 517, 519, 521, 523, 525, 527, 529, 531, 533, 535, 537, 539, 541, 543, 545, 547, 549, 551, 553, 555, 557, 559, 561, 563, 565, 567, 569, 571, 573, 575, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, 627, 629, 631, 633, 635, 637, 639, 641, 643, 645, 647, 649, 651, 653, 655, 657, 659, 661, 663, 665, 667, 669, 671, 673, 687, 717, 719, 721, 723, 725, 727, 729 and 731, and
- 15 f) a nucleic acid encoding a functional fragment of any of the nucleic acid sequences as specified in any of a) to d),
- 20 20. An isolated nucleic acid as defined in according to claim 19 which is DNA, cDNA, genomic DNA, synthetic DNA, or RNA wherein T is replaced by U.
- 25 21. An isolated nucleic acid capable of selectively hybridizing to a nucleic acid as defined in any of claims 18 to 20 or the complement thereof.
22. An antisense molecule comprising a nucleic acid capable of selectively hybridizing to a nucleic acid as defined in any of claims 18 to 21.
- 30 23. A nucleic acid probe which selectively hybridises with any of the nucleic acid molecules as defined in claim 18 or 19.
24. A nucleic acid primer which selectively amplifies any of the nucleic acid molecules defined in claim 18 or 19.



25. An expression vector comprising a nucleic acid according to any of claims 18 to 22.
26. An expression vector according to claim 25 which is an expression vector wherein said nucleic acid is operably linked to one or more control sequences allowing the expression in prokaryotic and/or eukaryotic host cells.
- 5 27. An expression vector according to claim 25 or 26 which comprises an inducible promoter.
28. An expression vector according to any of claims 25 to 27 which comprises a sequence encoding a reporter molecule.
29. A host cell transformed, transfected or infected with the vector of any of claims 25 to 28.
30. An isolated nucleic acid according to any of claims 18 to 22 for use as a medicament.
- 10 31. An isolated polypeptide which is involved in a pathway for programmed cell death of *Candida* spp. and encoded by a nucleic acid as defined in claim 18 or 19, wherein said polypeptide is selected from:
- (a) a polypeptide having an amino acid sequence as represented in any of SEQ ID NOs
- 15 434, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590,
- 20 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 718, 720, 722, 724, 726, 728, 730 and 732, or encoding a functional equivalent, derivative or bioprecursor of said protein;
- (b) a polypeptide having an amino acid sequence which is more than 70% similar to any of
- 25 the amino acid sequences as represented by any of SEQ ID NOs 434, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540,
- 30 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632,

634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 718, 720, 722, 724, 726, 728, 730 and 732,

- (c) a polypeptide having an amino acid sequence which is more than 70% identical to any of the amino acid sequences as represented by any of SEQ ID NOs 434, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 718, 720, 722, 724, 726, 728, 730 and 732, and
- (d) a functional fragment of any of said polypeptides as defined in a) to c).

32. A polypeptide according to claim 31 for use as a medicament.
33. An antibody capable of specifically binding to a polypeptide of claim 30 or to a specific epitope of said polypeptide.
34. An antibody according to claim 33 for use as a medicament.
35. A pharmaceutical composition comprising an antibody of claim 33 or 34.
36. Use of an isolated nucleic acid encoding a polypeptide which is involved in a pathway eventually leading to programmed cell death of yeast or fungi and which nucleic acid is selected from:
- (a) a nucleic acid encoding a protein having an amino acid sequence as represented in any of SEQ ID NOs 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 324, 326, 328, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396,

398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 692, 694, 696, 698, 700, 702, 704, 706, 708, 710, 712, 714, 716, 718, 720, 722, 724, 726, 728, 730 and 732, or encoding a functional equivalent, derivative or bioprecursor of said protein;

(b) a nucleic acid encoding a protein having an amino acid sequence which is more than 70% similar to any of the amino acid sequences as represented by any of SEQ ID NOs 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 299, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 324, 326, 328, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 692, 694, 696, 698, 700, 702, 704, 706, 708, 710, 712, 714, 716, 718, 720, 722, 724, 726, 728, 730 and 732,

- (c) a nucleic acid encoding a protein having an amino acid sequence which is more than 70% identical to any of the amino acid sequences as represented by any of SEQ ID NOs 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 299, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 324, 326, 328, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 692, 694, 696, 698, 700, 702, 704, 706, 708, 710, 712, 714, 716, 718, 720, 722, 724, 726, 728, 730 and 732,
- (d) a nucleic acid comprising a sequence as represented in any of SEQ ID NOs 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415,

- 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481, 483, 485, 487, 489, 491, 493, 495, 497, 499, 501, 503, 505, 507, 509, 511, 513, 515, 517, 519, 521, 523, 525, 527, 529, 531, 533, 535, 537, 539, 541, 543, 545, 547, 549, 551, 553, 555, 557, 559, 561, 563, 565, 567, 569, 571, 573, 575, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, 627, 629, 631, 633, 635, 637, 639, 641, 643, 645, 647, 649, 651, 653, 655, 657, 659, 661, 663, 665, 667, 669, 671, 673, 687, 691, 693, 695, 697, 699, 701, 703, 705, 707, 709, 711, 713, 715, 717, 719, 721, 723, 725, 727, 729 and 731,
- 5 (e) a nucleic acid which is more than 70% identical to any of the nucleic acid sequences as represented by any of SEQ ID NOs 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481, 483, 485, 487, 489, 491, 493, 495, 497, 499, 501, 503, 505, 507, 509, 511, 513, 515, 517, 519, 521, 523, 525, 527, 529, 531, 533, 535, 537, 539, 541, 543, 545, 547, 549, 551, 553, 555, 557, 559, 561, 563, 565, 567, 569, 571, 573, 575, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, 627, 629, 631, 633, 635, 637, 639, 641, 643, 645, 647, 649, 651, 653, 655, 657, 659, 661, 663, 665, 667, 669, 671, 673, 687, 691, 693, 695, 697, 699, 701, 703, 705, 707, 709, 711, 713, 715, 717, 719, 721, 723, 725, 727, 729 and 731,
- 10 (f) a nucleic acid encoding a functional fragment of any of the nucleic acid sequences as specified in a) to e), and
- 15 (g) the complement of any of the nucleic acid molecule as specified in a) to f),
- 20 for the preparation of a medicament for treating diseases associated with yeast or fungi.
- 25
- 30
- 35

37. Use of an isolated polypeptide which is involved in a pathway eventually leading to programmed cell death of yeast or fungi, said polypeptide being selected from:

- (a) a polypeptide having an amino acid sequence as represented in any of SEQ ID NOs
- 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60,  
5 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102,  
104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136,  
138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170,  
172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204,  
206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238,  
10 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272,  
274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 299, 292, 294, 296,  
298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330,  
332, 324, 326, 328, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364,  
366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398,  
15 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432,  
434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466,  
468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500,  
502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534,  
536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568,  
20 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592,  
594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626,  
628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660,  
662, 664, 666, 668, 670, 672, 674, 688, 692, 694, 696, 698, 700, 702, 704, 706, 708,  
710, 712, 714, 716, 718, 720, 722, 724, 726, 728, 730 and 732, or encoding a  
25 functional equivalent, derivative or bioprecursor of said protein,
- (b) a polypeptide having an amino acid sequence which is more than 70% similar o any  
of the amino acid sequences as represented by any of SEQ ID NOs 18, 20, 22, 24,  
26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68,  
70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108,  
30 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142,  
144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176,  
178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210,  
212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244,  
246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278,  
35 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 299, 292, 294, 296, 298, 300, 302,

- 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 324, 326, 328, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 692, 694, 696, 698, 700, 702, 704, 706, 708, 710, 712, 714, 716, 718, 720, 722, 724, 726, 728, 730 and 732,
- (c) a polypeptide having an amino acid sequence which is more than 70% identical to any of the amino acid sequences as represented by any of SEQ ID 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 324, 326, 328, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666,

668, 670, 672, 674, 688, 692, 694, 696, 698, 700, 702, 704, 706, 708, 710, 712, 714, 716, 718, 720, 722, 724, 726, 728, 730 and 732, and,

(d) a functional fragment of any of said polypeptides as defined in a) to c),

for the preparation of a medicament for treating diseases associated with yeast or fungi.

- 5 38. A pharmaceutical or fungicidal composition comprising a nucleic acid as defined in claim 36 or a polypeptide as defined in claim 37 together with a pharmaceutically acceptable carrier diluent or excipient therefor.
39. A vaccine for immunizing a mammal against yeast or fungal infections comprising at least one nucleic acid as defined in claim 36 or at least one polypeptide as defined in claim 37 in  
10 a pharmaceutically acceptable carrier.
40. A genetically modified yeast or fungus in which modification results in the overexpression or underexpression of at least one of the nucleic acids as defined in claim 36 or the polypeptides as defined in claim 36, which overexpression or underexpression of said nucleic acid or polypeptide prevents, delays or sensitizes for apoptosis of said genetically  
15 modified yeast or fungus.
41. A method of identifying compounds which selectively modulate expression or functionality of polypeptides involved in a pathway eventually leading to programmed cell death of yeast or fungi or in metabolic pathways in which said polypeptides are involved, which method comprises:
- 20 (a) contacting a compound to be tested with a genetically modified yeast or fungus according to claim 40, in addition to contacting wild type cells with said compound,
- (b) monitoring the growth and/or death rate and/or activity of said genetically modified cells compared to said wild type cells; wherein differential growth or activity of said genetically modified yeast or fungi cells is indicative of selective action of said  
25 compound on a polypeptide in the same or a parallel pathway,
- (c) alternatively monitoring the growth and/or death rate and/or activity of said genetically modified cells compared to genetically modified cells which were not contacted with the compound to be tested, wherein differential growth or activity of said genetically modified yeast or fungi cells is indicative of selective action of said  
30 compound on a polypeptide in the same or a parallel pathway,
- (d) alternatively monitoring changes in morphologic and/or functional properties of components in said genetically modified cells caused by the addition of the compound to be tested, and,
- (e) identifying the compound.



42. A method of identifying compounds which selectively modulate expression or functionality of polypeptides involved in a pathway eventually leading to programmed cell death of yeast and fungi or in metabolic pathways in which said polypeptides are involved, which method comprises:

- 5       (a) contacting a compound to be tested with yeast or fungal cells transformed, transfected or infected with an expression vector comprising an antisense sequence of at least one of the nucleic acid as defined in claim 36, which expression results in underexpression of said polypeptide, in addition to contacting one or more wild type cells with said compound,
- 10       (b) monitoring the growth and/or death rate and/or activity of said transformed, transfected or infected cells compared to said wild type cells; wherein differential growth or activity of said transformed, transfected or infected yeast or fungal cells is indicative of selective action of said compound on a polypeptide in the same or a parallel pathway,
- 15       (c) alternatively monitoring the growth and/or death rate and/or activity of said transformed, transfected or infected cells compared to transformed, transfected or infected cells which were not contacted with the compound to be tested, wherein differential growth or activity of said mutated yeast or fungi cells is indicative of selective action of said compound on a polypeptide in the same or a parallel
- 20       pathway,
- (d) alternatively monitoring changes in morphologic and/or functional properties of components in said transformed, transfected or infected cells caused by the addition of the compound to be tested, and,
- (e) identifying the compound.

25   43. A method of identifying compounds or polypeptides which bind to or modulate the properties of polypeptides which are involved in a pathway eventually leading to programmed cell death of yeast or fungi, which method comprises:

- (a) contacting a compound or polypeptides to be tested with at least one of the polypeptides as defined in claim 37,
- 30       (b) detecting the complex formed between the compound or polypeptide to be tested and said polypeptide,
- (c) alternatively, examining the diminution of complex formation between said polypeptide and a binding partner, caused by the addition of the compound or polypeptide being tested,

- (d) alternatively, examining the alteration in the functional activity of the polypeptide, caused by the addition of the compound or polypeptide being tested, and,
- (e) identifying the compound or protein.

5 44. A method for identifying compounds interacting with a polypeptide involved in a pathway eventually leading to programmed cell death of yeast and fungi comprising the steps of:

- (a) providing a two-hybrid screening system wherein a polypeptide of claim 37 and a protein interacting with said polypeptide or an interacting polypeptide obtainable by a method of claim 41, are expressed,
- 10 (b) interacting said compound with the complex formed by the expressed proteins as defined in a),
- (c) detecting a second complex, wherein the presence of said second complex identifies a compound which specifically binds to one of said polypeptide or to said second complex, and,
- (d) identifying the compound.

15 45. A method of identifying compounds which selectively modulate expression of polypeptides which are involved in a pathway eventually leading to programmed cell death of yeast or fungi which method comprises:

- (a) contacting host cells transformed, transfected or infected with an expression vector comprising a promoter sequence of a nucleic acid as defined in claim 36 joined in  
20 frame with a reporter gene,
- (b) monitoring increased or decreased expression of said reporter gene caused by the addition of the compound being tested, and,
- (c) identifying the compound.

25 46. A method for identifying polypeptides involved in a pathway eventually leading to programmed cell death comprising the steps of:

- (a) providing a two-hybrid system wherein a polypeptide encoded by a nucleic acid according to claim 36 or a vector according to any of claims 3 to 7 as a bait and a yeast or fungal cDNA library as a prey are used,
- (b) detecting an interaction between said polypeptide and a yeast or fungal polypeptide  
30 encoded by said cDNA library, and,
- (c) identifying said yeast or fungal polypeptide.

47. A method according to any of claims 41 to 46 wherein said yeast or fungus is chosen from *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Candida albicans*, or *Aspergillus fumigatus*.

48. A compound or polypeptide identifiable according to the method of any of claims 41 to 47.
49. A compound or polypeptide according to claim 48 for use as a medicament.
50. A method for preparing a pharmaceutical composition for treating diseases associated with yeast or fungi comprising admixing a compound or polypeptide according to claim 49 with a suitable pharmaceutically acceptable carrier.
51. A pharmaceutical composition comprising a compound or polypeptide according to claim 49 together with a suitable pharmaceutically acceptable carrier.
52. Use of a compound or polypeptide according to claim 48 or 49 or a pharmaceutical composition according to claim 51 or obtainable by the method of claim 50 for the preparation of a medicament for treating diseases associated with yeast and fungi.
53. A method for preventing infection with yeast or fungi comprising administering a composition according to claim 51 or obtainable by the method of claim 50 to a mammal in an effective amount to stimulate the production of protective antibody or protective T-cell response.
54. Use of an antibody capable of specifically binding to at least one of the polypeptides as defined in claim 37 or to a specific epitope of said polypeptide, for the preparation of a medicament for treating diseases associated with yeast and fungi.
55. Use according to any of claims 52 to 54 wherein said disease is associated with yeast or fungi, where the yeast or fungus is chosen from *Candida* spp., *Aspergillus* spp., *Microsporum* spp., *Trichophyton* spp., *Fusarium* spp., *Zygomycetes* spp., *Botritis*, spp., *Cladosporium* spp., *Malassezia* spp., *Epidermophyton floccosum*, *Blastomyces dermatitidis*, *Coccidioides immitis*, *Histoplasma capsulatum*, *Paracoccidioides brasiliensis*, *Cryptococcus neoformans*, and *Sporothrix schenckii*.
56. Use of a compound or polypeptide according to claim 48 or 49 or a pharmaceutical composition according to claim 51 or a genetically modified organism as defined in claim 40 for the preparation of a medicament for modifying the endogenic flora of humans and other mammals.
57. A genetically modified mammalian cell or non-human organism in which modification results in the overexpression or underexpression of at least one of the nucleic acids as defined in claim 36 or a human homologue thereof or at least one of the polypeptides as defined in claim 37 or a human homologue thereof, which overexpression or underexpression of said nucleic acid or polypeptide prevents, delays or sensitizes for apoptosis of said genetically modified mammalian cell or in said genetically modified non-human organism.

58. A genetically modified mammalian cell or non-human organism according to claim 57 wherein said modification comprises the expression of an antisense molecule to at least one of the nucleic acids as defined in claim 36 or an antisense molecule to a mammalian homologue of said nucleic acid.
- 5 59. A method for identifying compounds for stimulating or inhibiting apoptosis comprising the use of at least one of the nucleic acids as defined in claim 36 or a human homologue thereof and/or at least one of the polypeptides as defined in claim 37 or a human homologue thereof and/or a genetically modified mammalian cell or non-human organism according to claim 57 or 58.
- 10 60. A compound identifiable according to the method of claim 59.
61. A compound according to claim 60 for use as a medicament.
62. A method for preparing a pharmaceutical composition for treating proliferative disorders or for preventing apoptosis in certain diseases comprising admixing a compound according to claim 60 or 61 with a suitable pharmaceutically acceptable carrier.
- 15 63. Use of a compound according to claim 60 or 61 for the preparation of a medicament for treating proliferative disorders or for preventing apoptosis in certain disorders.
64. Use of a nucleic acid selected from any of the nucleic acids as defined in claim 36 or a human homologue thereof for treating an/or preventing and/or alleviating proliferative disorders or for the prevention of apoptosis in certain diseases.
- 20 65. Use of a nucleic acid selected from any of the nucleic acids as defined in claim 36 or a human homologue thereof for the preparation of a medicament for treating and/or preventing and/or alleviating proliferative disorders or for the prevention of apoptosis in certain diseases.
- 25 66. Use of an antisense molecule to at least one of the nucleic acids as defined in claim 36 or an antisense molecule to a mammalian homologue of said nucleic acid for treating and/or preventing and/or alleviating proliferative disorders or for preventing apoptosis in certain disorders.
- 30 67. Use of an antisense molecule to at least one of the nucleic acids as defined in claim 36 or an antisense molecule to a mammalian homologue of said nucleic acid for the preparation of a medicament for treating and/or preventing and/or alleviating proliferative disorders or for preventing apoptosis in certain disorders.

68. Use of a polypeptide selected from any of the polypeptides as defined in claim 37 or a human homologue thereof for treating and/or preventing and/or alleviating proliferative disorders or for the prevention of apoptosis in certain diseases.
69. A pharmaceutical composition for use as a medicament for treating proliferative disorders or  
5 for the prevention of apoptosis in certain diseases comprising a nucleic acid molecule as defined in claim 36 or a human homologue thereof or an antisense molecule to at least one of the nucleic acids as defined in claim 36 or an antisense molecule to a mammalian homologue of said nucleic acid or a polypeptide as defined in claim 37 or a human homologue thereof together with a pharmaceutically acceptable carrier diluent or excipient  
10 therefor.
70. A vaccine for immunizing mammals against proliferative disorders or for preventing apoptosis in certain diseases comprising least one nucleic acid as defined in claim 36 or a human homologue thereof or at least one polypeptide as defined in claim 37 or a human analogue thereof in a pharmaceutically acceptable carrier.
- 15 71. Use of an antibody capable of specifically binding to at least one of the polypeptides as defined in claim 37 or to a human homologue thereof or to a specific epitope of said polypeptide or said human homologue, for the preparation of a medicament for treating proliferative disorders or for the prevention of apoptosis in certain diseases.
- 20 72. An expression vector comprising a human homologue of a nucleic acid as defined in claim 36.
73. An expression vector according to claim 72 which is an expression vector wherein said nucleic acid sequence is operably linked to one or more control sequences allowing the expression in prokaryotic and/or eukaryotic host cells.
74. An expression vector according to claim 72 or 73 which comprises an inducible promoter.
- 25 75. An expression vector according to any of claims 72 to 74 which comprises a sequence encoding a reporter molecule.
76. A host cell transformed, transfected or infected with the vector of any of claims 72 to 75.
77. An isolated nucleic acid comprising a human homologue of at least one of the nucleic acids as defined in claim 36.
- 30 78. An antisense molecule comprising a nucleic acid sequence capable of selectively hybridising to the nucleic acid molecule of claim 77.
79. A polypeptide encoded by a nucleic acid of claim 77.

**Figure 1:**

YBL002W, 896 bp, CDS: 501-896 (SEQ ID NO 21)

TGTTTGATATTAGTAGTCATGTTGTAATCTCTGGCCTAAGTATACGTAACGAAAAATGGTA  
GCACGTCGCGTTTATGGCCCCCAGGTTAATGTGTTCTCTGAAATTCGCATCACTTTGAGA  
AATAATGGGAACACCTTACGCGTGAGCTGTGCCACCCTTCGCCATAATAAGCGGTGTT  
CTCAAAATTTCTCCCCGTTTTCAGGATCACGAGCGCCATCTAGTTCTGGTAAAATCGCGC  
TTACAAGAACAAAGAAAAGAAACATCGCGTAATGCAACAGTGAGACACTTGCCGTCATAT  
ATAAGGTTTGGATCAGTAACCGTTATTTGAGCATAACACAGGTTTTTAAATATATTATT  
ATATATCATGGTATATGTGTAAAATTTTTTTGCTGACTGGTTTTGTTTATTTATTAGCT  
TTTTAAAAATTTTACTTTCTTCTTGTAAATTTTTTCTGATTGCTCTATACTCAAACCAAC  
AACAACTTACTCTACAACTAATGTCCCTCTGCCGCCGAAAAGAAACCAGCTTCCAAAGCTC  
CAGCTGAAAAGGAGACCTATTCTCTTATATTTACAAAGTTTGAAGCAAACATCACC  
CTAAGGTTAGAAAAGGAGACCTATTCTCTTATATTTACAAAGTTTGAAGCAAACATCACC  
CAGACACTGGTATTTCCCAGAAGTCTATGTCTATTTTGAAGTTTTCGTTAACGATATCT  
TTGAAAGAATTGCTACTGAAGCTTCTAAATTGGCCGCTTATAACAAGAAATCCACTATTT  
CTGCTAGAGAAATCCAAACAGCCGTTAGATTGATCTTACCTGGTGAATTGGCTAAACATG  
CCGTCTCCGAAGGTACTAGGGCTGTTACCAAATACTCCTCCTCTACTCAAGCCTAA

YBL002W, 131 aa (SEQ ID NO 22)

MSSAAEKKPASKAPAEEKKPAKKTSTSVGKKRSKVRKETYSYIYKVLKQTHPDTGISQ  
KMSILNSFVNDIFERATEASKLAAYNKKSTISAREIQTAVRLILPGELAKHAVSEGTR  
AVTKYSSSTQA

YBL064C, 1286 bp, CDS: 501-1286 (SEQ ID NO 25)

TTGCCAACCTCAAAGAAGAAGATTATGGGCATATTGACCTTCTCCGGTTTTCCCTCCCGC  
GCTCTCGTATCCGTCTGCATTTGACCTCGAGCAAGCGCTCCACTATGTCTATATGTTTAC  
CAGTAAACTTCTTAACGTTTGTGATATTTTTGAACTTCAACCACATTCAGTATGCGTG  
TGTATATAAGATATTCCTGATAGCACTATGTTTATCTTTATACAATATACAAAAGGTCA  
CCCAGGACGAGCAGCGCGCTATTTTTCTATCATTCGGTGAATAGCGACCAACGGTCGGC  
GGCTATTTTTTTTTTTGCAATTTTTTCGGGATGGGTTCCTCCCGCAAAAGCTAGCCCCGGA  
GATTTTTTAATTACGTAAAGAAACAAGGGGCCGATGTTGCTGCTATTGGTATATAAAGAG  
AGAAGGAGAGATATAGAAAATTGTGCTTCTAGATTCTCGCAGTAGGATGAGATAAATTTTC  
AAAGAAGCAGGAAGCAAAGGATGTTTAGTAGAATTTGTAGCGCTCAATTAAAGAGGACGG  
CATGGACCTTCTTAAGCAGGCTCACTTGCAATCACAGACGATTAAAACATTTGCCACAG  
CACCTATTCTGTGCAACAATTCAAACAAGTGATCAACCAAGACTAAGAATAAACTCTG  
ATGCTCCTAACTTTGATGCTGACACAACGGTTGGTAAAATCAATTTTTACGACTACTTGG  
GCGACTCTTGGGGGGTCTTGTTTTCTCACCACGAGATTTACCCCTGTCTGCACCACCG  
AAGTCAGCGCATTCGCCAAATTGAAGCCGGAATTCGACAAGAGAAATGTTAAATTGATCG  
GGCTTTCAGTGGAAGATGTTGAGTCCCACGAAAAATGGATTCAAGACATCAAGGAAATAG  
CAAAGGTTAAAAATGTTGGTTTCCCAATAATTGGTGACACTTTTAGAAAACGTGGCATTTCC  
TATATGATATGGTAGATGCCGAAGGATTCAAAAATATCAATGATGGGTCACTGAAGACCG  
TGAGGTCTGTTTTCTGTCATCGATCCCAAGAAGAAGATTAGACTGATTTTTACCTACCTTT  
CCACCGTCGGAAGAAACACTTCTGAAGTGTTAAGGGTAATCGACGCTTGCAATTGACTG  
ACAAGGAGGGCGTAGTAACCTCAATTAATTGGCAGCCAGCTGACGATGTCATTATTCCTC  
CCTCTGTCTCCAATGATGAGGCGAAGCTAAATTTGGTCAATTTAATGAAATTAAACCTT  
ATTTAAGATTACCAAGTCGAAATAA

YBL064C, 261 aa (SEQ ID NO 26)

MFSRICSAQLKRTAWTLPKQAHLSQTIKTFATAPILCKQFKQSDQPRLRINS DAPNFDA  
DTTVGKINFYDYLGD SWGVLF SHPADFTPVCTTEVSFAFKLKPEFDKRN VKLIGLSVEDV  
ESHEKWIQDIKEIAKVKNVGFPIIGD TFRNVAFLYDMVDAEGFKNINDGSLKTVRSVFVI  
DPKKKIRLIFTYPSTVGRNTSEVLRVIDALQLTDEGVVTPINWQPADDV IIPPSVSNDE  
AKAKFGQFNEIKPYLRFTKSK

2/251

YBR089C-A, 800 bp, CDS: 501-800 (SEQ ID NO 47)

TTTTTTAGGTGGCGCGCAACTATAAAGTACAGCAAGTGAGGTTGAGGCAATACTGGGAG  
TTTACACTATGGGAGACAGCTCCTAACACCAAGCAGAAAAACGACTTTTTTCGCAAAGTAT  
GTAAGGCGCTGGGTGAGCCCAGCGGACGAGGATGGGCTTAATAAGAACGTACAGTTTAGC  
ACAGCTAGAACAGGATACAGCTAAGGGCAACTCTGCTTTTCGGGAGAAGTTAAAGAGGGG  
TAGACAATGATGGTAATCTTATAAACC GGCTACAATGAAGGTTGTAGCAGCAAGGAAGAT  
GATATTTTAATACGGTTCAGGTGAAATGAAATAGCCGCCCATACCGGCATGCTCAAGTTG  
TAAGTCAGGACTCTAGCTTTCTACTGTAGTATCCTCTAAAGGACTGCTGTTCTGTGCACC  
CCCTTCCTTTGTTTATCATAGCGCACGACAAGAGTACTAACTAATTAACCTTAGAACATTA  
ACATATATAAACTAGCGCTATGGCCGCAACTAAAGAAGCAAAGCAACCAAAGGAACCAA  
AGAAGAGGACCACCAGGAGAAAGAAGGATCCTAACGCCCTTAAGAGGCGGTTGTCTAGCTT  
ATATGTTCTTTGCTAATGAAAACAGAGACATTGTCCGTTCCGAGAATCCTGACGTAACCTT  
TTGGCCAAGTAGGCAGAATATTGGGTGAGAGGTGGAAGGCCTTAAGTCTGAAGAAAAGC  
AACCCTATGAATCTAAGGCTCAAGCAGACAAGAAGAGATACGAATCTGAAAAGGAATTGT  
ACAATGCTACACGTGCTTGA

YBR089C-A, 99 aa (SEQ ID NO 48)

MAATKEAKQPKPKKRTTRRKDPNAPKRRLSAYMFFANENRDIVRSENPDVTFGQVGRI  
LGERWKALTAEEKQPYESKAQADKKRYESEKELYNATRA

YBR149W, 1535 bp, CDS: 501-1535 (SEQ ID NO 57)

TTCGCAACATCAACTTCTCCTTAATCGACCAACTGACAATGAACTTCAGGTTCTACGAG  
AGATCTGCCAATTTCCAGAAGGAAACAATAGGTGGGTAAAGAATGATGCTACAAGATAAG  
GATAACTATATCAAAACACTGATGCAACATTTGAAGAAAAAGAGAGTACAAAGTTGATA  
AAAGACAGCAAGAATGGCGCCTCCACCTTAACATCTTAACAATTTTCGTTTACTGAAAATG  
CTACTAGTATATAATCATTAAGTATCTAACTATCACTCAATAAAAAATATTATAGATCGCT  
TAAAAACTCGTTTATTGCCGATTATAAATCCACCAAAGCCGCTCTACCCTTACCTCCGC  
CTGGA AAAATTATAATATATAAAGTGAGCCTCGTAATACAGGGGTAAAAAGGAAAGAGGG  
GGATATCAAGCATCTGGACTTATTTGCACTATCTCCGCCTTCAATTGATAAAAGCGTCTT  
GATTTTAATCAACTGCTATCATGTCTTCTTCAGTAGCCTCAACCGAAAACATAGTCGAAA  
ATATGTTTGCATCCAAAGACTACAGAAATATACTTTTCACTCAACAATGGTGTTCGTATCC  
CAGCACTGGGTTTGGGGACAGCAAATCCTCACGAAAAGTTAGCTGAAACAAAACAAGCCG  
TAAAAGCTGCAATCAAAGCTGGATACAGGCACATTGATACTGCTTGGGCCTACGAGACAG  
AGCCATTTCGTAGGTGAAGCCATCAAGGAGTTATTAGAAGATGGATCTATCAAAAGGGAGG  
ATCTTTTTCATAACCACAAAAGTGTGGCCGGTTCTATGGGACGAAGTGGACAGATCATTGA  
ATGAATCTTTGAAAGCTTTAGGCTTGGGAATACGTCGACTTGCTCTTGCAACATTGGCCGC  
TATGTTTGTAAAAGATTAAGGACCCTAAGGGGATCAGCGGACTGGTGAAGACTCCGGTTG  
ATGATTTCTGGA AAAACAATGTATGCTGCCGACGGTGACTATTTAGAACTTACAAGCAAT  
TGGAAAAAATTTACCTTGATCCTAACGATCATCGTGTGAGAGCCATTGGTGTCTCAAATT  
TTTCCATTGAGTATTTGGAACGTCTCATTAAAGGAATGCAGAGTTAAGCCAACGGTGAACC  
AAGTGGAACTCACCTCACTTACCACAAATGGAAGTAAAGAAAGTTCTGCTTTATGCACG  
ACATTCTGTTAACAGCATACTCACCATTAGGTTCCCATGGCGCACCAAACCTTGAAAATCC  
CACTAGTGAAAAAGCTTGCCGAAAAGTACAATGTCACAGGAAATGACTTGCTAATTTCTT  
ACCATATTAGACAAGGCACTATCGTAATTCGAGATCCTTGAATCCAGTTAGGATTTCTT  
CGAGTATTGAATTCGCATCTTTGACAAAGGATGAATTACAAGAGTTGAACGACTTCGGTG  
AAAAATACCCAGTGAGATTCATCGATGAGCCATTTGCAGCCATCCTTCCAGAGTTTACTG  
GTAACGGACCAAACCTTGGACAATTTAAAGTATTAA

YBR149W, 344 aa (SEQ ID NO 58)

MSSSVASTENIVENMLHPKTTEIYFSLNNGVRIPALGLGTANPHEKLAETKQAVKAAIKA  
GYRHIDTAWAYETEPFVGEAIKELLEDSIKREDLFITTKVWPVLWDEVDRSLNESLKAL  
GLEYYDLLLLQHWPLCFEKIKDPKISGLVKTPVDDSGKTMYAADGDYLETYKQLEKIYLD  
PNDHRVRAIGVSNFSIEYLERLIKECRVKPTVNQVETHPHLPQMELRKFCFMHDILLTAY  
SPLGSHGAPNLKIPLVKKLAEKYNVTGNDLLISYHIRQGTIVIPRSLNPVRISSSIEFAS  
LTKDELQELNDFGEKYPVRFIDEPFAAILPEFTGNGPNLDNLKY

3/251

YBR289W, 3218 bp, CDS: 501-3218 (SEQ ID NO 63)

GATACGATCTATAGTCTCTAAAAAGGTAAAAACAATCAAGCGGGCCTTTTGACTTCGAAGT  
GGAGGCTAAGCACCATAATTGAGCTTATTTATAACTGAGAAATACTTATAGACCTCTAA  
ATCTCTTCCAACCATTGAATGGTCTAAATAATCATCACTACTGCTATCTTCGAGCAATTG  
AGGACATGTGGTACGAACGCGGGTCCACAGGTGCTTGAAGGAGGGAGCTGTTGCACCTAA  
AAGATACTGGAAAATAAGTTTGTCTTTGTATCAGTGATATAGAATGACAAATACATCTA  
TTTTGGTTGGGTTGGTAAGGTTTACAGCCTCTGTTGTTGCCCAAGTCCTGTTATCGCCAA  
CTTTAAATAAATCTCTTCTTGTCTTTGACCAAAAATTTTCATTTTTTCGTCGCATTTAAAA  
GAAACTGAAATTTCAAACATAAACACCAAAACAAAGCATCATCAAGGGAACATATAGTAA  
AGAACTACACAAAAGCAACAATGAATAATCAGCCGCAGGGTACCAACAGCGTTCCAAATA  
GTATTGGAAATATATTTAGCAACATTGGAATCCATCTTTTAACATGGCGCAAATTCGCG  
AACAGCTGTATCAGAGCCTCACACCACAACAATTGCAGATGATTAGCAACGACACCAAC  
AGTTACTGAGGAGTCGTCTACAACAACAACAACAACAACAACAACAACAACTTCACCGCCAC  
CGCAAACGCATCAATCTCCACCCCTCCTCCGCAACAATCTCAACCCATTGCTAATCAAT  
CAGCGACTTCTACCCCTCCTCCTCCTCCAGCACCAACAACCTTACATCCCCAAATTGGTTC  
AAGTGCCCTTAGCTCCAGCGCCTATTAATTTGCCTCCACAAATTGCTCAGTTACCTTTGG  
CTACACAGCAACAAGTTTTGAACAAGTTGAGGCAGCAGGCCATAGCAAAAAATAATCCAC  
AGGTTGTGAATGCAATTACTGTTGCACAACAACAAGTGCAACGCCAAATTGAGCAGCAAAA  
AGGGACAGCAACCGGCACAACTCAGCTAGAACAGCAGAGGCAATTGCTGGTTTCAGCAGC  
AACAGCAGCAGCAACTTAGAAACCAAATACAGCGACAACAGCAACAACAGTTTAGGCATC  
ATGTGCAAATACAACAGCAGCAACAAAAGCAACAACAACAGCAGCAGCAGCATCAGCAAC  
AACAACAACAACAACAGCAACAGCAGCAACAGCAACAGCAACAGCAGCAGCAACAACAAC  
AGCAACAACAACAACAACAGCAGCAGCAGCAGCAGCAGCAGCAAGGACAAATACCGCAAT  
CTCAGCAAGTTCTCAAGTTAGATCCATGAGTGGACAACCTCCCACCAATGTTTCAGCCCA  
CTATTGGCCAACTTCTCAACTTCCAAAATTAAACTTACCCAAGTACCAAACTATTCAAT  
ACGATCCACCAGAAACCAAGCTACCATATCCAACCTATTGGTCAGACAAAAAAGCAGATA  
CGGATACTTTGTTGTACGAACAAATTATCCAGCGTGATAAAATTAAACAAATATTCGCTAA  
TAAGAGAAACCAATGGTTACGATCCGTTTAGCATTTATGGATTAGTAATAAAGAGTATA  
TTAGTAGACTGTGGCATACTGAAGTATTATCAAGATTTGAAGAACACTAGAATGAAAT  
CTATCACAAGCACTTCTCAGAAGATTCTTCGGCAAGTATTTGGGGAAATGGTTACTCAG  
GGTATGGTAATGGGATTACGAATACAACCTACCAGAGTTATTCCACAAGTAGAAGTTGGAA  
ATAGGAAGCATTACCTAGAGGATAAATTAAAAGTCTATAAACAGGCCATGAATGAGACAT  
CGGAACAGTTAGTTCCCATAGATTGGAGTTTCGATCAAGATCGTGACAGATTCTTCCTCA  
GGGACACTTTGTTATGGAACAAAATGACAAGCTTATTAATAATTGAAGACTTTGTGGACG  
ACATGTTGCGAGATTACCGATTTGAGGACGCTACGAGAGAGCAACACATTGATACTATTT  
GTCAATCTATACAAGAGCAGATTTCAGGAGTTTCAAGGAAATCCATATATAGAGTTGAATC  
AGGACCGTCTAGGCGGTGATGACTTGAGAATTAGAATCAAGCTGGATATTGTTCGTGGGAC  
AAAACCAAGTTAATCGATCAATTTGAGTGGGAGATCTCTAATAGTGATAACTGTCCAGAAG  
AGTTTGCAGAGTCCATGTGTCAAGAATTAGAATACCAGGTGAGTTGTGACTGCCATTG  
CTCACTCCATAAGAGAGCAAGTTCATATGTATCATAAATCACTGGCACTGTTAGGTTACA  
ATTTTGATGGATCAGCGATAGAAGATGATGACATTAGAAGCAGAATGCTCCCAACGATTA  
CTCTTGATGATGTTTATAGGCCTGCAGCGGAAAGCAAAATTTTACTCCAAACCTATTAC  
AGATTTTCAGCTGCAGAGTTAGAGAGATTGGATAAAGATAAGGACAGAGACACAAGAAGGA  
AAAGAAGACAAGGTAGATCTAATAGACGTGGTATGCTCGCATTGTCCGGCACATCTGCAA  
GTAATACATCTATGAACGGCGTTCACAACACAGTAGCAGCAGGAAATGCTTCATCGTTGC  
CACCAGGAGAGATTTTACTGCCAGATATTGCAGATATTCCAAGAACTTTCAGGACTCCAG  
TACCTAGCACTTTAATGCCTGGTGGTGTGACGTAGGCCCTTCTGTGGAATCGTACGAAT  
TGAGAAACACAACCACTTATAAAAGCAGGGCCAGATAGACCTAAGCCAGTTTACCTCCTT  
GTTATATTATTGACCATATTTCCGGGTCAATTCGCTACTACTTTCTATTAAACTGCCTGGGA  
AAGTTAATACAAAAGAAGAGTTTCGAGCAGCGCCCAATGACACAAGTAGTGGCACCAATG  
CAATGCTTCCGAGTCCAGAATCGCTGAAAACCTAAGCTGAATAGTAACATTTCGCGCTGGTG  
TGACGATACCTTCAATCCCAAACCCGATTGCCAATCACACTGTTACTAATTCACCCAATC  
CCACACTGCAGCCAGTAATCCCAGGTGGGGCAGCTAGTAAATCGGTACCTACACCTAGTC  
TTCTTATAGCACCTCCAGTAGCACCATGATAGCGAAGCGACATTGTTGACTAATAGCA  
ATAATGGTAGCAGTAACAATAACACACAGAATACATAG



4/251

YBR289W, 905 aa (SEQ ID NO 64)

MNNQPQGTNSVPNSIGNIFSNIQTSPFNMAQIPQQLYQSLTPQQLQMIQQRHQQLLSRL  
QQQQQQQQQTSPPPQTHQSPPPPPQSQPIANQSATSTPPPPFAPHNLHPQIGQVPLAPA  
PINLPPQIAQLPLATQQQVLNKLRRQAIKNNPVVNAITVAQQQVQRQIEQQKQQTAAQ  
TQLEQQRQLLVQQQQQQQLRNQIQRRQQQQQFRHHVQIQQQQQKQQQQQQQHQQQQQQQQQ  
QQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQIQPSQQVPQVRMSGQPPTNVQPTIGQLPQ  
LPKLNLPKYQTIQYDPPETKLPYPTYWSDKKADTDLLYEQIIQRDKINKYSLIRETNGY  
DPFSIYGF SNKEYISRLWHTLKYYQDLKNTRMKSITSTSQKIPASASIWGNNGYSGYNGIT  
NTTTRVIFPQVEVGNRKHYLEDKLVYKQAMNETSEQLVPIRLEFDQDRDRFFLRDRLWN  
KNDKLIKIEDFVDDMLRDYRFEDATREQHIDTICQSIQEQIQEFQGNPYIELNQDRLGGD  
DLRIRIKLDIVVGQNLIDQFEWEISNSDNCPEEFAESMCQELELPGEFVTAIAHSIREQ  
VHMYHKSALLGYNFDGSAIEDDDIRSRMLPTITLDDVYRPAAESKIFTNLLQISAAEL  
ERLDKDKDRDTRRKRRQGRSNRRGMLALSGTSASNTSMNGVHNTVAAGNASSLPPEGILL  
PDIADIPRTFRTFVPSTLMPGGVDVGPSVESYELRNTTTYKSRPDRPKPVSPPCYIIDHI  
PGHSLLLSIKLPKVNTEKEFAAAPNDTSSGTNAMLSPESLKTCLNSNIRAGVTIPSP  
NPIANHTVTNSPNPTLQPVIPGGAASKSVPTPSLPIAPPVAPHDSEATLLTNSNNGSSNN  
NTQNT

YCR004C, 1244 bp, CDS: 501-1244 (SEQ ID NO 69)

TTAAGAAAATGAACGTTACTATTTCTTCCTCGTTTTAGTTACATAAAAATTTACTAATGG  
TTGGAATTTGCGGAAGCTATCACGCGATACTAGGTACACACGCATTATTTTATAATC  
CCATTATTAATAAATCCGTTATGACCCTTTTAGTAATAACTTATTAAGAACCTCCGGGTA  
AAATACTGTACTGCGGGGAAAGAAGGCGCTTCCCCTTCTTGGAACCTAATATAAATAATA  
AATTTGCCTAAGGGCATTAGGCCTTACTGCCTTGGCTAGCGTACTTATTTTCGATTACATAC  
AATTTGCACTATTTCCGGCAGCTAGTTGATACTATAACATCCTACATTTTTACTTGTTTTA  
CGTTCATTTTTATTTGAAGTTTGTAACTTTATCAGAAAAGAAAACAAGAAGAGGAAAAAG  
GAAAAGAGGGGTACGGTGTAGTATCAATAAAAAAAGAGAGTAAACAAAACAATACAGAC  
TCAATTGAAGCACTATAAGAATGGTAAAGATTGCGATAATTACTTACTCTACCTACGGGC  
ACATAGACGTTTGTAGCCCAAGCTGTTAAGAAAGGTGTGGAGGCAGCTGGTGGTAAAGCTG  
ATATATACAGGGTCGAGGAACTTTACCTGATGAAGTCCTCACCAGATGAACGCTCCTC  
AGAAACCTGAAGATATTCTGTGGCCACTGAGAAAACGTTGCTCGAATATGACGCCCTTTT  
TGTTCCGGTGTTCCTCAACTAGGTTTGGTAATTTGCCGGCTCAATGGTCCGCCTTTTGGGATA  
AAACCGGTGGATTATGGGCCAAGGGCTCTTTGAACGGCAAAGCTGCGGGGATATTCGTTA  
GTACTTCCAGTTACGGAGGTGGTCAAGAAAGTACCGTTAAAGCCTGTTTGTCTTATTTAG  
CTCATCACGGAATTATCTTTTTACCACTGGGTATAAGAATTCATTTGCTGAGTTAGCCA  
GTATAGAAGAGGTACACGGTGGCTCTCCATGGGGTGCTGGTACCCTTGCAGGACCTGACG  
GCTCAAGAACTGCGTCTCCACTTGAATTGAGAATTGCTGAAATTCAGGTAAAACATTCT  
ACGAAACCGCCAAAAAACTTTTCCCTGCAAAAGAAGCCAAGCCCTCCACTGAAAAGAAGA  
CCACTACTTCTGATGCGGCTAAGAGACAACTAAACCTGCAGCAGCTACAACCTGCAGAAA  
AGAAGGAGGACAAAGGATTATTATCTGTGCTGTACTGTCTATGTAA

YCR004C, 247 aa (SEQ ID NO 70)

MVKIAIITYSTYGHIDVLAQAVKKGVEAAGGKADIYRVEETLPDEVLTKMNAPOKPEDIP  
VATEKTLLEYDAFLFGVPTRFGLNPAQWSAFWDKTGGLWAKGSLNGKAAGIFVSTSSYGG  
QQUESTVKACLSYLAHHGIIFLPLGYKNSFAELASIEEVHGGSPWGAGTLAGPDGSRTASP  
LELRIAEIQKTFYETAKKLFPAKEAKPSTEKKTTTSDAAKRQTKPAAATTAEEKKEDKGL  
LSCCTVM

YCR013C, 1148bp, CDS: 501-1148 (SEQ ID NO 77)

TGAAAAATGATGAAGGCACATTGTTAATTGAAGAAGAAGAAGAAGAAGAAAACAAAATTAA  
AACCGATTGACCAATATATGTCTCTGAATGCCAAGGATGGAAATTATTGCAGAAGATTAG  
ACTTTTTTTTGTGCAAGTGGGATGAGCTTGGAGCAGGAAGAATACACTATACTGGATCTA  
AAGAGTACAATAGATGGATAAGAATATTGGCAGCGCAAAAAGGCTTCAAGCTTACACAAC  
ACGGTTTATTTGCAATAATATCTTCTCGAAAGCTTTAACGAACGCAGAATTTTCGAGT  
TATTAACTTAAATACGCTGAACCCGAACATAGAAATATCGAATGGGAAAAAAAACCTG  
CATAAAGGCATTAAAGAGGAGCGAATTTTTTTTTTAATAAAAAATCTTAATAATCATTA

5/251

AGATAAATAATAGTCTATATATACGTATATAAATAAAAAATATTCAAAAAATAAAATAAA  
CTATTATTTTAGCGTAAAGGATGGGGAAAGAGAAAAGAAAAAATTGATCTATCGATTTC  
AATTCAATTCAATTTATTTCTTTTCGGATAAGAAAGCAACACCTGGCAATTCCTTACCTT  
CCAATAATTCAAAGAAGCACCACCACCAGTAGAGACATGGGAGATCTTGTCACTGACAC  
CGTACTTCTTAGCGACAGTGGCAGTGTACCACCACCAATGATGACGGTGTACCAGCAG  
CAGAGCTCTTGACAACCTTCGTCTAACAAAGCCTTAGTACCAGCAGCGAACCTTTTCGAATT  
CGAAAACACCTGGTGGACCGTTCAGACAATGGTCTTAGCCTTTGCAACAGTAGCAGCAA  
ACAACCTTTCTAGATTCTGGACCATTGTCCAACCTTGCCAGCCAGCTGGAATACCTTCCT  
TGTCAGTGACAGTCTTGGTGTGGCATCAGCAGAGAAAGCATCAGCAATGATGAAGTCGA  
CTGGCAAGACGACTTCGACACCCTTGGCCTTGGCCTTTTCCATCAACTTTGGAACGATTT  
CAGCACCAGCCTTGTGCAAGATGGAGTCACCGATTTCACTGTTTTCCAAAACCTTCTTGA  
AGGTGAAAGCCATACCACCACCAATGATGATAGAGTCGACCTTGTCCAACAAGTTGTCAA  
TCAATTGA

YCR013C, 215 aa (SEQ ID NO 78)

MGKEKRKKLIYRFQFNSIYFFSDKKATPGNSLPSNNSKEAPPPVETWEILSVTPYFLATV  
AVSPPPMMTVLPAEELLTSSNKALVPAANFSNSKTPGGPFQTMVLAFATVAANNFLDSG  
PLSNPCQPAGIPSLSVTVLVLASAEKASAMMKSTGKTTSTPLALAFSINFGTISAPALSK  
MESPISVFSKTFKVKAIPPPMIESTLSNKLIN

YDL059C, 1217 bp, CDS: 501-1217 (SEQ ID NO 83)

AAAGTATCAAGTTCGCTAAATTTACTTCGAAGACAGAAGCCAGTAAATTTTGTTCCTTC  
ATGGAAATAGTTTCCAAAAGTTCTTAGTAATTACCATATGTTCTTGTATGTGGCGCTGC  
GAAAGAAAGGTTAGCCGACCGGCATCACCATAATTGTATAATATAGCAATGAAGCAACT  
TGTTGAAGTTTTCTTTAAAGTACTATAGTATTGAATAATATCATGTTCACTTGATAAAAT  
TGGGTATTTTATTGACCATTATATCGCGTTGGACACTAATGTCTTTCAAGTTGGTGTAC  
GTCACGTGCTTTTCAATGTACTGGGGCAAATTGATTAGAGGAAGCCACAGTTTGGCAAGG  
GCAGATATGATAGGAAGCAGTAACGGCAAGGAAGGATAAGAACATCATTGAGGGAGTCTG  
TGGCAGTTTAGCACATGCTTTGGACCATTAAAGGGTTACGTAGAGGAGAAGAGCATATTT  
CAGGATAAACAGACAAAATAATGACGATACAAGCGAAGCCAGTTCGAGCATATCGTATG  
ATTTCGACTACATACGGCACAGCACCAGGCTTGGATATAAAAGAGTTCCAAATCATCGAAG  
ATTGGAATGGAAGACCTGCCAGCGCTTGGTCGGTGCAGAGGATTGGGCTTCTACAGTCCA  
AGATGGAAGGTACACGTACAATATTTACCACAATAATAAATATGGGAAGCACAACTTAT  
CTAAGCTGATACCAGGGCATGCTCTCATTCACTTCGCTAATGAAACATTCCGGGTATGATG  
GTTGGCGAATGGATGTTATAGATGTTGAGGCCCGGGAGTGCCAGCCCTTCACCGCAGTAA  
ATAATGGAGAAAACACCAACACTAGTGAGGTCAAGTATACAGTTGTGGCAGAAGCCCAAG  
TAAAGGTTACCTTAAAGGATGGCACCAACACACAGTGTGGTGGGCTAGGTAGAATTACTT  
TGTCCTCGAGAGGTGAATGTTATAACAGGTGCAAAAAAGAGGCTGTAGGCGATGCGTTAA  
AGAAGGCGTTATTGAGCTTTGAAAAATCATACTCGATTATGAGACTAAGATTACAAATA  
ATTACTATGTCGATGGCTTGTATGGCTCAAAAAAATTAAAAATGAAGCTAACACCAATT  
ACAACCTTATTGTGTCAGCGACTAATAGCAAGCCGACTTTTATCAAATTGGAGGATGCTAAAG  
GCACGCATATCAAATAA

YDL059C, 238 aa (SEQ ID NO 84)

MTIQAKPSSSISYDSTTYGTAPGLDIKEFQIIEDWNGRPASAWSVQRIGLLQSKIERYTY  
NIYHNNKYGKHNLSKLIPGHALIQFANETFGYDWRMDVIDVEARECQPFTAVNNGENTN  
TSEVKYTVVAEQVKVTLKDGTNTQCGGLGRITLSSRGECYNRSKKEAVGDALKKALLSF  
EKIILDYETKITNNYYVDGLYGSKKIKNEANTNYNLLSATNSKPTFIKLEDAKGTHIK

YDL147W, 1838 bp, CDS: 501-1838 (SEQ ID NO 87)

ACTCTTCTCTGATTTTCAATGGCCTTTTTTTTTTCTTACGATCATACTCCTTCGCTT  
GCTTTTTGGAATTCTTTTTATTCTTACTTTTGACGTTTGTGTGACCTGTGAGTCCACGGG  
CCTTCAAGGCGGCCTTTAAATTCTTAAGTTGTGAACCGCCATGATTTGATCTTCCCTT  
TTATTTGCTTCTCAACTGTACTATTTACAGTAATAATTAGTGCAACCTTCAGATGCTTCT  
CGCTAAATGCTCATCTCTAAATTATCATTATTATTCCTAATAAATCCTAAAATTTTTAC  
TCGTTCTGTACGGCTCATCGCCCAATATTACCGTCTTGTATGTGATCTTTTTGACTTT

6/251

TCGGTGGCAAAATGCAAAGGGGAATCCAAGGAAAAACCATAACAGGACACTACATCAGAG  
ATAATCTTGAATTAAGAGAGTAGAGGAATATACTGCTGGGCTCACTACCATTTTTGTTGC  
TAGAGTAAACGTAGAGAAAGATGTCAAGAGATGCACCAATTAAGGCTGACAAGGATTATA  
GCCAAATTTTGAAGGAAGAGTTTCCTAAGATCGATTTCGCTCGCTCAAAATGATTGTAAC  
CTGCTTTAGACCAACTGTTAGTGTGGAGAAAGAAAACCAGACAAGCTTCAGATCTGGCCT  
CCTCGAAAGAAAGTTTGGCCAAGATTGTAGATCTGCTAGCATCAAGGAATAAGTGGGACG  
ACCTAAATGAGCAATTGACTCTACTCTCAAAAAAGCATGGTCAGTTGAAATTGTCAATTC  
AGTATATGATACAAAAGGTTATGGAATATTTGAAAAGCTCGAAATCTTTGGATTAAACA  
CCAGAATTAGTGTCAATTGAACTATCAGGGTGGTTACAGAGAACAAAATATTTGTAGAAG  
TGGAAAGAGCTAGGGTCACCAAAGATTTGGTGGAAATTAAGAAAGAAGAGGGTAAGATTG  
ATGAAGCTGCAGACATCTTGTGTGAGTTACAGGTTGAGACCTATGGCTCCATGGAAATGT  
CTGAGAAAATTCAGTTTATATTAGAGCAAATGGAATTGAGTATATTAAGGTTGATTATT  
CCCAAGCCACGGTGTCTTCAAGAAAAATCTGAAAAAACTTTTAAAAATCCAAATACG  
AGTCATTTGAAGCTAGAAATATTATAATCTTCTGGTAAAAATTAGTTTGCACAAGAGAGAAT  
ACCTAGAAGTTGCGCAGTATCTGCAAGAAATTTATCAAAACAGACGCCATTAAATCAGATG  
AGGCTAAGTGGAAACCTGTCTTATCGCACATTGTATATTTCTTAGTCCTTTACCTTACG  
GCAATTTACAAAATGATTTAATTCACAAAATCCAGAATGATAACAACCTGAAAAAATTAG  
AAAGCCAAGAATCTTTAGTAAAAATTGTTTACTACGAATGAGTTGATGAGATGGCCAAATTG  
TTCAAAAAACCTATGAGCCCGTCTTAAATGAGGATGATTTGGCATTGGTGGAGAAGCTA  
ATAAGCATCACTGGGAAGATTTACAAAAAAGGGTCATCGAGCACAATTTAAGAGTCATTT  
CCGAATACTATTCCAGAATTACTTTACTAAGATTGAATGAATTGCTGGACCTAACGGAGA  
GCCAGACGGAACATACATCAGTGATTTGGTAAACCAGGGCATCATATACGCTAAAGTTA  
ATCGCCACGCCAAAATCGTGAAATTTGAAAAACCAAAAACTCAAGCCAATTATTGAACG  
AATGGTCACATAATGTTGACGAATATTAGAACATATAGAAACAATAGGCCATTTAATTA  
CAAAAAGAGGAAATCATGCACGGTTTGCAGCTAAATGA

YDL147W, 445 aa (SEQ ID NO 88)

MSRDAPIKADKDYSQILKEEFPKIDSLAQNDCNSALDQLLVLEKKTRQASDLASSKEVLA  
KIVDLLASRNKWDDLNEQLTLLSKKHGQLKLSIQYMIQKVMYLLKSSKSLDLNTRISVIE  
TIRVVVTENKIFVEVERARVTKDLVEIKKEEGKIDEAADILCELQVETYGSMEMSEKIQFI  
LEQMELSILKGDYSQATVLSRKILKKTFFKNPKYESLKLEYNNLLVKISLHKREYLEVAQY  
LQEIYQTDIAKSDEAKWKPVLSHIVYFLVLSPTYGNLQNDLIHKIQNDNNLKKLESQESLV  
KLFTTNELMRWPIVQKTYEPLNEDDLAFGGEANKHHWEDLQKRIVIEHNLRLVISEYYSRI  
TLRLNELLDLTESQTETYISDLVNQGIYAKVNRPAKIVNFEKPKNSSQLLNEWSHNV  
ELLEHIETIGHLITKEEIMHGLQAK

YDR253C, 1076 bp, CDS: 501-1076 (SEQ ID NO 113)

TTTCCCCGCTAAAATAACGCCAGATGCTTTCTATGCTTCTAATCTTTTACCATTTACCTT  
TGTTTATTTCAATATAAACTTTAATTTACAGTCCCTATCTATTGCCCGACTGGACTAACA  
TGCACGTGACATTTTGTGATGGTTTTTCGTCCCTTACTTAGTACGCTTAGTACGCCACAG  
TTTATATTTTCTTGACAATAATAAGAACCTGATTGTGGGTTAGAACTTGCTATACTTTT  
AGTTTAAAAATAAGCAGGAAATAATCTTGAGTTCTGTATCATTATTATAAAATAAACTATA  
TTTGTCTCTTTGTCGCCCTCGGAACCTTTCTCATTACATTGACGAGGTATATATAGATA  
TAGTAGATATACATATCTATCCATGGTATATATGTATGCATCTGGATAATTGAATAGGGT  
TTCATGTCAATATGCCAAGAATTTGTTAATAATATAGTGGAAAAAGTCAAGAGGTATTAT  
AAATTTCAAAAAAGTACCAAATGGAGGATCAGGATGCTGCATTTATCAAACAGGCTACAG  
AAGCAATAGTGGATGTATCATTTAAATATAGATAACATAGATCCTATAATAAAGAGTTAT  
TAGAAAGGGTAAGGAATAGGCAAAACAGGTTACAAAATAAAAAACCAGCACTCATACCGG  
CAGAAAATGGTGTGATATAAATAGTCAAGGCGGTAACATAAAGGTTAAAAAGGAAAAACG  
CATTACCAAAAACACCGAAGTCCAGCAAAAAGCAAAACCCCAAGATCGTAGAAATAGTACTG  
GTGAAAAAGATTTAAATGTGCGAAATGTTCTGTTGGAATTTTCAAGATCATCAGATTTGA  
GAAGGCACGAAAAGACACACTTCGCCATATTGCCTAACATTTGTCCTCAATGTGGCAAAG  
GTTTTGCAAGGAAAGATGCATTGAAAAGACATTATGATACACTGACATGTAGGAGAAACA  
GGACTAAATTACTAAGTGCAGGTGGTGGGGTATCAATGAATTACTGAAAAAGTCAAGC  
AATCCAACATCGTTTCATCGTCAAGATAACAACCACAATGGTAGCAGTAATGGCTGA

7/251

YDR253c, 191 aa (SEQ ID NO 114)

MEDQDAAFIKQATEAIVDVSLNIDNIDPIIKELLERVRNRQNLQNKKPALIPAENGVDI  
NSQGGNIKVKKENALPKPPKSSKSKPQDRNSTGEKRFKCAKCSLEFSRSSDLRRHEKTH  
FAILPNICPQCGKGFARKDALKRHYDTLTCRRNRKLLTAGGEGINELLKKVKQSNIVHR  
QDNNHNGSSNG

YDR276C, 668 bp, CDS: 501-668 (SEQ ID NO 117)

ACCTTTAGTTCTTAGCATCACCAATCGCAGACATCCAACGTATCCGTGCGCGTAATCCTT  
CTCTTGGTAGTTGAGCACAGCATACAGAAGAAGCCGCGCGCAAGCGGTAATGTCTTTCC  
TCCGGCCTTCTAACCACCAAAACCGATCTCGGAACATGGGGGGGGGAAGGTCTCTGAAT  
CGAAAAACCCGAGACAGCGAGAGGGATTTTGCAGAAAAATTACAAAGATCACTATTTACTG  
CTCCCCTCACTTCCGCAGTCCCCTAATAGCGGAAGATGCAATGGGTGTGGGCTCTGGGTG  
CCCTTTAACCACGCCCTCAAAGGGGGTCTGTTATTTGCGATGGGCGCCTCTATAAA  
TACAAAAGAGGAAGTGAGTGTTTTTGTTTTGGAAGAGGGAAAGGAAAAAGAAAGAAAT  
TTACTATCGTTGTGTTTTTCGCCAGTATAATACAATTGATTATACATTTTGAACATAA  
CAGCACAGCACAAATACAACAATGGATTCTGCCAAGATCATTAACATTATATTTACCTTTT  
TCTTACCACCAGTCGCCGTTTTTCTAGCCCGTGGGTGGGGTACTGACTGTATAGTGGATA  
TCATTTTGACCATTTTGGCTTGGTTCCCAGGTATGCTATATGCCTTGTACATTGTCTTAC  
AAGATTAA

YDR276C, 55 aa (SEQ ID NO 118)

MDSAKIINIILSLFLPPVAVFLARGWGTDCIVDIILTLAWFPGMLYALYIVLQD

YDR377W, 806 bp, CDS: 501-806 (SEQ ID NO 127)

AATACAAGACTTGGTGGTCAGCGGAGCGCTATCCTTAGAGAATTCTATCGACCTCTCTAA  
TATCAAGCACACCACATGGAAGGATTGGGAAAGAAATCAACAAGAGGAATTGCTTCGGGG  
CAAAAAGGAACACAAAACCTCGGTCAAAGTTTTTAACCTTTTGAAGAGTTGTGGAACGGTGT  
AGAAGGCATATAAAATAGATCGTTAATATATTTCTAACATCTTCTTGTAAATGTAAATAT  
TTTAAAGGGTTGATCTTATTACGGAGAGAACCAATCATATCGAAGGATTTCTCAATAGT  
AAGTATCCCGCGCGTGGTCTCCTCGGGGAAATAGAACGAGAACTTCAAGTACTTGATAGCA  
AGAAAGTGAGTGCTTGGCTTCCCCATTTTGATTATAAAGAAAGGCATTATTTCTAGGGC  
AAGAAAAGACATTGTTGAAATTGTTCCAGAACTTTTCATTTAAAGTCTTTTCGTGAAAGGA  
GTGGACGTCAAAAAGAAATAATGATTTTTTAAACGTGCAGTATCTACATTGATTCTCCCAA  
AAGTTGTGTCTTCCAAGAATATAGGTTCCGCCACCAATGCCAAGCGCATTTGCTAATGTTG  
TTCACTTTTATAAGTCTTTGCCCTCAAGGACCAGCACCAGCCATCAAGGCTAACACTAGAT  
TGGCCAGATACAAAGCCAAGTACTTTGATGGGGATAATGCTAGTGGTAAACCATTTGTGGC  
ATTTTGCTCTAGGTATAATTGCCTTTGGCTATTCCATGGAATATTATTTTCATTTGAGAC  
ATCATAAAGGTGCGGAAGAGCATTGA

YDR377W, 101 aa (SEQ ID NO 128)

MIFKRAVSTLIPPKVVSSKNIGSAPNAKRIANVVHFYKSLPQGPAPAIKANTRLARYKAK  
YFDGDNASGKPLWHFALGIIAFGYSMEYFHLRHHKGAEH

YEL039C, 842 bp, CDS: 501-842 (SEQ ID NO 141)

AGTAATTGTCTCCCATTTTTGGTATACGAGCTAGCAGGACCTTTTGCCCAATGACCATT  
CATATTCACTCCCACTCACCACCGTCATCGTTGGTATTATTATTATCATTCGCTTGAAGA  
AAAAGAAACGAAAAAGAAATGGATCAGCAGCCGGGTATAGCGCCCCCTTATTGAATTAT  
TTTCTTTCGTGCTTCTCTGAGAAGGGTCTGCAGTCCCCCGCCGAGGGGTCTTTTCCAC  
CTTCTCAAAGCTAATAGCGATAATAGCGAGGGCATTATTCAAGTTCCAACACTATAAG  
TGGCCGCAAGGGGCAAGACAAAGGCACACAACATATATATATATCGTGTGTGAAGCTC  
GAGAAGATTAGATCAGAATAGTTCTCTTTTTGTTGAGGTTGAAACAAAATCAAAGACTTA  
TACAAGAAGATCACATACAAGCATTTATTTCACATTACTTTAAGTAAACTTCAGTAAACTA  
CATTACATCATAAACAAAACATGGCTAAAGAAAGTACGGGATTCAAACCAGGCTCTGCAA  
AAAAGGGTGCTACATTGTTTAAACGAGGTGTCAGCAGTGTACATAATAGAAGAGGGTG  
GTCCTAACAAAGTTGGACCTAATTTACATGGTATTTTTGGTAGACATTCAAGTCAAGTAA  
AGGGTTATTCTTACACAGATGCAACATCAACAAGAACGTCAAATGGGATGAGGATAGTA

8/251

TGTCCGAGTACTTGACGAACCCAAAGAAATATATTCCTGGTACCAAGATGGCGTTTGCCG  
GGTTGAAGAAGGAAAAGGACAGAAACGATTTAATTACTTATATGACAAAGGCTGCCAAAT  
AG

YEL039C, 113 aa (SEQ ID NO 142)

MAKESTGFKPGSAKKGATLFKTRCQQCHTIEEGGPNKVGPNLHGIFGRHSGQVKGYSYTD  
ANINKNVKWEEDSMSEYLTNPKKYIPGTKMAFAGLKKEDRNDLITYMTKAAK

YER112W, 1064 bp, CDS: 501-1064 (SEQ ID NO 147)

TACTGAAGTCCCTCTAAACCTACTGCCTTTTATTTTAGGCTCTAAAATAACCATGGACA  
ACGTGAATTGGGTAGCATCTTTTTTTTAAATAGATAGTTTATTATGTATAACAATAATTTA  
AAGATATTCATAGTGATAAGTAATTTTAAATGAGTTTAAAGTACTACTTTTCCTTTACCG  
CCAGTTTCCGTACTATGAAAAAGGCAAATTCGCATTTGTAGCCGCCACACGCATTTTG  
ATCATCAATTACGAAATTTGCCGCACACGTGTACGTGATAAGCACCTCTTACTATCATGT  
TTTACGGAGTAGCAATGATGTTCAATTATTGCAGCTTTCTTTTCGTGAAATCGTAGTATCA  
TAGACCTTCCTAATGATGGAAGCGGTAAAGAAGGAAATCGTAAAAGTAAATTAACGGAAGT  
AGTATTAGTAAAACAGAGTTGAAAACTGATAAATCTTCAACTCGAACTGAAAAGAAACA  
CAATAGAATATTTTTTCTCAATGCTACCTTTATATCTTTTAACAAATGCGAAGGGACAAC  
AAATGCAAATAGAATTGAAAAACGGTGAAATTATACAAGGGATATTGACCAACGTAGATA  
ACTGGATGAACCTTACTTTATCTAATGTAACCGAATATAGTGAAGAAAGCGCAATTAATT  
CAGAAGACAATGCTGAGAGCAGTAAAGCCGTAAAATTGAACGAAATTTATATTAGAGGGA  
CTTTTATCAAGTTTATCAAATTGCAAGATAATATAATTGACAAGGTCAAGCAGCAAATTA  
ACTCCAACAATAACTCTAATAGTAACGGCCCTGGGCATAAAAGATAC TACAACAATAGGG  
ATTCAAACAACAATAGAGGTAAC TACAACAGAAGAAATAATAAACGGCAACAGCAACC  
GCCGTCCATACTCTCAAACCGTCAATACAACAACAGCAACAGCAGTAACATTAACAACA  
GTATCAACAGTATCAATAGCAACAACCAAAATATGAACAATGGTTTAGGTGGGTCCGTCC  
AACATCATTTTAAACAGCTCTTCTCCACAAAAGGTCGAATTTTAA

>YER112W, 187 aa (SEQ ID NO 148)

MLPLYLLTNAKGQQMQIELKNGEIIQGILTNVDNWMNLTLNVTSEYSEESAINSEDNAES  
SKAVKLNEIYIRGTFIKFIKLQDNIIDKVQQQINSNNNSNSNGPGHKRYNNRDSNNNRG  
NYNRRNNNGNSNRRPYSQNRQYNNNSNNINNSINSINSNNQNMNGLGGSVQHFNSS  
SPQKVEF

>YFR010W, 2000 bp, CDS: 501-2000 (SEQ ID NO 153)

GAAAAATTTCAACGGTGGTGTCTTAATGGTTTCCCATGATATCTCTGTTATTGACTCTGT  
TTGTAAAGAGATTGGGTTTCAGAGCAAGGTACTGTCAAGAGGTTTCAAGGTACAATTTA  
CGACTATAGAGATTACATCTTGCAGTCTGCTGATGCTGCAGGTGTGGTTAAAAAGCATTG  
ATTATTTAGGAAGCACCTCAGAATATATTTTCCATAGAAGCCTAAATTAAGTATGCATTC  
ATAGCCCCATGATACTTTTTTTTTTGACTACTTGTATTGGAATCTAATTGACCTAAGTGG  
GCATTCTGGGTCAATTGGTATATGTATCACTTTTTTACGTAAAAAAGTAGTGGCTAATATAA  
AACATAAAATCTACAAGAAGGGTGAAGTGCTTTTTCGAATTTTGCCACTGCAAGTAATTGG  
TGCAATTGAAATACGAGATTTCTGTTCTCTAAGAGGATATAAAAAAAGGAAATTAGCCCT  
ACCTATCCTTGTGTTAAATATGAGCGGAGAAACGTTTGAGTTCAATATTAGACATTTCTG  
GTAAAGTTTACCCAATAACACTTTCCACTGATGCTACTTCAGCAGATTTGAAAAGCAAAG  
CAGAGGAATTGACCCAAGTCCCAAGTGCCCGCCAAAAATACATGGTTAAAGGTGGCTTGT  
CTGGCGAAGAGTCCATTAAAAATATATCCCTTAATCAAGCCAGGATCGACAGTAATGCTAT  
TGGGGACTCCAGATGCTAACCTGATTTCTAAACCAGCCAAAAAGAATAATTTTCATTGAAG  
ACCTTGCGCCTGAGCAACAAGTCCAACAATTTGCTCAATTGCCTGTTGGTTTCAAGAATA  
TGGGCAACACCTGTTATCTGAATGCTACCTTACAGGCTTTATACAGAGTGAACGATTTAA  
GGGATATGATTCTTAATTATAACCTTCTCAAGGTGTGTCTAACAGTGGTGCACAAGATG  
AAGAGATTCACAAACAAATCGTTATTGAAATGAAGCGTTGTTTGAATAATTACAGAATA  
AAAGTTTCAAGAGTGTTTTGCCAATTGTGTTATTAAACACGCTAAGAAAGTGTATCCAC  
AATTTGCTGAACGTGATTCACAAGGTGGGTTCTATAAACAGCAAGACGCTGAGGAGTTGT  
TTACACAACATATCCATAGTATGAGTATTGTTTTTGGTGACAAATTTTCCGAAGATTTCA  
GGATTCAATTTAAACTACCATCAAAGACACAGCTAATGATAACGATATTACTGTAAAG

9/251

AAAATGAAAGCGATTCTAAATTACAATGTCATATTTCTGGTACTACAAATTTTCATGAGAA  
ATGGGCTCCTGGAAGGTTTGAATGAGAAAATTGAAAAAGATCAGACTTGACTGGCGCCA  
ATTCCATCTATAGCGTCGAAAAGAAAATATCAAGATTACCAAAGTTTTTAACTGTTCAAGT  
ACGTTAGATTTTTCTGGAAGGTCACCAACAAAAATCTAAAATATTGCGTAAGGTCG  
TTTTCCCATTTCAATTAGATGTTGCAGACATGCTTACCCAGAAATACGCAGCAGAGAAGG  
TAAAAGTTCGTGACGAAGTGAAGAAAGTTGAAAAGGAGAAAAATGAAAAGGAAAGAGAGA  
TCAAAAGGCGTAAATTTGACCCATCATCCAGTGAAAATGTCATGACACCAAGAGAACAAT  
ATGAGACACAAGTGGCTCTTAACGAAAGTGAAGAAAGATCAATGGCTCGAAGAGTATAAGA  
AACATTTTCTCCAACTTGGAAGGTTGAAAACCCATCTTGTGTTTATAACTTGATCG  
GTGTCATTACACATCAAGGTGCAATTCTGAGTCTGGACACTATCAAGCTTTCATAAGGG  
ACGAAGTGGACGAAAATAAATGGTACAAATTTAATGATGATAAAGTTAGCGTTGTTGAAA  
AGGAAAAAATTGAATCTTTAGCCGGTGGGGGCGAAAGTGATAGTGCATGATCTTAATGT  
ATAAAGGATTTGGTCTGTAA

>YFR010W, 499 aa (SEQ ID NO 154)

MSGETFEFNIRHSGKVYPITLSTDATSADLKSAAELTQVPSARQKYMVKGGLSGEESIK  
IYPLIKPGSTVMLLGPDPANLISKPAKKNFIEDLAPEQQVQQAQLPVGFKNMGNTCYL  
NATLQALYRVNLDLDMILNPNPSQGVNSGAQDEEIHQIVIEMKRCFENLQNKSFKSVL  
PIVLLNLTLRKCYQFAERDSQGGFYKQDAEELFTQLFHSMSIVFGDKFSEDFRIQFKTT  
IKDTANDNDITVKENESDSKLQCHISGTTNFMNRGLLEGLNEKIEKRSDLTGANSIYSVE  
KKISRLPKFLTQYVVRFFWKSTNNKSKILRKVVFPQLDVAADMLTPEYAAEKVKVRDEL  
RKVEKEKNEKEREIKRRKFDPSSENVMTPREQYETQVALNESEKDQWLEEYKKHFPNL  
EKGENPSCVYNLIGVITHQGANSESGHYQAFIRDEL DENKWKFNDDKVSVEKEKIESL  
AGGGESDSALILMYKGFGFL

>YFR052W, 1325 bp, CDS: 501-1325 (SEQ ID NO 157)

CAGAGACATGTTTTAATTCAAGTGATGAGGCGAAACGTGCAAGATCCTAAATGAAGGAT  
AAAAAGAGTTCTTAAAAAGGGAAGTAAGGAATAACAGAGTAGAAAAACCGAAAAGACAAC  
TTAACAAATCGGCAACACTTTTATGGGGCCCCGCTCGCCTGTGTGCAAGTAGTATTCGAC  
CTGGAACACGCAATTTACCACGAGAAGACAGCAATAGTCCGTACAACATTAATTAGTTTTCG  
ACAATTGCTCGCCTTTATAAGCCATGCTAGTGCCCAATCAAACACTTTACTTGCCCTGAA  
GTTCCTTTTTTTCGCTAGCCTGTAACTTAAATAAGCCATCTAACCTTTTTTTTCTAAAAAT  
TTTCTTTATTACCCTGTGCGCTTATTTTCTATTCTACACATTATTTGCCACCCATTGAAA  
TTGTAGCTTGTATTAATAGGGAAAAGCCGGAAGTATAACCGGTGGAAGTACTATTGAAG  
TGAGATAAGAAGCCATCGTAATGCCCTCGTTAGCCGAATTGACCAAGTCGTTAAGCATAG  
CCTTTGAAAACGGCGATTATGCCGCGTGTGAGAAGCTCTTGCCCCCTATCAAGATCGAAC  
TTATCAAGAATAACCTTTTAAATACCTGACTTATCCATTCAAATGACATCTATTTGAATG  
ATTTGATGATTACTAAAAGGATCCTGGAAGTAGGTGCCCTTGCTAGCATCCAACTTTCA  
ATTTTGACAGCTTCGAGAATTACTTCAACCAATTGAAGCCTTACTACTTTAGCAACAATC  
ATAAATTATCTGAATCTGACAAGAAATCGAAGCTGATAAGTCTGTATTTGTTGAAGTTAT  
TGTCTCAGAATAACACAACCAAGTTTCACTCGGAATTGCAGTATCTAGATAAACATATCA  
AGAACTTGGAAGACGATTCACTTTTGTCTTACCCTATCAAACCTAGACAGATGGCTCATGG  
AAGGGTCGTACCAGAAAGCATGGGATCTTCTGCAATCTGGGTGCGAGAATATATCAGAAT  
TCGACTCTTTTACCGATATCCTAAAATCAGCTATAAGAGACGAAATTGCTAAAAATACCG  
AGCTATCCTACGACTTTCTCCCTCTCTCCAACATAAAGGCTTTGCTCTTTTCAACAACG  
AAAAAGAACTGAAAAATTTGCACTAGAGAGAACTGGCCTATTGTCAACTCGAAAGTTT  
ACTTCAATAACCAATCAAAGGAGAAAGCTGATTACGAAGATGAAATGATGCATGAAGAAG  
ACCAAAAGACAAACATTATCGAAAAAGCAATGGATTATGCCATAAGTATTGAAAATATTG  
TGTA

>YFR052W, 274 aa (SEQ ID NO 158)

MPSLAELTKSLSIAFENGDYAAACEKLLPPIKIELIKNNLLIPDLSIQNDIYLNLDLMITKR  
ILEVGALASIQTFFNDFSFNQYFNNHKLSESDKSKLISLYLLNLLSQNNNTT  
KFHSELQYLDKHIKNLEDDSLSPYIKLDRWLMESYQKAWDLLQSGSQNISFDSFTDI  
LKS AIRDEIAKNTELSYDFLPLSNIKALLFFNNEKETEFALERNWPIVNSKVYFNNQSK  
EKADYEDEMMEEDQKTNIEKAMDYAI SIENIV

10/251

&gt;YGL072C, 860 bp, CDS: 501-860 (SEQ ID NO 159)

ACTCTTTTGTCTAGGGAGTTTCTGTCTGCTAAGAGGTTTGTCAATGACACCGAAAAGAGGAT  
AATAGGTAATACTTTTGTAACTGTAAAGAAATATTAAATCGTTTTCACGGAATTGGCCTC  
TTCCCTATATTCTATCCGAGGTTGTGTACTGTAGCGGTTTATACTTCAACCTGTGAAAGT  
TATGTAATATGCGAATTCTGTTTCTGCTTGATAATCTGAAGAATATAGTCTCGAGCACGC  
GATGGAGCAGAAAGGGGAGAAATGAATACTGATGAGCTTAACGATGAGGAGGCCGTTTCC  
GTTTCTCTTGATTACCCCTTTCATCCAACAGTCAATATAAGTACGCCAACTTGCGTTAAAA  
CGGCCAATGTGACACCAGTTCACCTCGGCAAGCCCTTCTCAGGCTCTCACTAGCTCGAATA  
ACGAGAACTCTTCACGACTCATCTACTTGGCATTTTCCGGGTGCAGTTCAACCTCACTCG  
CGTGCGGCGGTGTGAGGTGCATGGGTGCCGGTATTTTTTTTAGTTTCGCTCTGCGCCTTAC  
GCGATCAGCTTCGAGAACATACTATATTAAATGATTATATACGCTATTTAATGACCTTGC  
CCTGTGTACTATTCTTAGCTCGTTTGGGCAGGCGGTGATCGTTGTACTCTGTGCGGTCCTC  
TGTATTTGACTATAGCCGGTTCCGGTATTTCTCCACAAATCTTTCTTAGCGTTCTCG  
GGCGCGGTGTCGGCTGGGTGGAATACTGTGGTCATTAAAGCTTGGCAGGTTATCACTC  
ACTTTAGTGTTTTCACTGGCGCTGAACCTTATATCGGGGGACACCCTTGTAATTCCCTCA  
CTAGTGTATTGTCTGTTTAG

&gt;YGL072C, 119 aa (SEQ ID NO 160)

MGAGIFFSSLALRDQLREHTILNDYIRYLMTLPCVLFLLSFGQAVIVVLCRVLYFDYSR  
FRYFLHKSFLSVLGRRVGLGGITVVIKAWQVITHFSVFSGAELYIGGHPCTSLTSVIVV

&gt;YGL080W, 893 bp, CDS: 501-893 (SEQ ID NO 161)

GAAGAAAAAGAAGAGGGGATGATGAGGAAGGAGAAATAGAACTTGAAATTATTAGAGTA  
AAAAGAAATAAAGGCAGGACGAAGATAAAGAAGACGCTTACTTGCTTCTCGAAAAACAAG  
AAAATTATTACCCCTCAGCACTCCAATAGTATGTGGTTACTACTAATAGTAATCTTGATT  
TTTGACCGCCTACTATCGAATTAAATATAATTTTATAACCCAGTTCTATATTGCTGGGTG  
GTATTATAGCTTCATGGCTAGTCAAATAAGTGGAGTTTFTTGTCTCGACGTGGCCTGTA  
AAGTTCTCTTTTGCAGCGGCCCCCGCTTTAACCGAGGCGAAATGACAAGTGCTTTCTGG  
CAAAGAAGGAATAGCCACTACAACCTGCGGTCTCCACCTTTCTCCACCGATAATCTATTT  
AAACACTCACTTGCCAATCAGCAAACGTCAATACATCTACATATATACGTATAGATTTTA  
TTGCACTGTGATCAAAAAGAATGTCTCAACCGGTTCAACGCGCTGCAGCACGCTCATTTCC  
TTCAAAAATACATCAATAAAGAACTTTGAAATATATTTTACAACACACTTCTGGGGTC  
CCGTATCAAAATTTGCGGTATCCCAATTGCTGCTATATATGATCTGAAAAAAGACCCCTACAC  
TAATCTCTGGCCCAATGACTTTTGCTTTAGTTACCTATTCAGGTGTTTTTCATGAAGTATG  
CTCTTTTCAGTATCACCCAAAACTACTTACTGTTTGGATGCCACCTTATTAATGAAACTG  
CGCAATTAGCTCAAGGCTATAGGTTTCTCAAATACACGTATTTTCAACAACAGATGAGGAGA  
AGAAAGCTCTAGATAAGGAATGGAAAGAGAAAGAAAAAACTGGTAAACAGTAA

&gt;YGL080W, 130 aa (SEQ ID NO 162)

MSQPVQRAAARSFLQKYINKETLKYIFTTHFWGPVSNFGIPIAAIYDLKKDPTLISGPMT  
FALVTYSGVFMKYALSVSPKNYLLFGCHLINETAQLAQGYRFLKYTYFTTDEEKKALDKE  
WKEKEKTGKQ

&gt;YGR008C, 755 bp, CDS: 501-755 (SEQ ID NO 165)

CGCAATAGTTATGAACTTAACCGAGCTCAAATAATTTAAAGATAAAAAGATAAAAAGATAAA  
AGATAAAAGACAAAAGAAAATTCATAGCCCATGTTGAAGTATCCCAGCGGGAAATGTTGC  
TATCCAACAGAAAGTACCAAGCCAGTTTCAAAAAGGTACAGAATTAAGTGATGCTATCCG  
TCCCACAATAATTTTCTCCAGCGGAGGAAATATACGCGGAGGGGGGAGGAAAACCTCT  
CAGTAAGCAATGAAGGGATAGATAAATGGGGCGCGCCTGCCATAGCTTAGGCTAAGAACT  
CCTTCGAAAAACAGGGGGCTGCGAGCGCAGAAGCGAACACTTGTCATTTGTATAAAAGGAC  
TATTTATAAGTTTGTCTTTTGTCACTCTCTTGGCCCTAATTACCCATACTATTGTAACAA  
TTGTTGTGTAACTCAATTATACAAATAAACGAACAATCAACAGTAACAAACCGCTCAAG  
TGTACAACCAATCAGAAAAAATGACGAGAACAAACAAGTGGACCGAACGTGAAGGAAAGG  
CTGATCCAAAGTACTTTTCGCACACTGGTAACCTACGGTGAATCTCCAAATCACATCAAGA  
AGCAAGGTTCCGGCAAGGTAATTGGGGTAAGCCAGGCGATGAGATTGATGACTTAATTG  
ATAATGGTGAAATACCCCCAGTGTTCAGAAAGATAGAAGAGGCTCAAATTTGCAATCGC

11/251

ATGAACAAAAGTTTGAACCGTCCAAAAGGAATGA

&gt;YGR008C, 84 aa (SEQ ID NO 166)

MTRTNKWTTEREGKADPKYFSHTGNYGESPNHIKKQSGSGKNWGKPGDEIDDLIDNGEIPP  
VFKKDRRGSNLQSHQKFENVQKE

&gt;YGR023W, 2156 bp, CDS: 501-2156 (SEQ ID NO 167)

TTAGATCATGGCTAGGGGGATCTGGAAGTACAATGATGTGCTCTCCCCCTCTCAAACACA  
ACACCAGGATGAACTAAGGGCTCATCTCGAAAGTCGAAGGTGCCTCATTCAAGTTATTAG  
TGGTGCCTGTTGTGTCTTCCATGAACAAGGAGCACTTAATTACTTGTGTGTCATGAGAT  
ATCATTTTTTTTTTCCCTCTTTCTTGGGGTCTTGACAGTCATCAAATCGAAGTTTTTAG  
TTTTTCTTCTTCGGGAAGATCAATTTAGGTAGAAAAGTGTAGATGAAAACGAAGGATA  
CTGCTATTTACTGTAAGTACTCTTCGGTCCATATTGGAAGACCAAGGCATAATAAGGATA  
TATTCCGAGGAGATAAATTGGGATATAATCCTCCATTGCTTCCGAAATTTGTTTAAACACT  
TCTAGTTCATTTTCGGGTGGTTCGATCTTCGTTTCCACTTTTAACTTACTCCAGTTAGT  
ATAATATAAGTAGTTAAGGTATGGCAAGCTGCAATCCGACCAGGAAGAAGAGCTCTGCTT  
CAAGCCTATCTATGTGGAGAACGATTCTCATGGCGTTAACAACACTACCGCTAAGTGTTT  
TTTCGCAGGAGTTGGTTCAGCTAATAGCACAACATCGAGCACAGCTCCTTCCATCACTT  
CGCTTTCCGCAGTTGAGTCATTTACGTCCAGTACCGATGCAACGAGCAGCGCAAGTTTAT  
CAACGCCGAGTATAGCTTCAGTATCCTTTACTTCCTTCCCACAAAGTTCTTCACTGCTTA  
CTCTTTTCGTCAACATTATCCTCAGAACTTTCCTCTTCGTCCATGCAAGTTTCGTGCTCTT  
CAACATCGTCGTCTTCTTCGGAGGTTACGTCAATCATCGTCATCATCAATATCTCCTT  
CCTCTTCATCATCAACAATAATATCATCGTCATCATCACTGCCGACATTCACTGTGGCAT  
CAACATCTTCGACAGTTGCCTCCTCCACACTTTCCACTAGCTCATCGTTGGTTATCTCTA  
CGTCTTCGTCAACGTTTACGTTTAGTTTCGGAAAGTTCAAGCTCTTTGATTTCTCTTCAA  
TTTCAACATCCGTTTTCGACTTCTTCAGTGACGTTCCCTCCTCTTCAACTTCATCTCCAC  
CTTCGTCTCATCCGAATTGACATCATCCTCGTACTCATCATCCTCATCCTCATCCACCC  
TCTTTTCTACTCCTCCTCATTTTCATCATCCTCATCCTCATCCTCATCATCCTCTT  
CATCCTCATCATCATCATCATCATCATCATATTTACCCTCTCCACATCTTCTCTT  
CATCCATATACCTCGTCTTCGTCAATCCTTCATTTTCATCTTCATCTTCTCAAACCTA  
CCTCATCAATCACTTCTACATCCGCTCATCTTCTATTACTCCGCTTCCGAATATTCCA  
ATTTGGCAAAAACCATAACTAGTATAATAGAAGGCCAGACCATCCTCTCTAACTACTATA  
CCACAATAACGTATTCACCGACAGCATCCGCATCTTCAGGAAAAAATTCACATCACTCAG  
GCTTATCAAAAAGAATCGTAATATTATCATCGGTTGTGTGGTTGGCATAGGTGCCCCC  
TCATCCTAATTCTACTAATATTGATTTACATGTTTTGTGTTTCAGCCTAAAAAACGGATT  
TCATTGACTCTGACGGTAAAATTGTACAGCTTATCGTAGTAACATTTTACCAAAATAT  
GGTATTTCTTGCTGGGTAAAAAATTGGTGAAACAGAAAGATTACAGCTCAGATTCCCCCA  
TCGGCAGCAATAATATTCAGAATTTTGGTGATATCGATCCAGAAGATATACTTAACAATG  
ACAACCCCTACACCCCTAAACACACTAATGTTGAAGGCTACGACGACGACGACGACGACG  
ACGCTAATGATGAAAACCTATCATCCAATTCCATAACAGAGGCATAGATGATCAATACT  
CACCTACTAAATCTGCATCATATTCAATGTGCAATAGTAATAGTCAAGATTACAACGACG  
CAGATGAAGTAATGCACGATGAAAACATTATCGTGTATTATGATGACAGCGAAGCTAGCA  
TCGACGAGAACTATTACACGAAACCAACAACGGCTTAAATATCACGAACCTATTAA

&gt;YGR023W, 551 aa (SEQ ID NO 168)

MASCNPTRKKSSASSLSMWRTILMALTTPLSVLSQELVPANSTTSSTAPSITSLSAVES  
FTSSTDATSSASLSTPSIASVSFTSFPQSSSLTLSSLSSSSMQVSSSSSTSSSS  
EVTSSSSSSSISPSSSSSTIISSSSSLPTFTVASTSSTVASSTLSTSSSLVISTSSSTFT  
FSSESSSSLISSSISTSVSTSSVVPSSSTSSPPSSSELSSSYSSSSSSSTLFSYSS  
FSSSSSSSSSSSSSSSSSSSSSYFTLSTSSSSSIYSSSYPSFSSSSSSNPTSSITST  
SASSSITPASEYSNLAKTITSIIEGQTILSNYYTTITYSPTASASSGKNSHHSLSKNR  
NIIIGCVVGIGAPLILILLIYMFVCPKKTDFIDSDGKIVTAYRSNIFTKIWFLLGK  
KIGETERFSSDSPIGSNINQNFIDIDPEDILNNDNPYTPKHTNVEGYDDDDDDANDENL  
SSNFHNRGIDQYSPTKSASYSMSNSNSQDYNDADVMHDENIHRVYDDSEASIDENYYT  
KPNNGLNITNY



12/251

>YGR034W, 1244 bp, exon1: 501-525, intron1: 526-879, exon2:  
880-1244 (SEQ ID NO 169)

TATAAAAAAAAAATTCCTGTAGACAATAAAAAAAGAAATGCCCCATTTTGTAACTTAGCGAAA  
GATGCCCAGTACATCCCTTTTACACCCGTGCATTAAAGGTGTTTGGGTTTAATAGGAGCT  
TTATCATATCTCTTTGATTTTTTTTCTGCTGTCCTCGGCTTGAGGGACTCACAGAGATCT  
GGAAATTTTCAGATTGTCAGTGCCTTAGGATGGGTTGTCTAGTAGACGGTGGCCGCCGTGGA  
TGGGAAATCTCATACGTTTACACACATAGTGTGTTGGAAATTAATAGTAGCAATAGCTATC  
TGGCTACTGTTTTAAAGTATTAGCCCGTTCTCAGTGCCTCTTTTTTAAGGAATAACAACG  
GCAAGACCAAAGATATATCAAATATGGCTAAGCAATCTCTAGGTATGTTTGGAGGATACG  
AATAACGATAGAAAACATGAGTGAATTTCCGTCCACGAAAAAATGTTAACATAAAATGCA  
AGAGAACAATTAATCGAATAATGTTAAATTATTGTAAAAACAATGTGTATGATGAGGAGGA  
ATTGTACCTAAGCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGAAACAGCTTTTGCAT  
ATTCAATCCAGGCATAGGGCGACTATTTAGCACTCAACGATTTTAAAGCTTGTGTATTGCT  
TGACATAAATTTCCGGCTTTAGAATCCAATATTGAAAAACGTGAGTACGCAGAGGAGATAG  
AAGAAAAGTAGGAAGTTACCGTTTATATTGATTTGTGAAATGCATACTCCGTTTGGATGTG  
GGGCAACATAGATTTAAGTGTGGATGAAAAATTATGTGCTCATTGTGAAAAAAAAAGTTTTG  
CTTTTACTAACAAATTTTTTTTATTATTTGTTTTCAATAGACGTTTCCTCTGACAGAAGAA  
AGGCCAGAAAGGCTTATTTCACTGCTCCATCCTCTGAACGTCGTGTTTTGTTATCTGCTC  
CATTATCCAAGGAATTGAGAGCTCAATATGGTATCAAGGCTTTGCCAATCAGAAGAGACG  
ATGAAGTCTTGGTTGTTTCGTGGTTCCAAGAAGGGTCAAGAAGGTAAGATTTCACTGTGTT  
ACAGATTGAAGTTTGCTGTTCAAGTTGACAAGGTCACCAAGGAAAAGGTCAACGGTGCTT  
CCGTTCCAATTAACCTTGCACCCATCCAAGCTTGTTATCACTAAGTTACACTTGGACAAGG  
ACAGAAAGGCTTTGATCCAAAGAAAGGGTGGTAAATTGGAATAA

>YGR034W, 129 aa (SEQ ID NO 170)

MLNYCKTMYVSSDRRKARKAYFTAPSSERRVLLSAPLSKELRAQYGIKALPIRRDDEVLV  
VRGSKKGQEGKISSVYRLKFAVQVDKVTKEKVNGASVPINLHPSKLVITKLHLDKDRKAL  
IQRKGGKLE

>YGR069W, 836 bp, CDS: 501-836 (SEQ ID NO 171)

TTCGAATTATTTTTGTGAAAACAGGCTCGAAAGTGATCTCTTGCTTAGAAATATTGCGT  
TGCCGCTGGTGTCCATATCTTGGTTGCTTGTAAGTGCAGCCGCTACTACTGTTATGTTGAT  
TTTCCGCATTTTCCCCACCGACTAAAAACATCCCTTTTGAAGAAACCAATAAGTTGTCCC  
AATAGCATTCGAAAATCTTACGCTTTTCCCTTAAGTACTTGCCAAACTACTGCTATTCT  
TCTTATATCGGCCAACTTGCAAAACTCCAATTTGAATCTTCTACCAATCTCAGCGAAA  
TTTTCTTCACTACGATCTCATTTTTCACTGAAATCACTAAGTTTCTGATAAAGGTATAG  
ACGACAGTTCCAACGGTGACCCTTGGATCAAAATTATGTCCTTGTAAGGGGAGTTTATTC  
TAATATCAAAATAACTTATTCTCTCTTTTCTTCTGCTCTGAATGCCACCGCTGCTAG  
ATAGCGAACTAAGTGAACATGGTCTTGCTTCACCTATTCTCGCCGAGAGCTGTACAA  
GATATTTTTTACTTTTGCCATCTTATACTCATCCTAATCATCTGTTTCATTTTCTCTTA  
TTCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTCAGTTTTCGAAGAAACTGCCTTTTTTA  
GAATTGTAAAAGACGAAGTGAAGTATTCAGGAGTATATTATTACATACATACAAAGCAAG  
ACAAAGAAACATTTTAGATCTAACATTTTACTTCAATTGTTTTTGTATTCCCTTATAATA  
AGAAAGACCTGCTGTTTAATGTGGGAGTAATCCGTCCCCCTACTCGATCTTCAATAA

>YGR069W, 111 aa (SEQ ID NO 172)

MVLLHPILAESCTRYFLLLPSTHPNHLFHFPSISFFFFFFFFFFFFSFRNCLFRIVKDEV  
KYSGVVYIHTKQDKETFLDLTFYFNCFCIPYNKKDLLFNVGVI RPLLDLQ

>YGR070W, 3968 bp, CDS: 501-3968 (SEQ ID NO 173)

AAGAAACATTTTTAGATCTAACATTTTACTTCAATTGTTTTGTATTCCCTTATAATAAGA  
AAGACCTGCTGTTTAATGTGGGAGTAATCCGTCCCCTACTCGATCTTCAATAAATTGTCA  
TCTTGATATCTAAAGGAGCGCTCCAGTACTCCAATTAAGCACCACCTAGTGGCTCTAGTGT  
CGATTTTTTTTTTACGCATACGTTTGTATGTTTCTTAAATTTCCCATGATTTTTTGTGTC  
CAATGTCATATCTACAACTCTATACGAAAGTAAACGCACTTCATCTTTTTTGCCCTAAA  
ACGGCAATATTTAGACATATCATAAGGGGCCCAAGGGAGAATCGTTAATTTTAACTTTT

13/251

CTTTGCTCTTGAATGAAAAAGTAAATAAAATAAACTAAATCAAAAAAAGAACGCCACGT  
TTGAATTTTAAAGCAAAAATTTTGTGATTTAGTAATGATATAAAATAAAACCAAGTCGTT  
GGTAAGAATTTGGTTAGGTATGAATAGTAATGAACGGATCTAAGAAATAAATATTTTT  
ATGAGATATTCGGTAAGAAAAGAAAATCAGATACTTCAACCCCTACTCAGTTGTTCTCCG  
GCTCCAAAGTTCAGACAAACATCAATGAAATTTCTATCACTAACGATGAGGATGAAGATA  
GTACTGAAGATGAAATAAGGCTTCATTGAAGGATTATACACTAGGGCAGACACCGGTG  
CACGGTATAGGATAGCACCGGACTGTTCTTCCCACCAATTAAAGGCATCTCCTGTCTTAC  
ATATTTCAACAAACCTTAATTCAAGTCCACAATCCTTCACAGGCGATCAGATTTACCTA  
CTAATAAAAAAATTTCAATAAATGATTCGACCAGACAAGATAAAGGTAACAGTTGCACTA  
CCACTTCATCACCTTCTCAAAAAAGATCGAATGTTTTGCTTCTCAGTAAGAAAACATT  
CATCTCCTTCACTATTATCATTTTCCAAAAACAGTGGCAGTCATATGGGGGATCCAAACC  
AGCTATCTACGCCCTCAACTCCCAAAAGTGCAGGTACACGATGGAGTTACACAGTTTAT  
TCAATGGAAACATAGTTCTTCTAGCACCTCTTCTTTATTTGCATTAGAGTCACTGAAAA  
CCCAAAATAGACGCTCATCAAACTCTTCCAATCATTTCTAGTCAATATCGACGCCATACTA  
ATCAACACCAACGTCATCATTTCAAGGTCCAAATCAAGTCCCTGTCTCTCTGACGGAATAT  
CCATGATCAAAGGCACGCCTTTGGTTTTATCCTGCACTTTTATCACTAATAGCAATTAAT  
TCAAACAGACCATCAAATTGAGCACGCATAAAAAGATGGGGTTACTTTACAGAGATTCCT  
TTACAGGAAAACAAGCAATTGATACCTTTATGCTTGATCATAGGAAGCTTAGATCGTAATT  
TGGGCATGTTGATCGGAAAATCGCTGGAAGCTCAAAAATGTTCCATGACGTACTTTATG  
ACCATGGCGTAAGAGATTTCTGTACTGGAGATTTACGAGTTATCTTCAGAATCAATTTTTA  
TGGCACATCAGTCGCAGAGTTCTACTTCAATTGCCAACACATTTTCTTCATCATCTTCTT  
CAGTTAATTCGCTCCGTACTAAACTGAAATATATGGTGTTTTTGTCCCATTTGACACATT  
GTTATTCCTCTACATGCTCTCTGGA AAAACTTTGCTACTCTATTTCTTGCCCCAATCGTT  
TGCAACAACAGGCTAATTTACATTTAAAATTAGGTGGTGGTCTTAAGAGAAATATTTCTG  
TAGCACTCGATAAGGAGGATGATGAACGAATTTCTGACAAATTTCTGTACCAAAGAGCG  
TATGGGAATCATTTATCCAAACAACAAATCAAAAGGCAGGAGGCAATATATGAGTTGTTTA  
CTACAGAAAAGAAGTTTGTA AAATCTTTGGAATCATCCGAGATACTTTTCATGAAGAAAT  
TATTAGAAACGAATATTATTCATCTGATGTAAGGATAAATTTTGTAAGCACGTTTTCG  
CACATATCAATGAAATATATTCTGTCAATAGAGAATTTTGAAGGCTTTAGCACAAAGGC  
AATCATTAAGCCCAATTTGTCTCTGGAATTGCAGATATATTTTGCAGTATCTTCTCTTCT  
TTGATCCTTTTTCTGTCATACATAGCATCAAGACCATACGCAAGTATCTAATTGAAACCC  
AAAGATCAGTTAATCCCAATTTTGCTCGTTTTGACGATGAAGTGTCTAATTTCTTCCCTGA  
GGCATGGGATCGATTATTCCTATCTCAGGGTGTTCAGACCTGGTAGATATTCACTGT  
TGGTAAGAGAAATAATACACTTCTCGGACCCAGTAACAGACAAAGATGATCTACAAATGC  
TAATGAAAGTCCAAGATCTTTTAAAGGATCTAATGAAAAGGATTGATAGAGCAAGCGGTG  
CAGCACAAAGATCGTTATGACGTTAAAGTGTTAAAGCAGAAAATTTCTATTCAAAAATGAAT  
ACGTTAATCTGGGTTTGAATAACGAAAAAAGGAAAATCAAGCATGAAGGTTTACTCTCAA  
GGAAGGACGTGAACAAAACAGATGCGTCTTTTTCAGGAGACATTCAATTTTACCTACTCG  
ACAAATATGCTATTATTTCTTGAATCAAAAGCTGTAAACAAGTGGCACCAACACACTGTAT  
TTCAGAGACCAATTTCCACTCCCTTTACTGTTTTATTTGTCCGGCTGAGGATATGCCACCCA  
TAAAAAGATATGTGACAGAAAACCCAAATTGCTCAGCGGGTGTGCTCTTACCCCAATATC  
AAACGAGCAATCCCAAGAATGCTATTGTATTTCGCCTATTACGGTACGAAACAACATATC  
AAGTTACTTTGTACGCGCCGACGCCGCGGATTACAGACATTAATAGAAAAGGTGAAAC  
AAGAGCAAAAAAGGCTCCTTGATGAACTAAACATATTACTTTTAAGCAAATGGTAGGTG  
AATTTCTTCACTCATACATAAATACTAATCGCGTCAACGATGTCTAATCTGTCTATGCTG  
GTAAAATTTTATTGGTTGCAACAAATATGGGACTCTTTGTTCTTAATTATGCTACATCGA  
TCAATCAAAAACCAAGTGCACCTTCTGCACAAAATATCAATTTACAGATCTCTGTATTGG  
AAGATATAAAGTTATGATTTCTTAATTGACAAAAAAGTACGGCTGTCTCTTTAGACG  
TAATCGACGATGCAGAAAATGCAGATTTTCTTTTTCAGAAAAAATTTAAAGTGTTATTTA  
AATATGTTGCAATGTTCAAAGACGGTTTCTGTAATGGTAAAAGAATCATTATGATTGCAC  
ATCATTTTTTGCACGCCGCACAATTATTGATTGTTAATCCTTTGATATTTGATTTTAATA  
GCGGTAATTTTTAAAAAAAACCTAAAGGCAGGCTTGGTAGATTTTAGCGTTGATTCTGAAC  
CTCTGTCTTTTTCTTTTTTGGAGAATAAGATCTGCATTGGTTGTAAAAAAAATATCAAAA  
TATTAACGTACCGGAAGTGTGTGATAAAAATGGATTTAAATGAGGGAGCTTTTAAATC  
TACATGATAACAAAGTTTTAGCGAACATGTATAAAGAGACGTTCAAAGTAGTTTCCATGT  
TTCCGATAAAAAATTCAACTTTTGCATGTTTTCCAGAACTCTGCTTTTTTCTCAATAAGC

14/251

AAGGGAAGAGGGAGGAGACAAAGGGATGTTTTTCATTGGGAGGGGGAACCAGAACAGTTCG  
CGTGTTCCTACCCTTATATTGTGGCAATTAATAGTAACCTTTATTGAAATTAGACATATAG  
AAAATGGGAGAACTTGTCCGCTGTGTACTTGGAAACAAGATACGTATGTTAAAATCATATG  
CCAAGAAGATCTTATATTGTTATGAGGATCCTCAAGGATTTGAAATTATCGAACTGTTAA  
ATTTTTGA

&gt;YGR070W, 1155 aa (SEQ ID NO 174)

MNSNELDLRNKYFYEIFGKKRKSSTSTPTQLFSGSKVQTNINEISITNDEDEDSTEDENK  
ASLKDYTLGHDTGARYRIAPDCSSHQKASPVLHISTNLNSSPQSFTGDIPTNKKISI  
NDSTRQDKGNSTTTSSPSQKRSNVLLPHVRKHSSPSSLFSKNSGSHMGDPNQLSTPPT  
PKSAGHTMELHSSFNKGHSSSSSTSSLFALESKTQNRSSNSSNHSSQYRRHTNQHQHH  
SRSSSPVSLTEISMIKGTPLVYPALLSLIAIKFKQTIKLSHKKMGLLYRDSFTGKQAI  
DTLCLIIIGSLDRNLGMLIGKSLEAQKLFHDVLYDHGVRDSVLEIYELSSSIFMAHQSQS  
STSIANTFSSSSSVNSLRKTEIYGVFVPLTHCYSSSTCSLEKLCYSISCPNRLQQQANL  
HLKLGGLKRNISLALDKEDDERISWTNSVPKSVWESLSKQQIKRQEAIYELFTTEKKFV  
KSLEIIRDTFMKKLETNIIIPSDVRINFVKHVFHINEIYSVNREFLKALAQRLSPIC  
PGIADIFLQYLPFFDPFLSYIASRPYAKYLIETQSVNPNFARFDDEVSNSSLRHGIDSF  
LSQGVSRPGRYSLLVREIIHFSDPVTDKDDLQMLMKVQDLLKDLMKRIDRASGAAQDRYD  
VKVLKQKILFKNEYVNLGLNNEKRKIKHEGLLSRKDVNKTDAFSGDIQFYLLDNMLLFL  
KSAVNKWHQHTVFORPIPLPLLFICPAEDMPPIKRYVTENPNCAGVLLPQYQTSNPKN  
AIVFAYYGTKQQYQVTLYAPQAPAGLQTLIEKVKQEQRLLEDETKHITFKQMVGFHHSYI  
NTNRVNDVLICHAGKILLVATNMGLFVLNYATSINQKPVHLLHKISISQISVLEEYKVM  
LLIDKKLYGCPLDIVDDAENADFLFRKNSKVLFKYVAMFKDGFNGKRIIMIAHHFLHAA  
QLLIVNPLIFDFNSGNFKKLNKAGLVDFSVDEPLSFSFLENKICIGCKKNIKILNVPEV  
CDKNGFKMRELLNLHDNKVLANMYKETFKVVSMPFIKNSTFACFPELCCFLNKQGKREET  
KGCFWHEGEPEQFACSYPIVAINSNFIEIRHIENGELVRCVLGNKIRMLKSYAKKILYC  
YEDPQGFEEIIELLNF

&gt;YGR132C, 1364 bp, CDS: 501-1364 (SEQ ID NO 177)

CATACATGTATCAGACGTATAGCTCCTACGATTCTCAAGAATCCAGAAAGTTTGGCATATT  
ATGTATAAAGCGCATGATTATGTATATTTTATGTTGTCTCCAGTAAGTGGCAGCATAACC  
CGGCCAGTCTGCGCTGCGATGCTGTGAAGCAGTAATATGCGATATATACCACATATATTCC  
GCTTCCGTTTCAGGATTTTCGAAAAGAGAAAACCTTCAGTGAATGACTATGACTACATAGTTGG  
AGTCTTAGACCATTGCAAATGAGTTATTCAAGTATGAGAGATCAACACTGATGAGAAATAA  
ACTCGTCTTCATGATGATACGGGTAACGCGAATGTATCGCATCAATAAATTTTCAGGGAAA  
GGGAGTTTGACGATCTCATGGATGCAACGGTTGAGGTATATAATATTAAGCAGAAAAGAAG  
AGGAAAAAAAATAAATCGGTAAACCAACCATCAACGGTACGAACTTACATTCAAAATCA  
ATAATTTACTTTAGAAAAGAATGTCTAATTCGCCAAACTTATCGATGTCATACCAAGG  
TGGCGTTGCCCATTTGGTATAATTGCTAGCGGGATTCAGTACTCCATGTATGATGTGAAGG  
GTGGTTCTCGTGGTGTATTTTCGACAGAATCAATGGTGTAAGCAACAGGTTGTGGGTG  
AAGGCACTCATTTCTTGGTGCCTTGGCTACAGAAGGCGATCATATACGATGTGAGGACGA  
AACCAAAAGACATTGCTACCAATACTGGTACGAAGGATTTGCAAATGGTGTCAATTGACCT  
TGAGAGTCTTACATAGACCAGAGGTCTTACAGCTACCCGCAATATACCAAAATTTGGGTC  
TCGATTACGACGAAAGAGTGTTACCATCTATCGGCAATGAGGTTTTAAAGTCTATAGTAG  
CTCAATTTGATGCTGCTGAGTTAATTACTCAGAGAGAAAATATTTCTCAAAAAATCAGAA  
AAGAGCTTTCTACGAGGGCCAACGAATTCGGTATTAAGTTGGAAGATGTCTCTATCACTC  
ATATGACGTTTGGTCCCGAAATTCACGAAAGCAGTTGAGCAGAAGCAGATTGCACAGCAAG  
ATGCCGAAAGAGCCAAAATTCCTTGTGAAAAGGCAGAGCAAGAGAGACAAGCTTCTGTTA  
TCAGAGCTGAAGGTGAAGCAGAAAGTGCTGAATTCATTTCAAAGCCTTAGCTAAAGTTG  
GTGATGGTCTGTTATTGATTAGAAGATTAGAAGCTTCTAAGGACATCGCTCAAACATTAG  
CAAACCTCATCTAACGTTGTCTATTTACCAAGTCAACATTCTGGTGGTGGTAACAGCGAGT  
CTTCGGGATCACCAAAATTCCTTGTCTTTGAACATTGGCCGTTAA

&gt;YGR132C, 287 aa (SEQ ID NO 178)

MSNSAKLIDVITKVALPIGIIASGIQYSYMDVKGSGRGVIFDRINGVKQQVVGEGTHFLV  
PWLQKAIYDVRTKPKSIATNTGTKDLQMVSLTLRVLHRPEVLQLPAIYQNLGLDYDERV

15/251

LPSIGNEVLKSIVAQFDAAELITQREIISQKIRKELSTRANEFGIKLEDVSITHMTFGPE  
FTKAVEQKQIAQQDAERAKFLVEKAEQERQASVIRAEGEAESAEFISKALAKVGDGLLLI  
RRLEASKDIAQTLANSSNVVYLPSQHSGGGNSSESGSPNSLLLNIGR

>YGR135W, 1277 bp, CDS: 501-1277 (SEQ ID NO 179)

TTCTGAACTGAATCTGAAATTGTTAAACCTGTTTCCCTCAAAGCCTGCAAACAAAGACGA  
TAGTTCCCTTATTAACACGTTGCGTAGTTTTATCGCTGATTACTCCTTCGACACCCAGGT  
GAACCTCCAGGAAGAAGGTGGTGTCTACGATGGTAAGATTTTGCCATTGCCCAAAGC  
CGATAAGCCTATCCCACTTCATGAATATATAACACTCGCAGAGCTCGATGTTGGAGACAG  
TGAGTGAGCAGTGAATTGCTCATGTTTTCTCTGCATCCTCATTTAATGACAATTAGCCAT  
GTAATAACATCTTGAGGCAGTTAAATATTCTGTTACCCTGCAGGTGGCAAAAAATTTATAG  
AATAAAAGCATAAAAAGATGGATATCTATGTAATAAGGAAACATTGGCAGAGCGAAGAGA  
ACAGACTGCTTTCTATAAAAAGTTTTCGATCAGTCTCTATTTTAATAATTGATTATTGGA  
TATAGTTAGTAGTGTAAACATGGGTTCCAGAAGATACGATTCCAGGACAACAATTTCT  
CCCCTGAGGGACGTCTATATCAGGTTGAATACGCGCTAGAATCCATTTACATGCAGGTA  
CCGCAATTGGGATTATGGCATCTGATGGGATTGTTCTTGCAGCAGAACGCAAAGTCACAA  
GTACTTTACTAGAACAAGACACCTCTACCGAAAACTTTATAAGTTAAACGATAAAATTG  
CGGTTGCCGTTGCTGGACTGACTGCAGATGCAGAAATTTCTAATAAATACGGCTAGAATTC  
ACGCTCAAAATTACCTTAAAACCTATAATGAAGATATACCAGTAGAAATTTTGGTGAGAA  
GGCTAAGTGATATAAAACAAGGTACACGCAACATGGTGGTTTAAGACCATTGTTGGTGTGT  
CCTTTATCTACGCCGTTATGACGATAGATACGGTTACCAATTGTATACATCTAATCCAT  
CGGGAACTATACAGGGTGAAGGCTATTAGTGTGGCGCTAACACATCAGCAGCACAAA  
CCCTACTTCAAATGGACTACAAGGATGATATGAAAGTCGATGATGCCATTGAACTGGCTT  
TAAAAACGTTATCCAAAACCTACCGACAGTAGCGCGCTGACTTATGACAGGTTGGAATTTG  
CTACTATCAGAAAGGGTGCTAATGACGGAGAAGTGTATCAGAAGATTTTCAAGCCTCAAG  
AGATAAAGGATATATTGGTAAAGACTGGTATTACCAAGAAGGATGAAGACGAAGAAGCTG  
ATGAAGATATGAAATAA

>YGR135W, 258 aa (SEQ ID NO 180)

MGSRRYDSRTTIFSPGRLYQVEYALESIHAGTAIGIMASDGIVLAAERKVTSTLLEQD  
TSTEKLYKLNDKIAVAVAGLTADAELINTARIHAQNYLKTYNEDIPEILVRRLSDIKQ  
GYTQHGGRLRPFVGSFIYAGYDDRYGYQLYTSNPSGNYTGWKAI SVGANTSAAQTLQMDY  
KDDMKVDDAIELALKTLSKTTDSSALTYDRLEFATIRKGANDGEVYQKIFKPQEIKDILV  
KTGITPKKDEDEEDEDMDK

>YGR155W, 2024 bp, CDS: 501-2024 (SEQ ID NO 181)

GTGTTCTCATCCGACCCTCTGATTCATTTGGTGGCCATTACATTTTCCCTCAATGACACA  
TTCCCTTATTTTCATAACTGATTAATAATGGTAATGGCACGTGATAGTAGTGGCTCACAAAA  
CAAATTTTCTTTCTCAGCGCTGACAAAGCTTCATTTGCATTCTAACCTTATCACAACAA  
CTTCAACTTCACCCAAGTAAGGATAATCAGCTCTGTCTGCTGACTGATAAATGCTATATCCG  
GCATATGCAGTCCACACGGCATTACCGTTTCACTAATTTATTGCCATCTTCTCCACAGT  
TTTGCACCGAAAGGAAAAAAGAAACCAACACCGAAAATTTTTTCTCTAAAGGTTAAA  
GTAAACGCAAGGCACCTTACCAGGCTTGTATATATAAATGTCGTGATGCTTCTATGCCAA  
AGTAAAAGGCAACACTTGAAGATTTCTGTTGTAGGCCACTTGCTCAAAGGACATCTAGATA  
AATACGACGTAAGAATAAAAATGACTAAATCTGAGCAGCAAGCCGATTCAAGACATAACG  
TTATCGACTTAGTTGGTAACACCCCATTTGATCGCACTGAAAAAATTGCCTAAGGCTTTGG  
GTATCAAACCACAAATTTATGCTAAGCTGGAACATATAAATCCAGGTGGTTCCATCAAAG  
ACAGAATTGCCAAGTCTATGGTGGAAGAAGCTGAAGCTTCCGGTAGAATTCATCTCTCCA  
GATCTACTCTGATCGAACCTACTTCTGGTAACACCGGTATCGGTCTAGCTTTAATCGGCG  
CCATCAAAGGTTACAGAACTATCATCACCTTGCCGAAAAAATGTCTAACGAGAAAGTTT  
CTGTCCTAAAGGCTCTGGGTGCTGAAATCATCAGAACTCCAAGTCTGCTGCTGCTGGGATT  
CTCCAGAATCACATATTGGTGTGCTAAGAAGTTGGAAAAAGAGATTCTGGTGCTGTTA  
TACTTGACCAATATAACAATATGATGAACCCAGAAGCTCATTACTTTGGTACTGGTCGCG  
AAATCCAAAGACAGCTAGAAGACTTGAATTTATTTGATAATCTACGCGCTGTTGTTGCTG  
GTGCTGGTACTGGTGGGACTATTAGCGGTATTTCCAAGTACTTGAAAGAACAGAATGATA  
AGATCCAAATCGTTGGTGCTGACCCATTCTGGTTCAATTTTAGCCCAACCTGAAAACCTGA

16/251

ATAAGACTGATATCACTGACTACAAAGTTGAGGGTATTGGTTATGATTTTGTTCCTCAGG  
TTTTGGACAGAAAATTAATTGATGTTTGGTATAAGACAGACGACAAGCCTTCTTTCAAAT  
ACGCCAGACAATTGATTTCTAACGAAGGTGTCTTGGTGGGTGGTTCTTCCGGTTCCTGCCT  
TCACTGCGGTTGTGAAATACTGTGAAGACCACCCTGAACCTGACTGAAGATGATGTCATTG  
TTGCCATATTTCCAGATTCCATCAGGTTCGTACCTAACCAAATTCGTTCGATGACGAATGGT  
TGAAAAAGAACAATTTGTGGGATGATGACGTGTTGGCCCGTTTGTACTCTTCAAAGCTGG  
AGGCTTCGACGACAAAATACGCTGATGTGTTTGGTAACGCTACTGTAAAGGATCTTCACCT  
TGAAACCGGTTGTTTCCGTTAAGGAAACCGCTAAGGTCACCTGATGTTATCAAGATATTAA  
AAGACAATGGCTTTGACCAATTGCCTGTGTTGACTGAAGACGGCAAGTTGTCTGGTTTAG  
TTACTCTCTCTGAGCTTCTAAGAAAATCAATCAATAATTCAAACAACGACAACACTA  
TAAAGGGTAAATACTTGGACTTCAAGAAATTAAACAATTTCAATGATGTTTCTCTTACA  
ACGAAAATAAATCCGGTAAGAAGAAGTTTATTAAATTCGATGAAAACCTCAAAGCTATCTG  
ACTTGAATCGTTTCTTTGAAAAAACTCATCTGCCGTTATCACTGATGGCTTGAAACCAA  
TCCATATCGTTACTAAGATGGATTTACTGAGCTACTTAGCATAA

>YGR155W, 507 aa (SEQ ID NO 182)

MTKSEQQADSRHNVIDLVGNTPLIALKKLPKALGIKPQIYAKLELYNPGGSIKDRIAKSM  
VEEAEASGRIHPSRSTLIEPTSGNTGIGLALIGAIGYRTIITLPEKMSNEKVSVLKALG  
AEIIRPTAAAWDSPESHIGVAKKLEKEIPGAVILDQYNNMMNPEAHYFGTGREIQRQLE  
DLNLFNLRVAVAGAGTGGTISGISKYLKEQNDKIQIVGADPFGSILAQPENLNKTDITD  
YKVEGIGYDFVPQVLDRLIDVWYKTDDKPSFKYARQLISNEGLVGGSSGSAFTAVVKY  
CEDHPELTEDDVIVAI FPD SIRS YLT K FVD DEWL KKNLW DDDV LARFDSSKLEASTTKY  
ADVFGNATVKDLHLKPVSVKETAKVTDVIKILKDNQFDQLPVLTEDGKLSGLVTLSELL  
RKLSINNSNNDNTIKGKYLDFFKLNNFNDVSSYENKSGKKKFIKFDENSKLSDLNRFFE  
KNSSAVITDGLKPIHIVTKMDLLSYLA

>YHR095W, 935 bp, CDS: 501-935 (SEQ ID NO 207)

GACACCTTTTCCGGTGTGTTGGAGGGGCAACGGCGGGTGCACCTTGACTTTCACCTTAAGTT  
GTCGTGAAAACCTTCATTTTACCTTCGGAGTATTCATGGCCTTTGAACGACCAGATTC  
CAATTCATATGAGTTGGATGAATTGGATTTCTGAGGAGATATTAGATCGGGAGTTGAATT  
CATGATTTTACGTATATCAACTAGTTGACGATTATGATATCTTTATAGATTTTAAAGTGG  
GGAAAGAACATGAGACCCAGATGGAATTGATTATGGGGACATTGTTGCCCTTATATATA  
ATTTCAATATACTAATTCAAATGATTA AAAACGTGAGGGGGACACGCAACTTCGGGTGTT  
AAGAAATATTTTGTCTACATTAGATAATGGTGGAGTTTCCTGGCTTGTCGGATAAAAGCCA  
TCAAATGTCGCAGCAGCTCATGTTTACGTTTGTCTTCTTGCCACGTCATATGAGTGG  
TATTCCTCTATCAGCACTTGATGAATATTCTTTTCTCATATATCTGAAAGACAAAAGAT  
CGGCACGGCAATGCCCTGCAGCATTCTTCCTAGTTTTTCCGAATTTCCATTACGTATTG  
GATCTTGTGCGCATATTTGTGAGTCTTCACGGAAAAAAGAGCACTGGGTCACTT  
CGGAAAAACCTTTGACTCAATGCAACAGTGTCAATCCCTTTGCGCTGTCTCTTTGAAGA  
AAAATCAGGAGTGCAAGATATCGATTAATTCCTTGGAAGTTATGATGGTTAGTCTTAGTT  
TAACCTCTCTTGAAGAAGGGTTTTTTTCAAGTTGGTCAACACTCTTTAGAGGTAAAAA  
AAAAAAGAGAAATCTTCATGTAATTTACCATGATTCTACGTTTTTGCAAG  
CAAAATGAAGATAATCCGAGCGCATGCGAAGTAG

>YHR095W, 144 aa (SEQ ID NO 208)

MNIFLIYLDKRSARQCPAFLPSFSEFPLRIGSCAHICQSFTEKKKEHWVTSEKLLTQ  
CNSVILCAVSLKKNQECKISINSLEVMMVSLSLTLLKKGFFSWSTLFRGKKKKKKKKR  
ILHVIYHDSSTFLQAKMKIIRAHAK

>YHR138C, 845 bp, CDS: 501-845 (SEQ ID NO 209)

CTACGAAAATAAGCAAAAAATAAATAAAAAACAAAAACAAAAACAAAAACAAAAAC  
AAAAACAAAAACAAAAACACATATTGTTATGATGACTGGACGAAAGAAAGATCGTCGTTA  
CTTTCCTAATTGTTTGTCTTCAGTACAGTTATTATCAGTGTCTCTTTCTTTTTTATTGT  
ACTATGTGATGTTACTGATACATCACGCGCTTCCTTTATGTTTTCTTTTTTTATGTTTCGT  
TACAGGATTTATAGTTTTTACAGTATATTGACTTCAATAATTTCTAATATTCAAGTTCCTA  
TTAAATTTGATTATTCCGATTAGATCGGTGCGCGCTACCAAAAGAGGCGAAGAAAAGAG

17/251

GAAAACGCAAGTGGATAAAGGGGTGGGGGGCAAAGTATTTAAGAAAAAGCGATGCGATG  
GAGAGAACAAATGGATAAGTTGCGTTTCCCTCGTTATATTACAACATTTAAATCTATTGTG  
TAACAGACTATAGCATATATATGAAGGCCAGTTACTTAGTTTTGATTTTCATTAGCATAT  
TCTCCATGGCACAGGCATCTTCCTTATCATCATACATCGTAACCTTCCCCAAGACGGATA  
ATATGGCTACGGACCAGAAATAGCATTATTGAAGATGTCAAAAAATATGTGGTGGACATAG  
GGGGTAAAATAACACACGAATATAGCTTGATAAAGGGCTTTACAGTGGACTTACCTGATA  
GCGACCAAATTTTGGACGGTCTGAAAGAACGTTTGAGCTATATTGAAAGCGAGTACGGTG  
CTAAATGCAATTTGGAAAAGGATTCAGAAGTTCATGCTCTAAACCGTGACCATTTAGTTG  
CTTAG

>YHR138C, 114 aa (SEQ ID NO 210)

MKASYLVLFISIFSMAQASSLSSYIVTFPKTDNMATDQNSIIEDVKKYVVDIGGKITHE  
YSLIKGFTVDLPDSDQILDGLKERLSYIESEYGAKCNLEKDSEVHALNRDHLVA

>YHR179W, 1703 bp, CDS: 501-1703 (SEQ ID NO 215)

ATATCTTACGTAATGAACCTCCGTAATGAACCTCCGTAATTCAGATCTCTTAGCATCTC  
TTGTTCAATCTTCAGACTCTACTAAGTGTCTTACCAACCATTGGATGCTCATTAACAAAT  
GAATGAATATATTGCACGGAACGGAAGCGGCATGCTTTTTCCGTCTCGTGTGCTTAGTAA  
AGCAAAACGGAGTAGAATCGGTAAGAACTTCCTTTTTGGGTGGGAAAATCATTGCCATTG  
TTTGGACACCTTTCTTTTTCCGTATTGTTTCGAGCACCGCGTTTCTTTTTGGGTACTTGAT  
GAGGTAGCAGATTCCCTGGAACGTGCTTTCTCTCGAGGTAACTGCCTTGTTCCTCCCTGGT  
GACTTTCTAAAAATATAAAAGGAAAAGCATATCTCTAGTTTCGAGTTTTTTCTTCATACCTT  
TATTTCCCTTATGTTAAACGGTCCAGATATAGAATAAATCATCATATTAAGCTAAATATAG  
ACGATAATATAGTATCGATAATGCCATTTGTTAAGGACTTTAAGCCACAAGCTTTGGGTG  
ACACCAACTTATTCAAACCAATCAAAATTGGTAACAATGAACCTTCTACACCGTGCTGTCA  
TTCCCTCCATTGACTAGAAATGAGAGCCCAACATCCAGGTAATATTCCAAACAGAGACTGGG  
CCGTTGAATACTACGCTCAACGTGCTCAAAGACCAGGAACCTTGATTATCACTGAAGGTA  
CCTTTCCCTCTCCACAATCTGGGGGTACGACAATGCTCCAGGTATCTGGTCCGAAGAAC  
AAATTAAAGAAATGGACCAAGATTTTCAAGGCTATTCATGAGAATAAATCGTTCCGATGGG  
TCCAAATTATGGGTTCTAGGTTGGGCTGCTTTCCAGACACCCCTTGCTAGGGATGGTTTGC  
GTTACGACTCCGCTTCTGACAACGTGTATATGAATGCAGAACAAGAAGAAAAGGCTAAGA  
AGGCTAACAACCCACAACACAGTATAAACAAGGATGAAATTAAGCAATACGTCAAAGAAAT  
ACGTCCAAGCTGCCAAAACTCCATTGCTGCTGGTGGCGATGGTGTGAAATCCACAGCG  
CTAACGGTTACTTGTGTAACCAAGTTCTTGGACCCACACTCCAATAACAGAACCGATGAGT  
ATGGTGGATCCATCGAAAACAGAGCCCGTTTCACCTTGGAAGTGGTTGATGCAGTTGTCTG  
ATGCTATTGGCCCTGAAAAAGTCGGTTTGAGATTGTCTCCATATGGTGTCTTCAACAGTA  
TGTCTGGTGGTGTGTAACCCGTATTGTTGCTCAATATGCTTATGTCTTAGGTGAACCTAG  
AAAGAAGAGCTAAAGCTGGCAAGCGTTTGGCTTTCGTCCATCTAGTTGAACCTCGTGTCA  
CCAACCCATTTTTAACTGAAGGTGAAGGTGAATACAATGGAGGTAGCAACAAATTTGCTT  
ATTCTATCTGGAAGGGCCCAATTATTAGAGCTGGTAACCTTTGCTCTGCACCCAGAAGTTG  
TCAGAGAAGAGGTGAAGGATCCTAGAACATTGATCGGTTACGGTAGATTTTTTTATCTCTA  
ATCCAGATTTGGTTGATCGTTTGGAAAAGGGTTACCATTAAACAAATATGACAGAGACA  
CTTTCTACAAAATGTCAGCTGAGGGATACATTGACTACCCTACGTACGAAGAAGCTCTAA  
AACTCGGTTGGGACAAAAATTAA

>YHR179W, 400 aa (SEQ ID NO 216)

MPFVKDFKPQALGDTNLFKPIKIGNNELLHRAVIPPLTRMRAQHPGNI PN RDWAVEYYAQ  
RAQRPGTLIITEGTFPSPQSGGYDNAPGIWSEEQIKEWTKIFKAIHENKSFAWVQLWLVLG  
WAAFPDPTLARDGLRYDSASDNVYMNAEQEEKAKKANNPQHSITKDEIKQYVKEYVQAANKN  
SIAAGADGVEIHSANGYLLNQFLDPHSNNRTDEYGGSIENRARFTLEVVDVAVDAIGPEK  
VGLRLSPYGVFNSMSGGAETGIVAQYAYVLGELERRAKAGKRLAFVHLVEPRVTNPFLTE  
GEGEYNGGSNKFAYSIIWKGP IIRAGNFALHPEVVREEVKDPRTLIGYGRFFISNPDLVDR  
LEKGLPLNKYDRDTFYKMSAEGYIDYPTYEEALKLGWDKN

>YIL074C, 1910 bp, CDS: 501-1910 (SEQ ID NO 219)

TGGGAGTCTTTAGCAAGTTCCGGCAAATATCGATATCAATAGTATTGCTAAATAAACCTTT

18/251

TTTATTCCATTTACTGTCGTTTATACTGGCTGACCCTTAATTCCTTAGCAATCTTTGCCT  
GCACCCGTACCAGGAAGCGTGATAGAATCGGTAGCTACAAAATTTTAGCATAGTTAATA  
AGTGCTATTGTTTTTTCATAATGTCACGTGCACTATCAATAATATTACACTCTTGTCTTG  
CCAAATATACACAAAATGCCACATTTTTTTCTTTACACCGAAGAATTTGGCCGTCAGCCG  
GACAGCGCTCAGATTAATTGTGGGCTAGATTCTTCACGCTGGAACGAGTCACCGTTATG  
AAAACTAATGGAATCTCCAGGTTTAATACATAAGAAGGTTACGAGCTACTACATTAAAA  
AATACTTTGTCTGTTTTAGCTGTAGATTATTGTAACATTAAAAAGTAACAAACACTGATT  
TCGGGTATTTCTCCCTAACATGTCTTATTACAGCTGCCGATAATTTACAAGATTCAATCC  
AACGTGCCATGAATTTTCTGGCTCTCTGGTGCAGTCTCAACCTCACCAACTCAGTCAT  
TTATGAACACACTACCTCGTCGTGTAAGCATTACAAAGCAACCAAGGCTTTAAACCTT  
TTTCTACTGGTGACATGAATATCTACTGTTGGAAAATGTCAATGCAACTGCAATCAAAA  
TCTTCAAGGATCAGGGTTACCAAGTAGAGTTCCACAAGTCTTCTCTACCTGAGGATGAAT  
TGATTGAAAAAATCAAAGACGTACACGCTATCGGTATAAGATCCAAAAC TAGATTGACTG  
AAAAAATAC TACAGCATGCCAGGAATCTAGTTTGTATTGGTTGTTTTTGCATAGGTACCA  
ATCAAGTAGACCTAAAATATGCCGCTAGTAAAGGTATTGCTGTTTTCAATTGCCCATCT  
CCAATTCAAGATCCGTAGCAGAATTGGTAATTGGTGAGATCATTAGTTTAGCAAGACAAT  
TAGGTGATAGATCCATTGAAC TGCATACAGGTACATGGAATAAAGTCGCTGCTAGGTGTT  
GGGAAGTAAGAGGAAAACTCTCGGTATTATTGGGTATGGTCACATTGGTTTCGAATTAT  
CAGTTCTTGCAGAAGCTATGGGCCTGCATGTGCTATACTATGATATCGTGACAATTATGG  
CCTTAGGTACTGCCAGACAAGTTTCTACATTAGATGAATTGTTGAATAAATCTGATTTTG  
TAACACTACATGTACCAGCTACTCCAGAACTGAAAAAATGTTATCTGCTCCACAATTCG  
CTGCTATGAAGGACGGGGCTTATGTTATTAAATGCCCTCAAGAGGTACTGTCTGGACATTC  
CATCTCTGATCCAAGCCGTCAAGGCCAACAAAATTGCAGGTGCTGCTTTAGATGTTTATC  
CACATGAACCAGCTAAGAACGGTGAAGGTTCAATTTAACGATGAACTTAACAGCTGGACTT  
CTGAGTTGGTTTTCAATTACCAATATAATCCTGACACCACATATTGGTGGCTCTACAGAAG  
AAGCTCAAAGTTCAATCGGTATTGAGGTGGCTACTGCATTGTCCAAATACATCAATGAAG  
GTAACTCTGTCTGGTTCTGTGAAC TTCCAGAAAGTCAGTTTGAAGTCTTTGGACTACGATC  
AAGAGAACACAGTACGTGTCTTGTATATTATCGTAACGTTCTGGTGTTTTGAAGACCG  
TTAATGATATCTTATCCGATCATAATATCGAGAAACAGTTTTCTGATTCTCACGGCGAGA  
TCGCTTATCTAATGGCAGACATCTCTTCTGTTAATCAAAGTGAAATCAAGGATATATATG  
AAAAGTTGAACCAAACTTCTGCCAAAGTTTCCATCAGGTTATTATACTAA

&gt;YIL074C, 469 aa (SEQ ID NO 220)

MSYSAADNLQDSFQRAMNFSGSPGAVSTSPTQSFMTLPRRVSITKQPKALKPFSTGDMN  
ILLLENVNATAIKIFKDQGYQVEFHKSSLPEDELIEKIKDVHAIGIRSKTRLTEKILQHA  
RNLVCIGFCIGTNQVDLKYAASKGIAVFNSPFSNSRSVAELVIGEIISLARQLGDRSIE  
LHTGTWNKVAARCEVRGKTLGIIGYGHIGSQLSVLAEAMGLHVLVYDIVTIMALGTARQ  
VSTLDELNLKSDFTVLHVPATPETEKMLSAPQFAAMKDGAYVINASRGTVVDIPSLIQAV  
KANKIAGAALDVYPHEPAKNGEGSFNDELNSWTSSELVSLPNIILTPHIGGSTEEAQS SIG  
IEVATALSKYINEGNSVGSVNFPEVSLKSLDYDQENTVRVLYIHRNVPGLVLTVDILSD  
HNIEKQFSDSHGEIAYLMADISSVNQSEIKDIYEKLNQTSKVSIRLLY

&gt;YIR037W, 992 bp, CDS: 501-992 (SEQ ID NO 221)

GTTTTCCATGCTTTTGCCGATTTCCTCCACCAACGCTTCCATTCGAGACCTGTCCGTGA  
TGTCGAGGACACGATAGACAAATTTGTCTGCACCGTATTCTCTTTGCAAAGACTGCAGAC  
CAGCTTCCGTTCTTGCTACGCCGTAGACGATGCATTATCGTCTCTTTCGATAACAGTTT  
TCACCAATTGCAGGCCAATCCCACGGGAGGCACCTGTAATCAAATAACCTTGCCCATAT  
CCCTTCTTTGACAGATTATAAGTTGTTTCTCTTGTGCTGTTTCGCGACAGCCCTTATTTC  
CTGTATTCTCTTCTTTTCTGCATTATCTGTTTTTAGCCACTTTACGAAAAAGGTCAAA  
AAGTGAAAAAAGAGGGAAAAAACCATGAGGAACAGTATGCTCCCTTAATATCGGAAAAG  
CAATAGTAATAAAAAACAGCATCAGAGCTTTCCACGTCTCTCTCTTCCAAGCTGTCATCTC  
GTAAAGTATTCAAGTTTATCATGTGAGAATTCTATAAGCTAGCACCTGTTGACAAGAAAG  
GCCAACCATTCCCTTCGACCAATTAAAGGGAAAAGTGGTGTATTCGTTAATGTTGCCT  
CCAAATGTGGATTCACTCCTCAATACAAAGAACTAGAGGCCTTGTAACAACGTTATAAGG  
ACGAAGGATTTACCATCATCGGGTTCCCATGCAACCAGTTTGGCCACCAAGAACCTGGCT  
CTGATGAAGAAATTGCCAGTTCTGCCAACTGAACTATGGCGTGACTTTCCCATATTATGA

19/251

AAAAAATTGACGTTAATGGTGGCAATGAGGACCCTGTTTACAAGTTTTTGAAGAGCCAAA  
AATCCGGTATGTTGGGCTTGAGAGGTATCAAATGGAATTTTGAAAAATTCTTAGTCGATA  
AAAAGGGTAAAGTGACGAAAGATACTCTTCACTAACCAACCTTCTTCGTTGTCCGAAA  
CCATCGAAGAACTTTTGAAAGAGGTGGAATAG

>YIR037W, 163 aa (SEQ ID NO 222)

MSEFYKLAPVDKKQPFPPFDQLKGKVVLVNVASKGFTPOYKELEALYKRYKDEGFTII  
GFPCNQFGHQEPGSDEEIAQFCQLNYGVTFPIMKKIDVNGNEDPVYKFLKSQKSGMLGL  
RGIKWNFEKFLVDKKGKVYERYSSLTKPSSSLSETIEELLKEVE

>YJL161W, 1043 bp, CDS: 501-1043 (SEQ ID NO 229)

TCATAAGTCTGGCGCGTATTCCTTGACAATTTTCATATCTTCCCATATGAATACCTG  
TTAGTCCGTATCACCAAGTGTAACCTGTTCTTTACAATGAGAACATCTAGAGTCTTTCTG  
ATATGCGTAACCTCTGCCTCATTAATTTAAAAATTTCTTCATAGTAAATAGCTTATTTGC  
TTGGAGCAGATGATCGACATGTATTTTAGGAACATAAACTGCCTAAATATAATAGATCA  
GCCTAAAAATAAGAATGCCAATCAACAAAGTTGTATTTTCTATCTTCCGATATTTCGCAGT  
CCACCATTTCAGACCTCTGGTGAGATAGTTTGCTGCTTTTGCTCCCTTCCAAAGTGCTGA  
TAAAAACCTCCGTGATTTTTTGAATACTCCCCTGAATGTCTATTTTAAAGTATATTATAAA  
ATTAGTTTTAAGTTGGTGCGGATAACGAAAACCTTGATGCAAGGTAAATAAATCAAGTATAT  
CATAGAGTTCTTTTCATTCATATGCTATACACAAGGTTGTTACGTCACAACCTACAATTCA  
CCAAGTTTTCAGGCACATCGCCCAATCTTGGCTCAAAACCTTTATTTTTCGAAGGGTAATT  
TGTAAGTACTAGTCTTTTAGTGACAACACTGTATGGGACAGGTCTGGCATGCCTATATCTAG  
AATCAAAATAGCTTGAATAAGTCCAAAGAGCAAGAAGATCCCCATGCCATCGCAGAAGACG  
ACATTTGTAAATATAGTCCATGACGCTCCCAATAGAATATTCAAGCCAGCACTTGATACCT  
ATCAAGAGAAAAGAGCTTGACTTACAAAAGAGTGACCTCCATAAAAGTACTTCATTCTTTGA  
CGTACAGTGATGTCTCTCAATTTTCGATTGTTTGGGGGTTTCTCATTCAACTTTTCGAGCC  
TAATAGGCAATTCCACCTTAGGCAAAAAATCCATTCTTTATAAGGGAAGTGTGCTTAGTG  
TTTTAGGGTTCCACCGTTGATTTATATGGCACTTAACTTAGGATGAAACAGCTGGAAA  
AAGCTGGAGTGCGCTTTGAGTAA

>YJL161W, 180 aa (SEQ ID NO 230)

MLYTRLLRHNSQFTKFSGTSPNLGSKPLFSKGNLYTSLLVTTLYGTGLACLYLESNSLNK  
SKEQEDPHAIAEDDIVNIVHDAPNRIFKPALDITYQEKELDLQKSDLHKVLHSLTYSVDVSQ  
FSIVWGFILQLSSLIGNSTLGGKKSILYKGSVSVLGFPPLIYMALKLRMKQLEKAGVRFE

>YJR096W, 1349 bp, CDS: 501-1349 (SEQ ID NO 233)

GTATATTCAAGAAGATGACACACCAAGCCAAAGCCATTAAAGTAGATGATGAACAATG  
GGACTACAAAATGAAATAAAGAAAAATAGAAATAGGCTAGAAGATCAATTATTAATCGC  
CCTATTTCTTCTTATTACCTACACAAAATAAAGCAGCAACATAAGAAACAAAAACAAAT  
GAAAAACAAACCAATAAATCTATGTAAGCATACTCATTTCAATTTGATATTCAATTACTTG  
ACTTTTTTTGTCCTTATTTGAGGCTCCATAAGCGCGCCATTTTTCCCTACTCCCTTTTTTC  
GTAAATAGTAATAATGTGCTGAAAAGAACATGAAGTAGTTATCATACATATTCCGTCGT  
GTCGATATGAGGGGAGGTGTCTCTTTCTTTTCATCCCTTGTGCGCAACCTCCAATATATAAG  
AGCATAAGCAACTGATCTTACTTTAGTAATTAACCTTAGCATACCTAGCCCGAAGGAAGAA  
AAAAAATTCACCTCAACAACATGGTTCCCTAAGTTTACAAACTTTCAAACGGCTTCAAAA  
TCCCAAGCATTGCTTTGGGAACCTACGATAATCCAAGATCGCAAACAGCCGAAATTTGTGT  
ATGAAGGTGTCAAGTGCGGCTACCGTCATTTGATACTGCTGTCTTTATGGTAATGAGA  
AGGAAGTTTGGCGATGGTATCATTAATGGTTGAACGAAGATCCAGGGAACCATAAACGCTG  
AGGAAATCTTCTACACTACTAAATTATGGAATTCGCAAAACGGATATAAAAGAGCTAAAG  
CTGCCATTTCGGCAATGTTTGAATGAAGTCTCGGGCTTGCAATACATCGATCTTCTTTTGA  
TTCATTTCGCCACTGGAAGGTTCTAAATTAAGGTTGGAAACTTGGCGCGCCATGCAAGAAG  
CGGTTGATGAAGGATTGGTTAAGTCTATAGGGGTTTCCAACATATGGGAAAAAGCACATTG  
ATGAACCTTTGAACTGGCCAGAAGTGAAGCACAAGCCAGTGGTCAACCAATCGAGATAT  
CACCTTGGAATTATGAGACAAGAATTAGCAGATTACTGTAATCTAAAGGTCTCGTCGTCG  
AAGCCTTTGCCCATTTGTGTCACGGCTACAAAATGACTAATCCAGATTTATTTAAAGTTT  
GCAAAAGAGGTGGACCGTAATCCAGGTCAAGTTTGTATTCGTTGGTCTTTACAACACGGTT



20/251

ATTTACCACTACCGAAGACTAAACTGTGAAGAGGTTAGAAGGTAACCTTGCAGCCTACA  
ACTTTGAACTGTCAGACGAACAGATGAAATTTCTTGATCATCCTGATGCTTATGAGCCTA  
CCGATTGGGAATGCACAGACGCGCCATAA

>YJR096W, 282 aa (SEQ ID NO 234)

MVPKFYKLSNGFKIPSIALGTYDIPRSQTAEIVYEGVKCGYRHFDTAVLYGNEKEVGDGI  
IKWLNEDPGNHKREEIFYTTKLWNSQNGYKRAAAIRQCLNEVSGLQYIDLLLIHSPLEG  
SKLRLETWRAMQEAVDEGLVKSIGVSNYKKHIDELLNWPELKHKPVVNQIEISPWIMRQ  
ELADYCKSKGLVVEAFAPLCHGYKMTNPDLLKVCKEVDNRNPGQVLIRWSLQHGYPPLPKT  
KTVKRLEGNLAAYNFELSDEQMKFLDHPDAYEPTDWECTDAP

>YKL065C, 1121 bp, CDS: 501-1121 (SEQ ID NO 241)

CTGGGCTAGGTTTCACATATCAAAAAGAAGTTATGGCTTATGTGCTCTTTCTAAGTTTGA  
CTTTTATGCCAAAAATTTCTCCGTAGATCGCCGCCCGTTGAAGCAGCAGAATATTTTAAGT  
GCGCCATAAAAACCTAGATAGAAAAGAAGGGAGAGAACATAAACGCAGAACACCCTACT  
TTTAAGGCGTACGCAAACTGTTGGGCTTATCTATATTGTACTATCTACCTACTTGCAACG  
TCTTTTACCTCCTCGATACGTACTGCTTATGCCCTGAACAATTTACATGTAACCCGCGAGC  
TGCATGCTATATCACAGGATACGTTAACATAAAGGGGGCGCTACTAAACCCCTCTGGCGCA  
GTGCAAAAATAGAAATATATGCCAAGTGGGACCTTGTATAGTTTCTGGTTTAAAGCTATT  
CGTTCATTGCAACGCTCCTTTCTGCTATCCTTTTCGCAAAGTGGCAAGTACTGAAAACCGA  
GAAGAATAAATAATATTGCGATGAGTTTATACCTTTACGACATTATTTTATTGCTCACTG  
TTGAGGTGGTAATGCTCTTCATCTTCGTTTTGCTTTGCCATTCCGGATCCGTAGGGGTA  
TTTTTAGCACCTATAACCAATTGACAGCGAAGCAGCAAATAAAAACTATAATCTTTATAA  
CGGGTTGTCTTGTGGCCTGTTGTTTTATTGATTCATGGAAAAGGTCCAAATTCGTGTTT  
CATTATACCACAACGACAACAGTGGCTCAATCGGGTCATCTGCTGTAACCTCCAATACAGG  
CACTAGCATCAAGAGCGTACAATCAAAGAAATATGTATATTTCCGGGTTTCATATTGTACT  
TTTCTATCTGTATCCCAACTGTCATGTCTATTGTCAAGAGACTGGTGAAATACCAAGGCT  
TAATCAACGAACAAGAAAAGCAAAAATTGAACAAACCTTCCTCAAACAGCAAGAAAGACT  
CAAATGAAGCTGATTCCACCAAACCTCAAGAGGAACTAAGGAAAAGCAAATTTCTCTGG  
AGGGCCTACAAAAGCAAGTCAAAAACCTGGAGAAATATTTTGATGAGAAGAATCAACCTG  
GAAATGTAGCAGCTGCTGAAGCTTCCAAGAAAGGAAACTAA

>YKL065C, 206 aa (SEQ ID NO 242)

MSLYFTTLFLLLTVEVVMLFIFVLPLPFRIRRGIFSTYNQLTAKQQIKTIIFITGCLVGL  
LFIDSWKRSQIRVSLYHNDNSGSIGSSAVTPIQALASRAYNQNRNMYISGFILYFSICIPT  
VMSIVKRLVKYQGLINEQEKQKLNKPSSNSKKDSNEADSTKLQEELRKKQISLEGLQKQV  
KNLEKYFDEKNQPGNVAAAEASKGN

>YKL196C, 1103 bp, CDS: 501-1103 (SEQ ID NO 253)

AAAGAGGCTTCCTATTAGGAGCAATAAAATATAAAGCACCAGCCATAGAAAGAATCCCCA  
TTATAAAGCCCGCTGTTTTTTCCTGATTGGAGTTCTTACCGAACTGAGGGGAGGACGCCA  
TGAGACGCTCTGTTTGGTGTCTGGCATAACCCCTTGCCACTTGAATTGACGGCCTGTTTC  
TGCACGCATTCCTGACGACTAAGTTGCGAAGCATTTTACTGATAATATACACTCTTTGGA  
TCGAGCCTACTTCCAGTTGGTAATTGGTGTTCACAAATTTACGATTATATGTTTTTAAA  
CCAAAATTCGGCTCCTTTTCCCTTTTTTCTTATTGGGTGGCGTGCCGTACAGAACGATT  
GGCTTGGTGTGAAATCAAGAGCAAGCACAAATAGATATCAACATGAACAATATACAAAAGT  
CTCTGGCACAGTTTGACTGCGTTAGACCAGGCTAGGGCATTTCTGAAGCTTTACGTATCA  
CTAGAGAAGTTATTTTGGCAATGAGAATCTACTACATCGGTGTATTTTCGCTCTGGAGGAG  
AAAAGGCTCTAGAGTTGAGTGAAGTTAAAGACTTGTCACAATTTGGTTTCTTTGAAAGGT  
CTAGTGTGGCCAGTTTATGACTTTTTTTGCTGAAACGGTCGCTTCTAGAACTGGTGCAG  
GACAAAGACAAAGTATAGAAGAAGGCAACTATATTGGCCACGTTTATGCCAGGAGTGAGG  
GCATATGTGGTGTTTTGATCACCGACAAAGAATATCCTGTCAGACCAGCATACACACTAT  
TAAACAAAATATTGGATGAATATTTAGTCGCACATCCTAAGGAAGAGTGGGCAGATGTGA  
CTGAGACCAATGATGCATTGAAAATGAAGCAACTGGACACTTACATTAGCAAATATCAAG  
ATCCTTCACAGGCTGACGCTATCATGAAAGTTCAACAAGAACTGGATGAGACGAAAATCG  
TTTTGCACAAAACGATTGAGAATGTTTTACAAAGAGGTGAAAAGTTGGATAATTTGGTGG

21/251

ACAAATCGGAGTCATTAACGGCAAGTTCCAAAATGTTTTATAAGCAAGCTAAAAAATCCA  
ATTTCGTGTTGCATCATCATGTAG

>YKL196C, 200 aa (SEQ ID NO 254)

MRIYYIGVFRSGGEKALELSEVKDLSQFGFFERSSVGQFMTFFAETVASRTGAGQRQSIE  
EGNYIGHVYARSEGICGLITDKEYPVRPAYTLLNKILDEYLVVHPKEEWADVTEINDAL  
KMKQLDITYISKYQDPSQADAIMKVQQELDETKIVLHKTIENVLQRGEKLDNLVDKSESLT  
ASSKMFYKQAKKSNSCCIIM

>YKR076W, 1613 bp, CDS: 501-1613 (SEQ ID NO 259)

TAAATAGTTGAGGCTTTTCTGCATTCTGTCAAGAAGGGTATGTGTATGAACATGCAAAT  
GACACTGTAAAAATGATTTCATTACCTGATTATGGAGTGATTTTCTTTCTTTTCTTTT  
ACATTTTAGTTTTCATTATTATGCAAATTAGAGGGTATACAGTTGAGATTTTAACACTTTGA  
ATTAAAAAGTGTACAGAGGAAACCGACGCAAAAGGCCTGGTGACGCAAACTTTTCCATC  
TTTATTTTACCCTCTTCAGACGGTCCTAAGACCCTTTTGAACGTATCAATATAGTTTATCA  
TCTGTTCTCTGTTGTTCTCCGTTACTAAGATATTAGTCAGCTCTTGAAATTTACACCCCC  
TATTTATTTGTCTTAGCGTCCAACCCCTCTCAACCCTTTTCCATTTCTTGATAAAGGTA  
GTAAATTAGGTAACGCTGCTCTTACCATCACTACAGTGCTTACGAGAATTTACCCAAACC  
CTGCGCAAGATAAATAAGAAATGTCGAAACAGTGGGCGAGTGGTACAAACGGAGCTTTCA  
AAAGACAGGTTTCGTCCTTCAGAGAAACAATCTCTAAGCAACACCCAATTTATAAGCCAG  
CAAAGGGAAGATATTGGTTGTATGTTTCACTTGCATGCCCATGGGCCCATAGAACACTAA  
TTACGAGGGCTTTGAAGGGATTAACTCTGTTATAGGATGTAGCGTAGTCCATTGGCACC  
TTGACGAGAAAAGGATGGAGATTTTTGGACATGGAAAAGCAATTGGAGGACAGTGAAGATT  
TTTTGGAACATTGGGCACGATGTTGCAGGTGGTATTAGAAGTGCATAAGAGGATTCCAGCA  
AGAGCTTCGCCGAGATCAAGAATGACAGTCAAAGATTTCATGGTTGATGCTACCAATGAGC  
CTCACATATGGATACAAGAGAATCAGTGACTTATATTACAAGAGCGATCCTCAATACTCGG  
CAAGGTTTACCCTCCAGTCCCTGTGGGACTTAGAAACCCAAACAATTGTTAACAACGAAA  
GTAGCGAAATTATAAGGATTTTGAACCTCTAGTCCGTTTCGATGAATTTGTGCGACGACGATC  
ACAAGAAAACGGACCTTGTTCCTGCTCAGTTGAAAACACAGATCGATGACTTCAATTCTT  
GGGTTTACGACATCAACAATGGTGTATACAAGACCGGATTCGCAGAGAAAAGCAGAAG  
TTTACGAAAGTGAAGTCAACAACGTATTTGAACATTTGGACAAAGTGGAGAAAAATCTTGA  
GTGACAAATATTCCAAATTGAAGGCCAAATACGGTGAAGAAGATAGACAAAAAATCTTGG  
GTGAGTTCTTCACTGTGGGTGATCAATTAACAGAAGCTGACATTAGATTGTATACTACCG  
TCATAAGATTCGATCCTGTGTACGTCCAACATTTCAAATGCAATTTTACCTCTATTAGAG  
CCGGATATCCATTTATTCATTTGTGGGTAAGAAATTTATACTGGAATTATGATGCCCTTCA  
GGTACACAACAGATTTTGACCATATCAAGTTACACTACACGCGTTCCACACAAGGATCA  
ACCCCTTGGAATTACGCCCCCTGGGACCCAAGCCAGATATTCGTCCTTTATAA

>YKR076W, 370 aa (SEQ ID NO 260)

MSKQWASGTNGAFKRQVSSFRETISKQHPIYKPAKGRYWLIVSLACPWAHRTLITRALKG  
LTSVIGCSVVHHLDEKGRFLDMEKQLEDSEDFLEHWHDVAGGIRTAKEDSSKSFAEIK  
NDSQRFMVDATNEPHYGYKRISDLYYKSDPQYSARFTVPVLWDLETQTIWNNESEIIRI  
LNSSAFDEFVDDHKKTDLVPALKTQIDDFNSWVYDSINNGVYKTGFAEKAEEVYESEVN  
NVFEHLDKVEKILSDKYSKLKAKYGEEDRQKILGEFFTVGDQLTEADIRLYTTVIRFDPV  
YVQHFKCNFTSIRAGYPFIHLWVRNLYWNYDAFRYTTDFDHIKLHYTRSHTRINPLGITP  
LGPKPDIRPL

>YKR092C, 1721 bp, CDS: 501-1721 (SEQ ID NO 261)

TCAAGGATACCTGGTTGATTCTACGTCGTCCTTCACTTTGGTTAATTCACCTTTGCC  
TTCACCTTGTGGTGTGCGGGTGTGTCAGTCATTAATGTTCTTTATCGCGAGAGGGGGTCT  
ACATAATCTTGTTTTTTTCACTCCAATAAGGCAGTTATAGTGAATTTGTTTTATTACAGAA  
GGTGTACCTTTCGTTTCGAGTTATTTTACTCTTGTGTTTGTAGTTTGTACATCTCTTTATGT  
CTGGATCAAAACGATAATTGCAAGCTTATTGCAATTTAGTTCTCTTACCCATTTCTTTAC  
AACGGGCCGAGAAAAAGTGGAGTTGGTCCGAGGAAGCTTTGAACGGGAAGAGGAAAAAAC  
CTTCCCATCGCTCGAGCATACAATTTTTTTTTTTTCAATGCAGGCTGAAAAAAAATTT  
CACTTGATGATTGAACCTCATCGCACTTTTATACAAAGCAAGAAAGAAACCCAAGTCGCAG



23/251

AGGGGTGGGATGCGCGAAATTCATGCCTACAGTAGAAAGCGGTTGTTGCACAAATGATT  
AAATCTTTATCTCCAACCTACAATACTATCGCGATAGATGCATAATATGTGCAGCTTCTA  
AACAGCACGGAGTGATGATAAATACGCATATATGTATATATATATGTATGTGCATATGCA  
CGTCCTTTTAAAACTCAAAATACAACATTCTTAGTAAATCCTTTTGTGGACACACGTCGG  
AACAACTCAGGACGGAGTTAATGGATATGCTTCATAATAAATGTAGTGATGCTATCAAAA  
GCACCTCCAATAGCAATTTGAGTAATGAGGTAGACAAACAAAAATTGCAATACGATGACC  
TCGGGAACACCGGATTTTCTGAACATTTGAGATGGAATCTCAAGATAATAATGATAGCA  
TAGAGGATTTCTTGTCTTTAATATAAAATTTAACCCAGGAGGTTGAGTTGAGAACCAAA  
GACAATATGAGCACACGAAAAAGACAAAGAAGCATAACCCATTCTATGTACCGTCAGAGG  
TAGTGCGAGAGATGGTCAAGAAACACGCATTGAATGGCAGAATATAG

&gt;YLR053C, 108 aa (SEQ ID NO 272)

MDMLHNKCSDAIKSTSNSNLSNEVDKQKLQYDDLGNITGFSELFEMESQDNNDSDIEDFLFF  
NINLITQEVFENQRQYEHTKKTKKHNPFPVSEVREMVKKHALNGRI

&gt;YLR390W, 839 bp, CDS: 501-839 (SEQ ID NO 291)

GTGAAATGAGACTGATAGGTGAGAGGTGAACCAATTGAGTGAGGAGTGGTTTAGTTACA  
AATGCAGAAGAAGAAGCTAAAAGAGATACGCCCATACAGAGCAATATCAAAATGAGCAAG  
AATGAGGTCTTCCGAATGGTTGGTTCTGACTTACTATTTGATTTCACTTTCTCTGATTCA  
TTCAGGAAGAAAAGGGCGAAGTCCTCGAAATGAAAATTTCAACATCATTAACAGACCGGC  
GCGCGCCTTTACAATTTAGTATGTACGCCACCAATAAAAGCTGCTTAAACAATAAGCTAG  
AAAGCCCAAAGGGTGTTAAATAGTACAGCGAACCCCTTCAGCAACGGTACATCAACAACCC  
CTTGAAAAGAATAGAGACAATACAGCTACAGTCATCCCCCTTCTCTTGTATTTTTGGCCAC  
AATTGATTGTATTACATCATATTTTGCTGTGCGCTTCTTCTATCTTTTCCGCATAAACT  
AGGGGAAACGCGATGAAGAAATGGATTGGCTGAAAAATACAACAATTGTAGTGTTATTCA  
GTCATTCAACTGACAAAAGTAACAAACACAAGAACGTCAAGTCCAGTGCAATATGCGAA  
AGAACACTTTAGATATGGTCACTATAGGTATCGCATGCCTTGTGGGAGTCTACACGGGCA  
CGAGATTTTTCGAGCCCATTTGTATCGATAGATTGCGTAAGGATGGAAGCTTGAGAACGG  
ACATTCCCATCCCAGAATACGACGAGGACGGAAATCTGTTAAAGGTCACGCCGTCTTTAT  
CATCCACACCAGCTGCACCACCTACACCACCTACACCTCCTACTCCACCACAACAGTAA

&gt;YLR390W, 112 aa (SEQ ID NO 292)

MDWLKNTTIVVLFSSHSTDKSNKHKRQVQCNMKNTLDMVTIGIACLVGVYTGTRFFPEPI  
VIDRLRKDGNLRTDIPPEYDEDEGNLLKVTPSLSSTPAAPPTPPTPPTPPQQ

&gt;YMR251W, 1601 bp, CDS: 501-1601 (SEQ ID NO 315)

ACTCCAGAGCGCAAGAGTTCGTTTCATCTACGAAATGTTGCTGGCATTGGCATCTCCACAA  
GATGACATCCCAACGCCGGATGAAATCGAAAAGAAAAATAAGCTAAAGGAAACAACAACG  
AGAAACTATAGAGGAACATGTTGAGTTGAAAAGGTCATCCAATATACCGCCCCCTATATG  
TATGTACCTTTACCTTTTATTTAAGTACTAGTGCTGTTTAGTTAGGTTATGTGAAGGCAC  
GGGTTTTGTCTTTTTTTTTTTTTTTTTTTTACTATTACTTTCTTTTTTCAAGCTTTTAAGCG  
CCGAAATGATATTTAAGGGAAGATGACTAAAGGGACAGCGACGAGGATTCAGCCTGGACA  
GTGATAGAAAAGTTATGCGGGAATACGTATATATAGTTGTATAAATTGTGGTTATAGAAC  
ATCGCAGCGCCTTTAAATATATTGTCTTTTTATTTCATCTTATTCCATCTCTCTCTTGCA  
ACCACGGCAAAGCTGGAGCTATGTCTGAAAAATCAGCTAGCAATAACAAAGCTGAATCA  
AAAGGCAGTCATCGCCATTTCAGAGAAATCATCTCTGCGGATCACCCAATTTATAAACCTG  
CTAAGGGAAGGTAAGTGGCTGTATGTGGCGCTACCATGCCCATGGGCACAAAGAACCTTGA  
TCACCAGGGCCCTGAAAGGGCTAGCGCCTATAATCGGGTGCAGTGATAGCGCATTGGCACC  
TGGATGACAAAGGCTGGCGATTCTTTGAAGAAGGAGATGGGAAAACCAATGAAAGGCACT  
GGTTTGACATTGCAGGCGGAATTAGCTCAGTAAATTTAAATACCAGTACTCCTGTGGCTA  
ACATACCCAATAACGCGCATCGGTTGTTGGTGCACGGAACAGATGAACCGCATTACGGGT  
ACAAGAGACTAAGCGACTTCTATTTCAAAACAAAGCCAGACTATAAGGGAAGATTACCGG  
TACCTGTTCTTTGGGACTTGGAACATGCACTATAGTAAACAATGAAAGCAGTGATATCA  
TCGGAATTATGAATTCGCTGCGTTTGATGAGTTTGTGCGGCAAGAATACCGTCAAGTCC  
GTCTGGTACCTCGGTCTCTAGAGGCACAGATTACAGAGTTCAACTCTTGGGTGTACGATA  
AAATCAACAACGGTGTATACAAGGCCGGTTTTGTCAGAATGTGCAGAGGTATACGAGAGGG

24/251

AGGTAACAAGCCTTTTTCAATATCTTGACAAATTGGAAAATCTTCTGGACAAGAAGTACA  
CAGATTTGGAGGCGGAGTATGGTAAGAACAACAAGGACAAGATACTAGATCGCTACTTTG  
CCATCGGAGACACTCTGACCGAGGCGGACGTGAGACTCTACCCAACGATAGTAAGGTTCCG  
ACGTGGTATACCATCAACACTTCAAATGCAATCTGGCCACCATCAGAGATGATTATTCCC  
GTATACACACGTGGCTCAAGAATATATACTGGCGCCACGAAGCCTTCCAGCGCACAAACGG  
ACTTTACCCACATAAACTCGGATATACTCGCTCGCAGCCACGGGTCAACCCGATTGGGA  
TCACCCCACTGGGGCCCAAGCCTGATATCCGACCTCCATGA

&gt;YMR251W, 366 aa (SEQ ID NO 316)

MSEKSASMNKAEFKRQSSPFREIISADHPIYKPAKGRYWLIVLPCPWAQRTLITRALKG  
LAPIIGCSVAHWLDDKGWRFLEEGDGKTNERHWFDIAGGISSVNLNTSTPVANIPNNAH  
RLLVDGTDEPHYGYKRLSDFYFKTKPDYKGRFTVPVLWDLETCTIVMNESSDIIGIMNSA  
AFDEFVGEERYQVRLVPRSLEAQITEFNSWVYDKINNGVYKAGFAECAEVYEREVTSLFQ  
YLDKLENLLDKKYTDLEAEYGNKNDKILDRYFAIGDTLTEADVRLYPTIVRFDVVYHQH  
FKCNLATIRDDYSRIHTWLKNIYWRHEAFQRTTDFTHIKLGYTRSQPRVNPIGITPLGPK  
PDIRPP

&gt;YMR273C, 3248 bp, CDS: 501-3248 (SEQ ID NO 321)

AAATTGGTCTCAATCTGGAATAAGTGCTACTTCGCACTGCTGGTCCTTGGATTAATATCC  
CTGAAGGATACCTTACAACTCTGGTAGGAACTCCTGGTTATAGAATAACCTTTAGCCT  
TTTTTACGTACTTGTATACCGTTTAAAATTTCTATGTACTATAACCTTTTTTCACTACT  
ATTATGGAATTTCTATCGAGCGACCGGGCTTTTGTACGGAAGAGTGAAAAAATCGAGTTT  
TGGTGTTTTGGTGAAAGAATTTGGAGGACTATAAAGTACCTATACTTTGTATTACGGACT  
CAATAACAAGTCGTTCTGTGTCAGTGGTATTGAAGTTGTCAGATCTAAGAGTAGAGAGAAG  
GTGGCATCTAATAGGTTTCGACGTTTTTCTTTTTTTAAGGTTTTTATTTGGTCTCCTAGA  
ATTTAAGGTCTTAGTTAGTTTGGTTTGTGTGTGGGTTACATATTTTCAATTCAAAGGA  
GAATTTAGCTGTCTTTTATAATGTCCAATAGAGATAACGAGAGCATGCTGCGTACTACAT  
CAAGCGATAAGGCGATCGCTAGTCAAAGGGATAAACCGGAAGTCTGAAGTTTTGATTGCTG  
CACAGTCCCTTGACAATGAAATCCGCAGCGTAAAAAACCTAAAAAGATTGTCGATTGGGT  
CAATGGATTTACTTATTGATCCAGAATTAGATATAAAATTCGGTGGGGAATCTAGTGGGA  
GACGATCATGGTCTGGCAGGACATCCAGTTCTGCGTCAATGCCAAGTGACACAACCAACCG  
TTAATAACACACGATATAGCGATCCAACCTCCGCTAGAGAACTTGCATGGGAGGGTTAACT  
CAGGGATAGAATCCTCCAATAAGACTAAACAAGGTAAGTACTTAGGTATAAAAAAAGGTG  
TTCCTCTCCATCCAGGAAATTAATGCTAACGTATTAAAGAAAAACTTATTATGGGTTT  
CCGCCAATCAACACCTTAACGTTAAGCCTGATAATTTCTTAGAGCTTGTACAAGATACTT  
TACAAAATATACAACTAAGCGACAATGGTGAAGATAATGATGGGAATAGCAATGAAAATA  
ACGATATTGAGGATAATGGGGAGGATAAAGAATCACAATCATATGAAAATAAGGAGAACA  
ACACTATCAACTTGAACAGGGGGCTGTCAAGGCATGGAAACGCGTCACTAATACGAAGGC  
CTTCAACATTGCGGAGGTCATATACAGAGTTTGATGATAACGAAGATGACGATAATAAGG  
GAGACAGTGCCTCTGAAACAGTAAATAAAGTCAAGAAAGAACTCTCCAAAATAAAAGAGA  
GACCAGTGTCGTTAAGAGATATAACTGAAGAACTGACAAAGATCTCAAAATAGTGCAGGAC  
TAACCGACAATGATGCCATTACATTAGCCAGAACTCTTAGTATGGCTGGTTCATATTAG  
ATAAAAAAGATCAACCACAACCGGAAGGGCATTTATGATGAAGGAGATATTGGTTTTTCAA  
CTTCACAAGCGAATACTTTGGATGATGGTGAATTTGCCCTCCAATATGCCCATCAATAATA  
CCATGACATGGCCTGAACGATCGTCACTGAGAAGGAGTAGATTCAACACTTATCGAATCA  
GGTCACAAGAGCAAGAAAAAGTAGAACAAAGTGTGGATGAAATGAAAAACGACGACG  
AAGAAGCTCTAAAAATTGACCAAGAATACAATAAAGGTCGAAATAGATCCGCACAAATCCC  
CTTTTAGACAGCAAGATGAGGATTTCTGAGAATATGAGTTTCGCCCTGGGTCAATTGGTGATT  
TTCAAGACATTTTATAATCATTTACAGACAGTCTAGTGGCGAGTGGGAACAAGAAATGGGAA  
TAGAGAAAGAAGCCGAAGAGGTACCCGTCGAAGTTTGAATGACACAGTAGAACAAGACT  
TAGAGTTAAGAGAGGGAACAACAGACATGGTAAAGCCAAGCGCAACGGATGACAACAAG  
AAACGAAGCGACATCGTCGAAGAAACGGATGGACATGGTTGAACAATAAATGAGCAGAG  
AAGACGATAACGAAGAAAACCAAGGGGACGATGAAAATGAAGAAAACGTGGATTACAAA  
GAATGGAGCTCGACAATTCCAAAAAACATTATATTTCTCTATTTAATGGCGGTGAGAAGA  
CGGAGGTGTCAAATAAAGAAGAAATGAACAATTCAAGTACTTCCACCGCCACATCACAGA  
CAAGACAGAAAATCGAGAAAACTTTTGCGAACCTATTCAGAAGAAAGCCACACCACAAGC

25/251

ATGATGCATCATCATCACCTCGTCGTCACCATCATCGTCACCATCAATACCAAATAACG  
ATGCCGTGCACGTTTCGCGTGAGGAAAAGCAAAAAGCTTGGTAACAAAAGTGGAAGGGAGC  
CGGTTGAACCCATTGTGTTGCGCAATCGCCCTCGTCCCTACCGTCACCATCACAGCCGTC  
ATGGTTCCCAAAAAATAAGCGTAAAAACCCTTAAAGATTCTCAGCCGCAGCAGCAGATAC  
CATTACAACCACAATTGGAAGGCGCAATAGAGATAGAAAAGAAAGAGGAAAAGCGATTCCG  
AGAGCTTGGCCCAACTACAGCCGGCCGTTAGTGTAAGTAGTACCAAAAGTAACCTCTAGAG  
ACAGAGAAGAAGAGGAGGCAAAGAAAAAGAACAAGAAGAGGAGCAATACGACAGAAATTT  
CCAACCAACAACACTCCAAACACGTCCAAAAGGAGAATACCGATGAGCAAAAAGCTCAAC  
TACAAGCTCCAGCTCAAGAACAAGTCCAAACTTCAGTCCAGTTCAAGCTTCAGCCCCAG  
TCCAAAATTTCAGCCCCAGTCCAAACTTCAGCCCCAGTTGAAGCTTCAGCTCAAATCAGG  
CTCCAGCGGCACCACCATTGAAACATACCTCCATATTGCCCCCAAGAAAGCTTACATTTG  
CAGAGTCAAAAAACCTGACAAACCAAACTCCCCGGTTCAATTACAGACAGTGCCTTTG  
GGTTCCCACTGCCTTTGCTGACAGTGTCTACGGTTATCATGTTCGACCACCGTCTACCAA  
TTAACGTCGAAAGGGCCATATACCGGCTGAGTCACCTGAAATTGAGCAATTGGAAGAGGG  
GACTGCGCGAGCAGGTATTACTAAGTAACCTTCATGTATGCTTATCTGAACTTGGTTAATC  
ACACTCTGTACATGGAGCAGGTAGCCACGACAAAGAACAACAACAACAACAACAACA  
AACCTGA

>YMR273C, 915 aa (SEQ ID NO 322)

MSNRDNESMLRTTSSDKAIASQRDKRKSEVLIAAQSLDNEIRSVKNLKRLSIGSMDLLID  
PELDIKFGGESSGRRSWSGTTSSSASMPSDTTTVNNTRYSDPTPLENLHGRGNSGIESSN  
KTKQGNYLGIKKGVHSPSRKLNANVLKKNLLWVPANQHPNVKPDNFLELVQDTLQNIQLS  
DNGEDNDGNSNENNDIEDNGEDKESQSYENKENNTINLNRGLSRHGNASLIRRPSTLRRS  
YTEFDDNEDDDNKGDSASETVNKVEERISKIKERPVSRLDITEELTKISNSAGLTDNDAI  
TLARTLSMAGSYSDDKKDQPPQEGHYDEGDIGFSTSQANTLDDGEFASNMPINNTMTWPER  
SSLRRSRFNTYRIRSQEQEKEVEQSVDEMKNDDERLKLTKNTIKVEIDPHKSPFRQODE  
DSENMSSPGSIGDFQDIYNHYRQSSGEWEQEMGIEKEAEVVPKVRNDTVEQDLELREGT  
TDMVKPSATDDNKETKRHRRRNGWTWLNKMSREDDNEENQDDENEENVDSQRMELDNS  
KKHYISLFGGEKTEVSNKEEMNNSSTSTATSQTRQKIEKTFANLFRKPHKHHDASSP  
SSSPSSSPSIPNNDVHVVRVRSKKLGNKSGREPVEPIVLRNRPVRPHRHHHSRHGSQKIS  
VKTLKDSQPQQQIPLQPQLEGAIEIEKKEESDSESLPQLQPAVSVSSTKSNRDRREEEEA  
KKKNKKRSNTTEISNQQHSKHVQKENTDEQKAQLQAPAEQVQTSVPVQASAPVQNSAPV  
QTSAPVEASAQTQAPAAPLKHTSILPPRKLTFADVKKPKPNSPVQFTDSAFGFPLPLL  
TVSTVIMFDHRLPINVERAIYRLSHLKLNSKRGLREQVLLSNFMYAYLNLVNHTLYMEQ  
VAHDKEQQQQQQQP

>YNL112W, 3143 bp, exon1: 501-1773, intron1: 1774-2775, exon2: 2776-3143 (SEQ ID NO 327)

CTTGATGGATTTATGTGACGTTGTAGAATCTAAGTTTACTGAAAAATCAAGAGCATGTA  
GATGTTACGGATCGACTCAAAGACCCTCTGTCACTCTGAAATTTCTAATAATTATGCACA  
CCACGCTAGTATAGATACAGCTTGATTTGTGTATCCCGTTTATAGTCGTGCTATTTAAAA  
TCTATGTATAATATAACCAGATAAAAAATACACCTTCGTACAAGGTGCTAATAATGTTGAG  
AATTCGAAATTCCTTTTTTAAAGGCGTATTCGTTGTAATGATTGAAAAATTTATTTCTT  
TTTTTATTTCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTACGCCGATGCTCATCGCAGAAAAT  
TTTCTCCTTCAGTTTATTTGTCTTATAAAAAGACTGTCCTACGCTCAAATAACTTATACTT  
TTCTGTATCTCATTCAAATTATTTTCTTGTCAACAACCTGTAACAGAATTAAGCACTATT  
AAGGCAAATTTAGAGCAAATATGACTTACGGTGGTAGAGATCAGCAATATAACAAGACTA  
ACTACAAGTCTAGAGGTGGCGACTTCCGCGGTGGAAGAACTCTGATAGAACTCTTACA  
ATGACAGACCACAAGGCGGTAACCTACCGTGGTGGTTTCGGTGGTCGTTCCAATTACAACC  
AACCCAGGAATTGATCAAACCAAACCTGGGATGAAGAATTACCCAAATTGCCAACTTTTCG  
AAAAGAATTTCTATGTTGAACACGAAAGTGTTCGCGACAGATCGGACAGTGAGATTGCTC  
AGTTCAGAAAGGAAAATGAAATGACTATTTCCGGACACGATATTCAAAGCCAATCACCA  
CTTTCGATGAAGCTGGTTTCCCAGACTACGTTTGAATGAAGTGAAGGCTGAAGGATTTG  
ACAAACCAACTGGCATTCAATGTCAGGGTTGGCCAATGGCTTTATCTGGTAGGGACATGG  
TTGGTATTGCTGCCACTGGTTCCGGTAAGACTTTGTCTTATTGTTTACCAGGTATTGTTT  
ATATCAACGCTCAACCATTATTGGCTCCAGGCGATGGACCAATTGTTTTGGTTTTGGCTC

26/251

[illegible]

>YNL112W, 546 aa (SEQ ID NO 328)

MTYGGRRDQQYNKNTNYKSRGGDFRGGRRNSDRNSYNDRPQGGNYRGGFGGRRSNYNQPQELIK  
PNWDEELPKLPTFEKNFYVEHESVRDRSDSEIAQFRKENEMTISGHDIPKPITTFDEAGF  
PDYVLNEVKAEGFDKPTGIQCQGWPMALSGRDMVGIAATGSGKTLSYCLPGIVHINAQPL  
LAPGDGPIVLVLAPTRELAVQIQTECSKFGHSSRIRNTCVYGGVPKSQQIRDLSRGSEIV  
IATPGRLIDMLEIGKTNLKRVTYLVLEADRMLDMGFEPQIRKIVDQIRPDRQTLMWSAT  
WPKEVKQLAADYLNDP IQVQVGSLELSASHNITQIVEVVSDFEKRDRNLNKYLETASQDNE  
YKTLIFASTKRCDDITKYLREDGWPALAIHGDKDQRE RDWVLQEFRNGRSPIMVATDVA  
ARGIDVKGINYVINYDMPGNIEDYVHRIGRTGRAGATGTAI SFFTEQNKGLGAKLISIMR  
EANQNI PPELLKYDRRSYGGGGHPRYGGGRGGRGGYGRRGGYGGGRGGYGGNRQRDGGWGN  
RGRSNY

>YNL131W, 959 bp, CDS: 501-959 (SEQ ID NO 329)

CAAAAAGAGCTAATCAACTCCTTGAACCTAGATAAAATACGCCATAAATGATAACAGTGAG  
GAATGGGCTGAATCTCAAAAATCTTTAGAAAATAGCTGCCAAGGCCAAAGGCGTCGTCAGT  
TTAAAAACTGGTAAAAAGAGAACGACTGAAAAGGCTGAAGATATCTATAGACAAGAGATG  
AAAGCTATGAAAAAACCAAGAAAGTCTAAAAAGGCTGCAAAATTAAGCGTTCTACTCTTTG  
TCAACCCCTTTTATAGCTAAACGTTTACTTAAATTTGTACAATAATATAGAATAGAAACAT  
AGTTGATGTTTGAACCTTTACATATTCTTTCAATCGTGTCGAGCGATATAAGTATTACG  
ATTATGCCGGCGAAAACCTGAACCCGTTTTAGACAATTTCAATCAACATACTCCACTCCGT

27/251

AGTGAGTAACTTTTGGAGTAATACGAAGTAACCAAAGAGGTCAAAACGGAACATATATACC  
CCAAAATAAGCATCATTCAAATGGTCTGAATTAAGTAAAGACGATGTCGTTCAAT  
TAGACGAACCACAATTTTCCAGAAATCAGGCCATCGTGGAAGAAAAGGCCTCTGCAACAA  
ACAACGACGTTGTGCGATGATGAAGATGACTCTGATAGTGATTTTGAAGATGAATTTGATG  
AAAATGAAACATTGTTGGACAGAATCGTTGCTTTAAAAGACATTGTCCCCCAGGTAAGA  
GACAAACAATTTCTAATTTTTTTGGTTTTACTAGCTCTTTTGTGAGAAATGCTTTCACAA  
AATCCGGAAACCTTGCTTGGACTTTGACCACCACTGCTTTGTTACTCGGTGTGCCACTAT  
CCTTATCTATACTTGCCGAACAACAGCTAATCGAAATGGAAAAGACATTTGATTTACAAA  
GTGATGCTAATAACATATTGGCCCAAGGTGAAAAAGATGCTGCAGCAACAGCCAATTAA

>YNL131W, 152 aa (SEQ ID NO 330)

MVELTEIKDDVVQLDEPQFSRNQAIVEEKASATNNDVVDEDDSDSDFEDEFDENETLLD  
RIVALKDIVPPGKRQTISNFFGFTSSFVRNAFTKSGNLAWTLTTTALLLGVP LSLSLILAE  
QQLIEMEKTFDLQSDANNILAQGEKDAAATAN

>YNL143C, 893 bp, CDS: 501-893 (SEQ ID NO 333)

GAAAATACACACGGCGGAAGCCATCATCGAGGCCCAAAGCAAGGATAAAGCATGCTTTTT  
CCTGGATAAACCAGAATATAATAAACCAGATACCTGGGACCATAATCCACACACCTGCTGA  
AGCCACACCGATCCATCCCATGTTGGCCAAGTCAAATTGTGTATTCAAATCTGTTGTCAA  
CGAGTTACCACCCGTTCCCTTCGCCTGTAGGCGTACCTGTAAAATTGTAAGACATTGTTGA  
TATTGTATTGTAATATATTAAGTATGATATATTACAAAATAAACTTCTTTCAAAGCTCT  
GTGCAGACTTATTATTTAAGAAGGATATTTAATTTGAAAGGACGTGAAAGCACGAATGAT  
TACTACCCACTGATGTTTGGTTAGCACATGTGTAATACTACTGCTTATATATGGTGCAGAAA  
AGTGGCTCGGAATGAACACCTCTTGTACTGAATACTTCATTGATAAGGCACAGGGCTTTC  
ACGCCGCTTAGTATTTCGTGATGCGTGAGCAATTGAAGCTTTTACGAGGGAAATAGTCG  
ATTTTACATTTCTTATCTTATCTGGCTTTGACTATTACCAGACACTCTTGATAAGCAGTA  
ACAGCAGTAAGAAGAGACCGAAGGATTCTTCTTTGTTATCGGAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAGATGTCTTATCTTATCTTCTTATCTTAAAGACCTACCATTGTTC  
CTTTTCTATTTTGGCAGCCCGGTTATTCGAAAGGGAAAAAAAAAACCAAGACAGCATTCCT  
TGTTTATTATGACTATTACAAAGCCAGGAATGATTTTCGATGGCCGACATGAATTACGTCG  
TTTCCAAGAACAGAAGCTTAAACCGTCCTGCTGAGCGGGGCGGTAATCGGTGA

>YNL143C, 130 aa (SEQ ID NO 334)

MREQLKLFRTREIVDFTLILSGFDYYQTLISSNSSKKRPKDSLLSEKKKKKKKKKDV  
LSYLSYKLDLPFVPFLFWQPGYSQREKNPRQHSFLFIMTITKPGMISMADMNYVVSKNRSL  
NRPAERGGNR

>YNL179C, 938 bp, CDS: 501-938 (SEQ ID NO 335)

ACAGCGGTTAATTTCAAATACCCTAATCGGAGGTCTTATCTTATTTTTCAAGGGCAAGGC  
TCTCCACATCGGTAAGTGATGACCAGATAATGGAAAGTAGCAGAATTTTATTTATGTGCC  
ATACAAGCCCGGAGAAACAGAGTAGCTAAAAAATTAAGGTGTGCAAAAGTGGTTTTGTTC  
CCCGACGCCCGGGCCTTTCTCTCCCTGAATCTTTTCGTTCCGGCCCCCTCTCTCAATA  
CCAGATCTGCATCTATACTAAAGCTGCAGTGAGAGTAAACCGGAAAATTATCCTGCGTGT  
TTGCTTCGGTCTTAGCTTTTACTTGGGTATGCGAGAACCTCTAAGAGCTTAGACCGGTCT  
TCCTCCCTAAAAAGAAATATAAAAGGTTATTATCTGGACTAAAGCAAAAAAAAAAACAA  
CGTTTCGGCGTCCGCTCAAATTTTTCATTACGCTTCTTGGTCAAATCAGTTACGTAACGG  
GTTATGACGAATACGATGAGATGAGTAATTGCAGAAGGCTCCTATGCAGACAGCTAAGCA  
GTGCTTACTTGAATTACCTTCCCTTTTATTTCTTGATATATCGTCCTTTTTTCTCTATC  
TTAGTTCTTGCGAGTACTGGCAATCATGTTTCTCCTTTTTTTTTTCTTTTTTTTTTATTTT  
TTTTTTTTTTTTTTTACTTTTTCAGTTTCTCGTAGCTTTTCTTATTTTGCTATTTAAAGTAA  
GTTTAAATAGTACCCTCACTAAACACGTACGGCCGATCCACCAACGAACAAAAGCACGAT  
CCTTGACCCATCATTGTATTCCAAAGCGTTGGAACATTCACTTTTTTTTTTCCGGTCTAT  
TGCACAAGACAATATCCAGAATATTCAGTTGGATAGGAAATACAAGACAGGTGGCACCCA  
CAAAGCACACGCCGAAATATTTATTAAATACAATATAG



28/251

&gt;YNL179C, 145 aa (SEQ ID NO 336)

MSNCRRLLCRQLSSAYLNYLPFYFLIYRPFSLYLSSCEYWQSCFSFFFLFFLFFFFFTF  
QFLVAFPIILLFKVSLNSTLTKHVRPIHQRTKARSLTHHCIPKRWNHFFFSGLLHKTISR  
IFSWIGNTRQVAPTKHTPKYLLNTI

&gt;YOL150C, 812 bp, CDS: 501-812 (SEQ ID NO 349)

TTCCCATTTCCACTGCTATTCCTGTTGCTATTGTCAGAACCATTGTTTACTTGAATGTTA  
TTACTACCATTTTGTGAATCAAAAATATCTACTTCTTGTGGGGAGACGGGTAGAAGATTT  
GTATTTTGGGAGACGTCCTCTCAAATATATGGCCAAAACACCTTGATATTCTAGTTTATTC  
CATTCGTCCTTCTTGAAGTCCCATTATACAGTGACGCATGTGGTGTGTGAAAAAGTAGT  
TGCTTTATTTTGGATCGTATCTCCCAATAACGTTGAAATTCAAAGCTTTTCTATAGAAT  
TCTAACGTGTGTGGCAGAGTTTCTGCTGCAGTTGCTGCTCCGGTCATTGTGCACAGCTTT  
TCTTGTGATGTGTGCAAAGATAAATGCTTATCTGAACGTTTCTCTATTGTTTTTTCGTC  
AATTTTCTTTTCTTTCTTGCCTTCGCGTTTTCGACATATTAAGCTGTATATAGAAGAGAAA  
AATGCGCAGAGATGTACTAGATGATAAAAAATAATTGTAATAACGTTAATATATATAAAAT  
ATTATCTATTTTTCATTTTAAAGTTTATATTCTGCCCTCAAATTTTAAATTTGGGAGGCAG  
TGTCGTCAATGGTCTCTTTCAAGTTCTCTGAACCTTGAAACCTAACAATTTCTTACTCTTTT  
TATTATCAAGAGTAGCACCAGGGGTGTTATGGGTAGCACCAGAACCTGGTTTCCCCACTG  
GAATATTGCCCTTTTAGAACAGGGAAGTCTTCGTTAAGGATATCGAGAACATCCTGCATAG  
TAAATCTGGCCTCCGATACGATTAGTCTTTGA

&gt;YOL150C, 103 aa (SEQ ID NO 350)

MIKNNCANNVNIYKYLFSEFKVYILPSNFKIWEAVSSMVSFKFLNLKPNNFLLFLLSRVAP  
RVLWVAPEPGFPTGILPFRTGKSSLRISRTSCIVNLAASDTISL

&gt;YOL151W, 1529 bp, CDS: 501-1529 (SEQ ID NO 351)

GCGTGAACATATGTCATATTTGCGATTTTAGGTACAATAAATATTATCATTATTATATTAT  
GTTTGCATGTAGGTTCTACAAATACATTTGTTGTACGCTATAGTTTCCTTTCAAACCTAGA  
AAGAATTCGTAACAAAATAATCTCCAATATTTTATAGCACCTTATTAATATCAATGCTGC  
AATACCTTCTCATTTCAACAATTTGGCCCTCACCTCTTTTGTACAAAAACGTCGCCATTG  
ATAAAATAAGTAAGAAGCATATAAATTGGAATGTCCATTACGTAAAAGAAAAAAATCATG  
TGTACATATTACGTAATAGAAATACGGAATTTTCTCGCGGAAGTAGATCTTCCGTGGAAAA  
AAAGGAAAAAGTCCGATCAATATTGAAAAAGGGATCCTTAGTTTCCCAACTATATAAGGA  
GGAAAAGTCTATCTCTGTAGCGTTGATATAACGTGTACGATTTTCAAACAAACAGATAGC  
AGTATCACACGCCCGTAAATATGTCAGTTTTCGTTTTCAGGTGCTAACGGGTTCATTGCC  
AACACATTTGTCGATCTCCTGTTGAAGGAAGACTATAAGGTCATCGGTTCGCCAGAAGTC  
AAGAAAAGGCCGAGAATTTAACGGAGGCCCTTTGGTAACAACCCAAAATTTCTCCATGGAAG  
TTGTCCCAGACATATCTAAGCTGGACGCATTTGACCATGTTTCCAAAAGCACGGCAAGG  
ATATCAAGATAGTTCTACATACGGCTCTCCATTCTGCTTTGATATCACTGACAGTGAAC  
GCGATTTATTAATTCCTGCTGTGAACGGTGTAAAGGGAATTCCTCACTCAATTAATAAAT  
ACGCCGCTGATTCGTGTAACGTGTAGTTCTCACCTCTTCTTATGCAGCTGTGTTTCGATA  
TGGCAAAAGAAAACGATAAGTCTTTAACATTTAACGAAGAATCCTGGAACCCAGCTACCT  
GGGAGAGTTGCCAAAGTGACCCAGTTAACGCCCTACTGTGGTTCTAAGAAGTTTGTGAAA  
AAGCAGCTTGGGAATTTCTAGAGGAGAATAGAGACTCTGTAAAATTCGAATTAAC TGCCG  
TTAACCCAGTTTACGTTTTTGGTCCGCAAATGTTTGACAAAGATGTGAAAAAACAATTGA  
ACACATCTTGCGAACTCGTCAACAGCTTGATGCATTTATCACCAGAGGACAAGATACCGG  
AACTATTTGGTGGATACATTGATGTTCTGTGATGTTGCAAAGGCTCATTTAGTTGCCCTTCC  
AAAAGATGGGAAACAATTGGTCAAAGACTAATCGTATCGGAGGCCAGATTTACTATGCAGG  
ATGTTCTCGATATCCTTAACGAAGACTTCCCTGTTCTAAAAGGCAATATTCAGTGGGGA  
AACCAGGTTCTGGTGCTACCCATAACACCCCTTGGTGCTACTCTTGATAATAAAAAGAGTA  
AGAAATTGTTAGGTTTCAAGTTCAGGAACCTGAAAGAGACCATTGACGACACTGCCTCCC  
AAATTTTAAAATTTGAGGGCAGAATATAA

&gt;YOL151W, 342 aa (SEQ ID NO 352)

MSV FVSGANGFIAQHIVDLLLKEDYKVIGSARSQEKAE NLTEAFGNNPKFSMEVVPDISK  
LDAFDHVFQKHGKDIKIVLHTASPFCDITD SERDLLIPAVNGVKGILHSIKKYAAD SVE

29/251

RVVLTSSSYAAVFDMAKENDKSLTFNEESWNPATWESCQSDPVNAYCGSKKFAEKAWEFL  
EENRDSVKFELTAVNPVYVFGPQMFDDKDKVKKHLNTSCELVNSLMHLSPEDKIPELFGGYI  
DVRDVAKAHLVAFQKRETIGQRLIVSEARFTMQDVLIDLNEFVPLKGNIPVGKPGSGAT  
HNTLGATLDNKKSKLLGFKFRNLKETIDDTASQILKFEGRI

>YOR131C, 1157 bp, CDS: 501-1157 (SEQ ID NO 359)

TCCTGAACGGAAGCTGCAGTTTGCCTCAGTACCTACACGCTCCTCTGACATAGAAGATGAT  
CCATCTGTGGTTGTTGCAGCAGGTTTCAAGATCTTCTCTCTGGGGCTCAGCAAATGGATTG  
TTATCCAGATCATCATATGGATCATAAGGTACAGCCGAAGTCATTGTTTCAAGAGGATAGAT  
GGATTGACTAAGGGTACAGTACGGCAAAAAAATTAGATCAGCTTTTCAAACAAACTA  
TTTTGGCGTTTACCAAACCAAACAGTATATTCAACTAGTTCAATCACTCTTGAAAACG  
TCCCCTTTCTACAAAATTAGGCTTTGAACCGGTGCTATGGAAAAAGTGTAAGAAAACG  
AAAAAACAGAAAAGTCATATATATCTTATAACGAAATATCAGGGTGTTCGACTCAATCG  
CCAGGTGCCGCTAACACAATCATTAGGATAGTCGGGCAATATATACGGTTCAATAGTCAC  
TGAAAGTGTTATCACAGAATAATGACAAAGCTACAAGGACTACAGGGATTAAAACACATCA  
AAGCGGTTGTATTTGATATGGATGGCACATTATGCCTACCCAGCCTTGGATGTTTCCAG  
CAATGAGAAACGCCATAGGATTGGAGGACAAATCGATTGATATCCTTCATTTTCAATTGATA  
CATTTGCCACAGAAAAAGAAAAAAGAAGCGCATGATAGAATAGAATTAGTTGAGGCAA  
AAGCCATGAAGGAGATGCAACCGCAGCCTGGTCTGGTTGACATAATGAGGTATTTGACGA  
AAAATGGTATTAGCAAGACATATGTACTAGAAATGTCGGAGCCCCGGTAGAGACTTTTG  
TTAAAAGATTTATTCATCCGAGCTTTTCGAGGTTTGACTATATTGTGACAAGGGAGTTTA  
GGCCTACAAAACCGCAACCAGACCCATTATTACACATCGCCTCGAAGCTAAATATAAGGC  
CCTTGGAATGATCATGGTAGGAGATTCAATTGACGACATGAAATCCGGTAGATCTGCTG  
GATGTTTACCGGTATTACTCAAGAATCATGTGAATGGACATTTACTGCTCGAACATAAAG  
AACTAGTAGACGTTTTCAGTAGAGGATCTTTCCGAAATAATTGAATTGATTCAAAATATGA  
ATAAAGAAAGTTTCTAA

>YOR131C, 218 aa (SEQ ID NO 360)

MTKLQGLQGLKHIKAVVFDMDGTLCLPQPMFPAMRNAIGLEDKSIDILHFDITLPTKEKE  
KKEAHDRIELVEAKAMKEMQPQPLVDIMRYLTNGISKNICTRNVGAPVETVFKRFIPS  
ELSRFDYIVTREFRPTKPPQDPLLHIASKLNIRPLEMIMVGDSFDDMKSGRSAGCFTVLL  
KNHVNGHLLLEHKELVDVSVEDLSEIIELIQNMNKESF

>YOR286W, 950 bp, CDS: 501-950 (SEQ ID NO 367)

CATCTGAGTACTCGATTGTTTCATATTCCTGCTTCCATCAATGTGCCATATAGATCGCACC  
CTGACGCATTTGCCCTTAGATCCTTTAGAATTTGAGAAACAGATTGGCATCCCCAACCTG  
ACAGTGCCAAGGAGCTAATATTTTATTGTGCTTCTGGCAAACGCGGGGAGAAGCTCAA  
AAGTCGCCTCCTCATGGATATTCAAACACCTCACTATATCCTGGCTCTATGAATGATT  
GGGTTTCTCATGGGGGTGATAAACTTGACTTATAGCCTTGTATACCTTAGGTATGTACCC  
TGTGTATTTTCGTAAGCTAGTAACGTATTATGCCATTTATGTCACACCGTTTCATAATATT  
TGCCTATTGCATTGGCTGTGATAGCGCGCGCAAAGAAATTAGGAAGTATAAAAAA  
AATACAAACTTAATCTGAATGGAATAAGATAGCGATAACTCTCAACAAATGGAAGCGAG  
ACAGAAGAAAAAGACCAACGATGTTCAAGCATAGTACAGGTATTTCTCTCGAGGACAGTTT  
CTGCAAGATCGCCTACATTTGGTCTTGAGAACATTTACAACGAAGGCTCCAAAGATCTATA  
CTTTTGACCAGGTCAGGAACCTAGTCGAACACCCCAATGATAAAAACTATTGGTAGATG  
TAAGGGAACCCAAGGAAGTAAAGGATTACAAGATGCCAACTACAATAAATATTCCGGTGA  
ATAGTGGCCCTTGGCGCTCTTGGATTGCCCGAAAAGGAGTTTCACAAAGTTTTCAAATTG  
CTAAACCACCTCACGATAAAGAATTGATTTTCTTTGTGCGAAAGGAGTAAGAGCCAAAA  
CTGCCGAAGAGTTGGCTCGATCTTATGGGTACGAAAACACTGGTATCTATCCTGGTTCTA  
TTACTGAGTGGTTAGCTAAAGGTGGTGTGACGTTAAGCCCAAAAAATAA

>YOR286W, 149 aa (SEQ ID NO 368)

MFKHSTGILSRTVSARSPTLVLRFTTTKAPKIYTFDQVRNLVEHPNDKLLVDVREPKEV  
KDYKMPPTTINIPVNSAPGALGLPEKEFHKVQFAKPPHDKELIFLCAKGVRAKTAEELAR  
SYGYENTGIYPGSITEWLAKGGADVKKPKK

30/251

&gt;YOR382W, 962 bp, CDS: 501-962 (SEQ ID NO 375)

AGTAAGCTCCTACAGTGAAATATCTGGGTGCTACTGACGCCAAGCCCTACAGCGATCGGA  
ATGCGGGAACGGAAGTTAACGGGGCTTCCAGAACGGCGGAAGCGAATTGAACGAGGACGG  
CAAACAAAAACACCCAAAATTTCTATTACTTAGAATGACCCTCAAGAGCAGGGTGCAATTT  
ATCAAGCGATCATTGAACTAACTAAGTTCATATCCTGTATAGGATTTAAAACAATGCACC  
CTAAGTTCAAATGCACCCCCCTCGCCCCGAGCGGACCCTTGAACAGAGAACGTGTTTCG  
AGGTTACCCCAATTGGATCACTTGTATAATTTGTAATCGAGTTCGGATAAGATGTATACG  
AATCTAACTGGGTGCAGTATAATTAGCATTTTATATTACCTAGCAATATATGTATAAAAC  
AGGAATGTGTGCGTGCTTCAGGCAGAATTTACGGTCCTTGTAAGAAAGTCTATCATAAA  
GCCATCACAAAACAATAATAATGAAATTTCTCAACTATTTTCGGAGCTACTACAGTTATGA  
CTGCCGTCTCGGCAGCAGCTGTGTGAGTGTAAATGACCACTAAGACTATTACTGCTACTA  
ACGGTAATAAGTTTACACTAAGTTCGTTACCGACACCGCTGACCCTATCATTTGTACAG  
GTACCCTAGAACTGTGCTTGTGTCAGTAATAGTGATGCTACTTACACAAAGGTTGTCACCG  
AAGGACCAGATACCACCTCTGAAAAGAGTACAACAAAGACACTTACTTTGACAAACGGTT  
CAGGTTTCATCAACCAACCTTTACACCAAGACCGTCACTCAAGCCGTCGAATCATCTACAT  
CCTCCTCATCCTCCTCATCCTCCTCCTCCTCCTGCTCCTCCTTCTGCTGCTGCTCCTG  
CTGCATTCCAAGGAGCAAGTGTGCGGTGCATTGGCCCTTGGTTTGATTTCTTACCTATTAT  
AA

&gt;YOR382W, 153 aa (SEQ ID NO 376)

MKFSTIFGATTVMATAVSAAVSSVMTTKTITATNGNNVYTKVVTDADPIISYSTTRTVV  
VSNSDATYTKVVTGPDTTSEKSTTKTLTLTNGSGSSTNLYTKVTQAVESSTSSSSSSS  
SSSSSSSSGAAPAFQGASVGLALGLISYLL

&gt;YPL078C, 1235 bp, CDS: 501-1235 (SEQ ID NO 379)

TAAACTGTGTTGTGACGCAACTGCAACTCCCAGATGAAATACGGTCCGGTAAAGATAGGA  
ATATTCTACTCTACAAGCATGAATATTTTAAACGCGGCGCAGTACTATACAGCATAACA  
GGTCTTCCACGCATGAGAACTGTCCATGGCTAAATTAGTTCCTCACACAGAATTAGAAA  
TGTGCTGTGACAAATGGCACATACGTAGATAAAAGATAAATATAATTGAGAATGGCTGTGG  
CGACAACCTATTATCATAGAGGTGTCCCATCGAGCGAGCCTCATTGGCCGGGTAATCGACA  
TCAATATTGAACCAATCACGACGCTTTTTCTCTTCACCGCTCATTTCGGACCTTCACCACA  
GGTTTGGGTAATTAAAATAGCAAGGGATTATAATTGCAGTTAGCAGTTTATGTTGACAAG  
TTTATACTGTGCTAGGAAGGGTTATATTTTATTAAAAGACTGACGAGAATTCAGTACCTC  
CTAAGTGCAGCAAGAGATAAAATGAGCATGAGTATGGGTGTCCGTGGCCTAGCGTTAAGGT  
CCGTTTCTAAAACATTATTTAGCCAAGGTGTTTCGTTGTCCTTCGATGGTGATTGGAGCCC  
GTTATATGTCTTCCACTCCAGAAAAACAGACAGATCCAAAAGCAAAGGCTAACTCTATCA  
TCAATGCCATTCCAGGTAATAATATTTTGACAAAGACGGGGGTTTTGGGGACTTCTGCTG  
CCGCTGTCAATTTATGCCATTTCCAATGAATTGTACGTTATCAACGATGAAAGTATTTTAT  
TGCTGACTTTTTTGGGTTTCACTGGTTTAGTGGCAAAGTATTTGGCGCCAGCATATAAAG  
ATTTTGGCGATGCAAGAATGAAGAAAGTCTCCGACGTTTTAAATGCCTCGAGAAACAAGC  
ATGTCGAAGCTGTTAAAGATAGAATCGACTCTGTCTCTCAACTACAAAATGTTGCTGAAA  
CTACAAAGGTTTTGTTTGATGTTTCCAAGGAACTGTTGAACTTGAAAGCGAAGCCTTTG  
AATTGAAACAAAAGGTAGAATTAGCTCACGAAGCAAAGGCAGTCTTAGATTTCGTGGGTTA  
GATATGAAGCTTCCTTGCCTCAATTGGAACAAAGGCAACTAGCAAAATCTGTCTATCTCA  
GAGTTCACTCAGAAATTGGGTAATCCAAAATCCAAAGAGAAAGTTTTGCAACAGTCTATAT  
CTGAAATTGAACAATTGCTTTCTAAATTGAAGTAA

&gt;YPL078C, 244 aa (SEQ ID NO 380)

MSMSGVRGLALRSVSKTLFSQGVRCPSMVIGARYMSSTPEKQTDPAKANSIINAIPGN  
NILTKTGLVLTSAAAVIYAI SNELYVINDESILLTFLGFTGLVAKYLAPAYKDFADARM  
KKVSDVLNASRNKHVEAVKDRIDSVSQQLQNV AETTKVLFVDSKETVELESEAFELKQKVE  
LAHEAKAVLDSWVRYEASLRQLQRLAKSVISRQSELGNPKFQEKVLQQSISEIEQLL  
SKLK

&gt;YPL085W, 7088 bp, CDS: 501-7088 (SEQ ID NO 383)

TTTTTCATGAGGAAGAGCCAGTGACAGTAAATAATAAAAGGTGAAATGATTAAACAATGA

31/251

AAGCGGCAGAAAAATAAAATCAAACAGTGGCAGTATTGACTTTTGAAAAATCAGAAGTTCA  
TCCTAAGTTAAGACTTTCTTCTTTTAAGTGCTTTCTCCTTCTCTCACTGTCTTATCGCTG  
TATATCTCATTGTTGAATAATATAACACAACGTTATAAGTGATCATCACTTTCTGATCCA  
TAATTTCAAACCTCAAGCGACCGTACATGTGGCATTTCCTACTATAAACTTACGAGCAAG  
AGAAAGATATACGGAAAAGGTTAATTGGCAGGTTACACAAGATTTTGGTCATTGAATATT  
TGCAGCCCTCCTGCTTGAGAACTGGACAACAACCTGTTATCAATATTCCCTTTTCAAAAT  
AGTGGTATTTAACTGGCCATAACCAAGGAAACCGTTGTACCTATTATTTTGTATAGTCTT  
CATTTAATAACGTGTTAAGAATGACACCTGAAGCCAAGAAAAGGAAAAACCAAAAGAAAG  
AGTTGAAGCAAAAAGCAAAAAAAGCTGCTGAGAAAGCTGCTAGCCACAGTGAAGAACCAC  
TTGAATTACCAGAAAGTACGATTAACAGCAGCTTCAACGACGACTCGGTGAACCGTACAG  
AATCTGACATAGCTTCAAAATCTGATGTTCTCCGGTCTCATCATCTACCAATATCTCTC  
CGGCTAATGAAACACAACCTAGAAATACCTGATACTCAAGAATTGCATCATAAACTGCTCA  
ACGACTCTGATCAACATGATATTACCGCGGACTCAAATGATTTGCCAGACAACCTCAATCG  
TTGAACATGACTCTGTTATTACCCAAACAAAACCAGCCATGTCTCAAGAATACGAAGATA  
CTGCCGCTCACTTATCTTCGAGAAATCCATCGCTCGATGTAGTCGCGGAGAACTTCACA  
ATAATAATGAACATACCCAGAAAATTGCCGTATCCGCTGTGGAAGAGGATTCTTTCAATG  
AAGAAGAGGGTGAAAAATCACGACAGCATAATAATTTTCATCATTAACGATGCTACCCCTT  
CTCAATATAATCATTTTCTCCCATCCGATGGCAATCTTCTTTCTCCAGAATTATCTTCTG  
GTGATACGCCAACTCACAATGTTCTCTAGGCACAAAAGACAATGAAATAAATGACGATG  
AGTATTGTAATGATAAGGAAATTAGTTTGAACGCAATAATGTGCTTCTGTATGAACTTT  
CAAAGGAAGAAGATGAAAGATTAAAACTAGAAACGCATGTATCAACCGAAGAAAAGAAAC  
AGGATATCGCTGATCAGGAACTGCAGAAAACCTTATTTACGTCTAGTACAGAACCATCTG  
AGAATAAAATAAGAAATTCTGGTGATGATACCTCCATGTTGTTTCAAGATGACGAAAGTG  
ATCAGAAGGTTCCATGGGAGGAAGATGTGAAGAAAAGATTTTCATAATGAGAACACAAATA  
ATACTCAAGAATCGGCACCGAACACAGATGATCGTGATAAGGGTTATGAAGGAAACGAAG  
CTTTGAAAAAGTCCGAAAAGTTGTACAGCCGCGGACGAGAGGTGCTACTCTGAAGAAAACCT  
CAGAAGATATCTTTCACGGACACGACAAAACAGGTAGTTGAAGGCCAAAATGATTTCACTG  
GGAAAAATATTGAGAATGAAAGCCAGAAATTAATGGGGGAAGGGAATCATAAGTTACCGT  
TGTCTGCCGAAGCTGACATTATAGAACCTGGTAAGGATATTCAAGATCAAGCCGAGGATT  
TGTTTACGCAGAGCAGCGGAGACTTGGGAGAAAGTTTGGCATGGGAATCTACTGATAAAA  
ACGCTGATGTAAACGAGCAAAATCCCAAGAGAAAACATGAAGATTATTTGCTGCTTCTGGAA  
ACGATGAGAAAACCTTCCCTTGGGAAGTTTCTGACGGTGAAGTATCATCGGGAAAAGACGAAA  
ACAGCATGCAGACTAGTACTGAGAAAATAGCTGAGCAAAAAGTTTTCGTTTGTGGAAAACG  
ACGACGACCTTTTGGACGACGACGACAGCTTTTGGCTTCTTCTGAGGAAGAAGACACAG  
TACCTAATACCGATAATACAACGAATTTAACCTCAAAACCAGTTGAAGAAAAAAGGCTT  
CAAGATATAAACCTATTATCGAGGAGGAAGCAGGAATGCGTCAAGAGCAAGTTCATTTTA  
CCAATACTACTGGCATTGTAACACCGCAGCAGTTCCACGGTTTGACTAAAACCTGGACTAG  
GCACCCCCAACCAACAAGTCAGTGTACCAATATAGTTAGTCCTAAGCCTCCTGTGGTAA  
AAGACAATCGTTCAAATTTTAAGATAAATGAGGAGAAAAAGAGTCTGATGCTTACGATT  
TTCCACTGGAAATTATTTTCAGAAAAGTTCCAAGAAAGGGTCACGCAAAAGCCGGTTGCCGTT  
CTACTCAAAGGTTTGGCTCAGGGAATCTTTTATGTTCTTTGGACAAAACCAATTCACAGA  
GCAGGAAAGGCTCTAATAACTCAAATAGGCCACCCGTGATCCCATTGGGGACGACGAGGAGC  
CTCGATCTTCGAGAACTAACTCAGCGATCTCGCAATCTCCCGTTAATTATGCTPTTCCCTA  
ACCCATACAAAATTCAACAACCTACAACAGGCTCCTATCCAATCAGGTATGCCTTTACCAA  
ATACCAACAGATACCTCCCCAGCATTAAGAGTGGAACCACCGTTTCTGCTCCTCCAATTC  
GGCAAGAGGGGTCAGCAATGCCTCCGTGGGAAGTTCAGCGTCTTTTGGTGCTAGACATG  
CAACACAGTACGGCTCAATAACGGGGTACCTCCGGTTTCGCCATATGGTCAAGCTACCA  
TAAATTTGCCAACTGCGAATAAGTATGCCCGTCTCTCTTACAGTTCAGCAGAAAGCAAT  
ATCCATCAGTTGTGCAAAAACCTTGGCGCTTCGGCCGTAAATACCCCCAATTTTGTAAAGA  
CCCATAGAGGCCATACAAGCTCTATTAGTTTCGTATACACCAAAACCAGAATGAACACGCTT  
CTAGATACGCACCCAACCTATCAACAATCTTATCAGGTGCCATATACCTCACAACTGTGTG  
GTCCTGTAGCTGGGAATTCAAGCTATCAAAGCCAAACCCGAAGTTCTTATGCAGTTCCCTA  
TGATGCCCCAGGCTCAAACCTTCAGCAAGTATTCAGCTCACGCGAACATTCAACCGCCTA  
CTGGCATTTTACCTTTAGCCCCCTTACGACCTCTAGACCCCTTACAAGCCGCTACGAACCT  
TGCAACCCCGTGCAAGCAACATAACGGCTGCAAAATTCATACCTCTTGCAAATTTGCCAC  
TTGCTGAAAAACATACTGCCAGAAATTATCACGCATCGAGCTACAAGTAGTGTGCACCAC

32/251

CACGACAGGAAAATAATCCAATTAATAAGACAACGAGGCTTTATTACGCCGTCAATTTTC  
CGATTTTTTCATTGGAGTGTGCAAAACAAGGTCTGTACGCAGTCCCCCTATCCCTGACC  
AATCGCAGTACATGATTTTCATCAAGCATTTGTACAGGAAATAAAGTGACACCAATTGACC  
AGATAATTAACCGAACGATATGCTCAAAAGCTTCCCAGGTCCCTTTGGGTAGTGCCAAAT  
TAAAAAAAAGGATTTAACCATAATGGATGGAAACCACTATTAAATCCATATCTGAAAATG  
AATCATCCACTGATATGACTATATGGCAACTATTGGAAATGAACTAAACGATAAAGTTA  
ACTGGAAAAATATTTCAAACTACTATACAATTCTGACGAACTTTTAATGTACCTATCTC  
AGCCCTTTTCCAAACGGTGACATGATTCCAAATGCATATAGACTGGATATAAATTGTGAGA  
TGAGAGTCCCTGGCGTTCTTACAAACGGGAAATCAGATGAGGCACCTTCGCTTAGCTTTAA  
GCAAGAGGGGATTATGCCATTGCACATTGGTTGGCAGTTTAATGGGTAAAGACAGATGGT  
CTGAAGTCAATTCAGAAATATTTATATGAAGGGTTTACTGCGGGGCCAAACGACCAAAAAG  
AATTGGCACACTTTCTGCTCCTTATCTTTCAAGTATTTGTTGGTAACCTCCAAAATGGCCA  
TAAAAAGTTTCTACACTAATAATGAGACCAGTCAATGGGCATCCGAAAACCTGGAAGAGTA  
TCGTTGACAGCTGTCTGATTAATATCCAGAAAATAATGAAGATCCACTACTTATACCAC  
CTGTTGTCTCTGAATTTTTTGATAGAGTTCCGGTATATTTCTCACCAAAAGGGCTTGACAG  
CCGCAGCTAGTACATTATTTATTTATTTGGTAACGTACCACTTTCTAATGAGCCAGTAATGG  
CAGATTCAGACGTTATATTTGAAAGTATTGGAAACATGAATACTTTTGAAAGCATTCAT  
GGGATGAAATCTACGAGTATATATTTCTCGTATGACCTTAAATTCAAAGGATTTTCATCTA  
TTTTTGCCCCAGAAGATATACCATGCATCTCTTTTACAAGAACAAAGGTTTGAAACAGCCTGG  
GGACAAAGTATACTGATTACCTCAGTTCTCAGTTTCGAAAACCTGCCTAAGAAAGATATTT  
TAACAATAAACCTCACTCGTGAATTGAGTGAGGTGGCTAGTAGGCTTTCCGAGTCTAATA  
CAGGATGGCTTGCAAAACCAAACTAAGCAGCGTATGGGGTCAATTAGATAAAATCCTTCA  
ATAAATATATTTGGTGGCGATGATATTTGATGCATGAATAAAAAAATGATAAAAAGAAAG  
TTTTTGATGGGTTTACACCGGGATCTTCTGCCAATTCGTCAACTGTGGATCTCACCCAAA  
CATTCACACCTTTTCCAAGCTCAAGTTACTTCGCAAAGCTATGTGGATACTACAGCTCTTT  
TGCATAAATGCCATAATGTACCAAGCCATAGTGTGCTGCATTCAAAGCCTTCCAATGTGT  
CAAAGGGGTTAGTTGAAGCAAACCTACCGTATACGCATAGGATCGGTGATAGTTTTCAGG  
GATCTCTCAGCGCATTCATAATACACAGTTTCGCTGCTGCTGAGCCTCAAATGGCTTCTTT  
TGAGAAGAGTTAGAACAGACCAGCATACAAACGAAAAGGCTTTGAAGAGTCAGCAGATTT  
TAGAGAAAAAGTCTACGGCTTACACTCCACAATTTGGACAGAACCATAGCGTTCCAATGG  
AAAAGTCTAATTCGAATGTGCCATCTTTATTTGCCGACTTCCCTGCTCCACCCAACTTG  
GAACAGTGCCGCTCAATTTATGTGTCTAGTCTGACTTAGTAAGAAGGGAGTCTATCATAT  
CTACCGGATCAGAATTTCTTCTCTCTCCCAAAATTTGGGGTACCTACTAAAGCTAATTCCT  
CGCAGGGATCGCTTATGTACTACCAAGTGTGGAAGCTTTGCCATATCGACCTGTGCTCC  
CGCAAGTTTCATGAGACGGGATACAATGATTTTGGTAACAAACATTCTCAAAAAGTATGC  
CTGAAGATGAATCTCACACATCACATGATAATAGCAATGCTGATCAAAAATACATTAAAAG  
ACTCTGCAGATGTTACAGATGAAACAATGGATATTGAAGGACCTGGCTTCAACGATGTGA  
AGAATCTTCTTCCATATGGAGCCCAACCACGCTTACGCTTACAGTAAATCCTATACAAA  
CTATTAGTGACGATATCCAACCGATTCTTCAAACCTAACGTGGAGGTCCGGGGTACTGATG  
CATCGAAAATGGAAAATTCACCTTCCCTCCATTGAAAATGAAAGAAAGTAGCGAGGAGCAGC  
CAGAAAACATTTCAAAATCAGCATCATCAGCATATTTACCATCAACTGGTGGATTGTAC  
TCGAAAACAGACCGCTAACTCAGGATGAAAACAGTATCTCAGAGACAGTTCAATCCACAT  
ACTTGCCAGCAGGAAGTATTTCAAATGGAAGCTAAACCAATTTCTCAAGTGCAAGATGTTT  
CAAGAAATGTTAATAATAAAGCATCCAACTTGTGGAGCAACATATGGCACCACCAAGC  
CAAAAAGTACTGACGCAACCAAAATGAACCTACTCACCATACGTGCCCTCAATCAACTGCCG  
CTAGTGACAGATGGCGATGAATCAACGATTTCTGAAAACATCGCCTGCTATATATGCAAGAA  
CTCACCAGCACATGCATCCAATCCATCACAATACTTTCTTTGGTCAACCAAGCAATG  
AAACTGCTTCATTTCGAATTTATCTGAATCAACATCCCAGGCACAAAGTAATGGAAATGTTG  
CTTCAGAAAATAGATTCAGCCCAATAAAGAAAGCCGAAGTCGTCGAGAAAGACACTTTTC  
AACCTACTATTAGGAAGGCTTCAACTAACCAATACAGGGCTTTTAAACCGTTGGAATCAG  
ATGCGGATAAATAAATGACGTTATTGAAGATGAATCCGATGACGACAATATGTCTACTG  
ATGAGGCAAAAGAACAGAAAGGAAGAAAAAAGAAATGTGAATATGAAAAAGGAAACAAAAC  
CAAGTAACAAGGACATAGATGACAAGTCTAATGGTTGGTTTGGTTGGTTGAAGAAAGATA  
CTGGCGACAAAAAGTGTATAAGGCCAAGCTAGGTCATAAAAACACACTATACATGATG  
AAAAATTGAAACGTTGGGTGAATAAGGACGCAACCGAAGAGGAAAAACAAAAATTTATG  
AAAGTTCCGGCACCACCCTCTCCATCGTGAACGTAAGATGGCGGCCCAAGACAA

33/251

AGCCACGTTTCAGGCCCATCAATAATTCCTACCTCCAGTACATGCCACATCAGTTATTC  
CGAACAAATCCAATCACTGGTGAGCCTTTGCCGATCAAAACATCCCCTTCTCCTACAGGAC  
CCAATCCAAACAATTCTCCATCACCATCCTCTCCCATATCAAGGATTTCTGGCGTAAACT  
TGACTAGCAAAAAGGCAAACGGTTTGGATGATTTATTGAGTTTGGCAGGAGGACCCAAAC  
CAGCAAGTACGAGAAGGAAGAAGAAAACAGCGAGAGGCTATGTTAATGTAATGGATAACA  
TACAATAA

>YPL085W, 2195 aa (SEQ ID NO 384)

MTPEAKKRKNQKKLKQKQKKAEEKAASHSEEPLELPSTINSSFNDDSVNRTESDIASK  
SDVPPVSSSTNIS PANETQLEIPDTQELHHKLLNDSQHDITADSNDLPDINSIVEHDSVI  
TQTKPAMSQYEETA AHLSSRNPSLDV VAGELHNNNEHTQKIAVSAVEEDSFNEEEGENH  
DSIIIISSLN DATPSQYNHFLPSDGNLLSPELSSGDTPTHNVPLGTDNEINDDEYCNDKE  
ISLNANNVLPDELSKEEDERL KLETHVSTEEKQDIADQETAENLFTSSTEPSENKIRNS  
GDDTSMFLQDDSDQKVPWEEDVKKDFHNENTNNTQESAPNTDDRDKGYEGNEALKKSES  
CTAADERSYSEETSEDI FHGHDKQVVEGQNDFTGKN IENESQKLMGEGNHKLPLSAEADI  
IEPGKDIQDQAE DLFTQSSGDLGEVLPWESTDKNADVTSKSQEKHEDLFAASGNDEKLPW  
EVS DGEVSSGKTENSMQTSTEKIAEQKFSFLENDDDLLDDDDSLASSEEDTVPNTDNT  
TNLT SKPVEEKASRYKPIIEEEAGMRQEQVHFTNTTGIVTPQQPHGLTKTGLGTPNQV  
SVPNIVSPKPPVVDNR SNFKINEEKKSDAYDFLEII SESSKKGHAKPVA VPTQRFGS  
GNSFSSLDKPIQSRKGSNN SNRPVPIPLGTQEPRSSRTNSAISQSPVNYAFPNPYKIQQ  
LQQAPIQSGMPLPNTNIP PALKVETTVSAPPIRARGVSNASVGSSASF GARHATQYGLN  
NGVPPVSPYQATINLPTANKYAPVSP TVQQKQYPSVVQNLGASAVNTPNFVKTHRHTS  
SISSYTPNQNEHASRYAPNYQQSYQVPYTSQPVGPVAGNSSYQSQTRSSYAVPMPQAQT  
SASIQPHANIQPPTGILPLAPLRPLDPLQAATNLQPRASNITAA NSLPLANLPLAENILP  
EII THRATSSVAPPRQENNP IKIDNEALLRRQFP IFHWSAANKVYVAVPPIPDQSQY MIS  
SSIVQEIKVTPIDQIIKPNDMLKSFPGLGSAKLKKDLTKWMETTIKSISENESSTDMT  
IWQLLEMKLN DKVNWKNISKLLYNSDELLMYLSQFPNGDMIPNAYRLDINCQMRVLAFL  
QTGNHDEALRLALSKRDYAIALLVGS LMGKDRWSEVIQKYLEGFTAGPNDQKELAHFLL  
LIFQVFVGN SKMAIKSFYTNNETSQWASENWKSI VAAVLINIPENNEDPLLI PPVLEFL  
IEFGIFLT KKGTLAAASTLFIIGNVPLSN EPMADSDVIFESIGNMNTFESILWDEIY EY  
IFS YDPKFKGFSSILPQKIYHASLLQE QGLNSLGTKYTDYLSSSVRKLPKKDILTINLTR  
ELSEVASRLSESNTGWLAKPKLSSVWGQLDKS FNKYIGGDDIDALNKKNDKKKVF DGFTP  
GSSANSSTVDLTQTFTPFQAQVTSQS YVDTTALLHNAHNVP SHSVLH SKPSNVSKGLVEA  
NL PYTHRIGDSLQGS PQRIHNTQFAAAEPQMASLRRVRTDQHTNEKALKSQQ ILEKKSTA  
YTPQFGQNH SVPM EKSN SNVPSLFADFP APPKLGTVPSNYVSSPDLVRRESII STGSEFL  
PPP KIGVPTKANSSQGS LMYSPSVEALPIDPVVPQVHETGYNDFGNKHSQK SMPEDESH  
SHDN SNADQNTL KDSADVTDETM DIEGPGFNDVKNLLPMEPNHQPTSTVNPIQTI SDDIQ  
PILQTNVEVRGTDASKMENS LPSIENERSSEEQENISKSASSAYLPSTGGLSLENRPLT  
QDENSISETVQSTYLPAGSISMEAKPISQVQDVPRNVN NKASKLVEQHMAPPKPKSTDAT  
KMNYSPYVPQSTAASADGDESTILKTSPAIYARTHQA HASNPSQYFPLVNQANETASFEL  
SESTSQAQSNGNVASENRFSPIKKA EVVEKDTFQPTIRKASTNQYRAFKPLESDADKYND  
VIEDESDDDN MSTDEAKNRKEEKNVMKKE TKPSNKDIDDKSNGWFGWLKKDTGDKKVY  
KAKLGHKNTLYYDEKLKRWV NKDATEEEKQKII ESSAPPPPIV KRKDG GPKTKPRSGPI  
NNSLPPVHATSVIPNNPITGEPLPIKTSPTSPTGPNPNNSPSPSSPISRISGVNLTSSKAN  
GLDDLLSLAGGPKPASTRRKKKTARGYVNVMDNIQ

>YPL190C, 2909 bp, CDS: 501-2909 (SEQ ID NO 387)

TAATCTTCGCTACTTCAAGTTTCAATAATCAATCGACTTCTGTATGGGTAAGCATCTGGT  
GTGATGCAGTTTTCATTATGACACCACAAAATACAAAAGAGACTATTAAATATGTATATAG  
ATCACATTCAAAAAAGAAAACCATTAATAATATCACTCTTTAATATTCCAAATTGAAAC  
GAAAAAGCGCTATTCTTATTCGCTTCC TAACTACCGCCCTAGTTCTGTGCTTG CATTTTTT  
TG TAGAACGATAAAATATGGTATCCCACGTGATTGAGTGTAACCC TGAATTGTTGAAGAG  
AAAATGAAGCGGAAGCAAGCAAAGGACAAAAACAATTCA TTTGATTTTGCCACTTCTAAA  
TGAAGGTCTAATAAAAGCTATCTTGAGCATCTTTATTAGATTCTGCACAGCAACAAGCGA  
TTTTCTTTGGTCAAAATATAATAATTGACTTACGTTTTTCCCGGACTGTCTTTTCATAAT  
ATAATAACCATCTGCAAGCCATGTCAGATGAAAACCATAACAGTGATGTTCAAGATATTC

34/251

CTTCACCTGAACTATCCGTCGATAGTAACCTCTAACGAGAATGAATTGATGAATAACTCAA  
GCGCAGACGATGGAATCGAATTTGACGCCCCAGAGGAAGAAAGAGAAGCCGAAAGGGAGG  
AGGAAAATGAAGAACAACACGAACTGGAAGATGTGAACGATGAAGAGGAGGAAGATAAGG  
AGGAAAAGGAGAGGAAAACGGGGAAGTAATAAACACAGAAGAAGAAGAAGAAGAAGAAC  
ATCAACAAAAAGGCGGAAATGATGATGACGATGATGATAATGAAGAGGAAGAAGAGGAAG  
AAGAGGATGATGACGATGATGATGATGACGACGATGATGATGAAGAAGAAGAAGAAGAAG  
AAGAAGAAGAAGGCAACGACAACAGTTCGGTAGGCTCAGATAGTGCCGCTGAAGACGGTG  
AGGATGAGGAAGACAAAAGGATAAAACCAAAGATAAAGAGGTGCAACTTCGCCCGTGAAA  
CATTTGGAAGAAAGAACAAAAGGACGTAGATGAAGCTATAAAAAAATAACTCGTGAAGAAA  
ATGATAATACTCACTTTTCCAACATAATGGAAGAAATGTTAATTACGATCTTTTACAAAAGC  
AAGTCAAGTACATTATGGACAGTAACATGCTAAATTTGCCTCAGTTTCAACATTTACCTC  
AAGAAGAAAAGATGTCTGCGATTTTAGCAATGTTAAATTCAAATCTGACACAGCTCTTT  
CCGTACCTCCTCATGATAGTACTATCTCAACAACAGCTAGCGCCTCAGCCACAAGCGGCG  
CAAGAAGCAATGATCAAAGAAAACCTCCATTGTGTCAGATGCCCAAAGACGTATGAGATTTT  
CTAGGGCGGATTTATCTAAGCCGATTACCGAAGAAGAACACGACCGTTATGCAGCCTATT  
TGCACGGTGAAAAATAAATCACCGAGATGCACAATATTCTCTCCGAAGTCAAGATTATTCA  
TTGGTAATTTGCCGCTAAAGAACGTTTCTAAGGAGGATTTATTTAGGATTTTCTCTCCAT  
ACGGTCATATCATGCAATCAATATCAAAAATGCCTTTGGATTCAATTCAGTTTGACAACC  
CTCAAAGCGTTAGAGATGCAATTGAATGCGAGTCTCAAGAAATGAACTTTGGCAAAAAGT  
TGATCCTGGAAGTTTCTAGCTCGAATGCTCGTCTCAATTTGATCATGGTGATCACGGTA  
CAAACAGTAGTTCTACTTTTATTTCTTCCGCAAAACGACCATTTCAAACGAATCTGGTG  
ACATGTACAATGACGACAATGGTGTGGCTACAAGAAATCCAGAAGACACACCGTTTCTT  
GCAACATTTTCGTTAAAAGAACCGCAGATCGTACGTATGCCATTGAGGTTTTC AACAGGT  
TTAGGGACGGGACTGGTTTGGAAACTGATATGATTTTCTTGAAACCAAGAATGGAACCTGG  
GAAAGCTTATCAATGATGCCGCATATAATGGGGTGTGGGGCGTTGTTTTAGTTAATAAAA  
CACACAATGTAGATGTTCAAACTTTCTACAAAGGCTCACAAGGTGAAACGAAATTTGATG  
AATATATTAGCATATCCGCTGATGACGCAGTTGCCATTTTAAATAACATCAAAAACAACA  
GAAATAATTCTCGTCTTACTGATTACCGTGCTATGAGCCATCAGCAAAACATATATGGCG  
CTCCTCCTCTTCTGTTCCAAACGGGCCAGCTGTCCGACCTCCTCCTCAAACAACTATT  
ACCAGGGTTACAGTATGCCCTCTCCACAACAACAACAGCAACAGCCATATGGTAAATTATG  
GGATGCCACCACCATCCCATGACCAAGGATATGGTTCTCAACCTCCAATTCCAATGAATC  
AGAGTGACGGTTCGTACCAGACTTCTATTCCACCACCCTCCACAACAACAATCTCTC  
AAGGGTATGGTCTGTTATCAGGCTGGTCCGCCCTCCTCAACCACCTTCTCAAACCTCCAATGG  
ACCAGCAACAACATATTATCTGCCATTCAAACCTTCCACCTAACGTTGTATCGAATTTGC  
TTTCAATGGCCCAACAACAGCAACAACAACCTCATGCTCAGCAGCAATTGGTTGGTTTAA  
TACAATCAATGCAAGGCCAGGCTCCTCAACAACAGCAACAACAGTTGGGTGGATATTCCT  
CTATGAACATCATCTCTCCCCCTCCTATGAGTACCAATTACAATGGTCAAAATATATCTG  
CAAAACCTCTGCCCCACCAATGTACACCAACCTCCGCCACCTCAACAACAACAACAAC  
ACAACAACAGCAACAGCAACAGCAACAGCAACCTGCTGGCAATAATGTTCAAAGTCTAT  
TAGATAGTTTAGCAAAACTACAAAAATAG

&gt;YPL190C, 802 aa (SEQ ID NO 388)

MSDENHNSDVQDIPSELSVDSNSNENELMNNSSADDGIEFDAPEEEREAREEEENEEQH  
ELEDVNDEEEEDKEEKGEENGEVINTEEEEEEEHQKGGNDDDDDDNEEEEEEEEDDDDD  
DDDDDDDEEEEEEEEEEGNDNSSVGSDSAEDGEDEEDKKDKTKDKEVELRRETLEKEQK  
DVDEAIKKITREENDNTHFPTNMENVNYDLLQKQVKYIMDSNMLNLPQFQHLPPQEEKMSA  
ILMLNSNSDTALSVPPHDSTISTTASASISGARSNDQRKPLSDAQRRMRFPADLSK  
PITEEHDRYAAYLHGENKITEMHNIPPKSRLFIGNPLKKNVSKEDLFRIFSPYGHIMQI  
NIKNAFGFIQFDNPQSVRDAIECESQEMNFGKKLILEVSSSNARPQFDHGDHGTNSSSTF  
ISSAKRPFQTESGDMYNDNGAGYKKSRRHTVSCNIFVKRTADRTYAIEVFNRFRDGTGL  
ETDMI FLKPRMELGKLINDAAYNGVWGVVLVNKTHNVDVQTFYKGSQGETKFDEYISISA  
DDAVAIFNNIKNNRNSRPTDYRAMSHQQNIYGAPPLPVPNGPAVGPPPQTNYQGYSM  
PPQQQQQQPYGNYGMPPPSHDQGYGSQPPIPMNQSYGRYQTSIPPPPPQQQIPQGYGRYQ  
AGPPPQPPSQT PMDQQQLLSAIQNLPPNVVSNLLSMAQQQQQQPHAQQQLVGLIQSMQGG  
APQQQQQQLGYSMNSSPPPMSTNYNGQNISAKPSAPPMHQPPPPQQQQQQQQQQQQ  
QQQQPAGNNVQSLDSLAKLQK

35/251

&gt;YPL201C, 1886 bp, CDS: 501-1886 (SEQ ID NO 389)

ATTTTCATCACTTCATTAGTTATAAAAAGGAGTTCCCATTGCAGGAGAAAATAATCATTGT  
TTATTGTCGCTAATTTTCTTTCCAATAACGATAACTGCAGTTTCCATTTCCAGGTCGCCA  
ATTGGTTGGACAACGTTGATGTTACCTTCCTTGTTATGGAACCATCCATCATTTTCTAGT  
TCTTCTTCTGCAATATTGCCTTTTGGGAAGAAGGATCGAAAAGTAGCCATTTGCAGACACG  
TTTTTACTATATTTACTGTATCTTCGATTGCGCGGCTAAAGTTGCCATATTATTATTATA  
TTGCAGCTCAACCCCGCATTTCCGGAGTTTTCTTTTTTTTTATTGTTGGGTAATTTGGAGG  
TCGGCGGCTATTGGTGGGCGGAAATGGTGACACACTTGTAATATATAAGGAGGAAATCC  
TACATGTGTATAAGCGAAATCACAAGGATAATAATGTATTGCTAAACACCCTCAAGAAAG  
AAAATAATCATAACGAAATCATGGGTATACCTATGCAAATATACCAGGATGGGAAGGGGG  
TGCAATTTTACCACACGAGATATCAGAACGTATTTGACGAACGGGCGAGCAAGTATGGCA  
ACTACACGGTGAATAATGATTACCCACAGCTTCCAGATACGATAAAGGAACATATCGACC  
AGCTTACCTTTAGCAATGTCGGAGAGGATGGTGGAGATGTTGGAACTATTCTGAAGAAG  
ACGATGATGGTGACGAAGAAAAGGAACCTGAAGATGTTTTTTCGAAGTAACCGTGGGTGG  
AATTTGTACGGATTAATAACTATTTTACTACCCACGATTTACAAAGTTTCAAAGTTTTTA  
GAAATTTCAATAGCAAGTACTGGATTTTTTATTCTAATCAAGCAGAGGACAAAAAATTAC  
TGCTGTATGACTTTAACGGCCAACATTTGATTTTTTATTAAGCAGCAATTTTACGGGCAGT  
TGAATTTACTGCTATCGGACGCAATAATATGTATGGACTGCAATTTTGGTTATAATTCAA  
ACACCATTCAAATTTTAGTTGGATTTTCAAGATGGAAAGTTGTTAAAGCTAAACTGCGACT  
TGAACGGAAACGTAAACAATCACTTGCTTTTGAAGGATCCTTCAACTTCCTCTCATCAA  
GCCACCTATCTATATTAAATGTCTGGGCAGGTTTGTGGCCACATTTCTGTTGTTTCTTTTA  
GTTTGAAAGATGGGCTGCTAATAACTTCTTTAGATCACCAACAAAGCAATGGAAGTTTTTC  
AAAGTTTCCATACCAACATTGATTTGCCTGTAGATCTACGCACGACCACAAATGTCAAGT  
CCGTTTTTAAATTTCCCTCAGTTTACTTTATACAAAGGAAATGATATGATTTTCCACTGCA  
AGAATCTATTAGGATCGGATGCTTCCACGCTAAACAAGGAAATAAACTTTATGCTTAAAA  
TAGACGAAGACGTTCAAAGATCGACTATCTTCTTAAACGAATCACATTTTACTCGAAA  
CCAACATGAGATATCTGTCCATTCCAACAAGAGACCCCATAGAGAATTCAAATTTCTTCTC  
CACCCGTCTCAGACAGCGAGGTTTATCCAATATTTTACAAGACACAAGAACTTCATGTCC  
ATGCTTCTCAGGAACAGGACGTCAGATAGCAAACAATGGGAAGTATATTTTATAACCGAGC  
AACATCTCTACGGAACAGCGTTATCGGTATACAAGTACTCTATATCTTTCAAACGGTGGC  
TGTTCTGTGGGCTACTCAGACATTAGGGCCAAATACGGTATAAGGAGTGTCAAAGATCTCT  
TTGTTGGTAACTGTCCCTCTGTAAATAGCCAGTCTGACAATTCTTACTGATGACAATA  
ACATTCAAACAATTCTTCTTAAATAA

&gt;YPL201C, 461 aa (SEQ ID NO 390)

MGIPMQIYQDGKGVQFYHTRYQNVFDERASKYGNVTVNNDYPQLPDTIKEHIDQLTFSNV  
GEDGGDVGNYSSEDDDGDEEKELEDVFRSNRGLFVRINNYFTTHDLQSFKSFNFNSKY  
WIFYSNQAEDKKLLLYDFNGQHLIFIKQQFYGQLNLLLSDAIICMDCNFGYNSNTIQILV  
GFQNGKLLKLNCDLNGNVNHLKDPSTSSHQSHLSILNVWAGLLPHFVVSFSLKDGLL  
ITSLDHQQSNGSFQSFHTNIDLPLVLRITTNVKSVLNFPQFTLYKGNMDMIFHCKNLLGSD  
ASTLNKEINFMLKIDEDVQKIDYLLKTNHILLETNMRYLSIPTDPIENSNSPPVSDSE  
VYPIFYKTQELHVHASGTGRQIANNGKYIFITEQHLYGTALSVYKYSISFKRWLFVGYSD  
IRAKYGIRSVKDLFVGNCPSVNSPVLTLTDDNNIQTILLK

>YPR028W, 1176 bp, exon1: 501-551, intron1: 552-684, exon2:  
685-1176 (SEQ ID NO 393)

ACAAACCCTGTCAATCTCCTGAAAAACAAAATTAAGTGCTTGAGAAGACCTTCAGAAGA  
GTTGCATAGATAGGATGGGTGAGCGCAATTACTAGTTACGCAGTAAGTAGGTTATATGGC  
TGCTGGAGGGGCGAGTACTGATTTAATCACAATCCGGATTAAACTTCCTCCTGAAAAAAA  
AAACTACATCAAGTCAAAAGATTTTCATTCACTCTTTGGAAGGCTGTGTGGCATTCTAA  
CCTTTATTTTTTATCACCATTCTCGAATTTTCGTGGTTTCGCTTCTTAGCGCCGTATT  
CTCTCTTCTGTCCACGTCAAAGGGAGTATGCGTAACCCCTTTCAAGGTTGAACGAAAA  
AAAAAAATATGTCCTTCAAATTTTTTTTGATTTAAACTAAAAACATTCCCTTGAAG  
CTTGTTATTCCGAAAGAAAGAATCTAAAATTGCAATTGGTAGTGAACAAATAAACAAA  
GACATAACCGCACTCCAATCATGTCCGAATATGCATCTAGTATTCACTCTCAAATGAAAC  
AATTCGATACCGTATGTAAGATGGTTTTATTGGTTCCATCGTCATCATGGTTCAAACAGC



36/251

CAATGACCCGACACACGTAACCGAAGCAGTTATACTAACAAGAAAGCTAATTTTCACCC  
TCCTTGCTACATTTTTTTCTACAGAAGTACTCTGGTAATAGAATTTTACAGCAATTAGAA  
AATAAACTAATTTGCCTAAATCTTATTTAGTTGCTGGTTTAGGTTTCGCTTATCTCCTT  
TTGATTTTTTATTAACGTCGGAGGTGTAGGTGAAATTCCTTTCCAATTTTGCTGGGTTTGTG  
TTGCCAGCATATTTATCGTTGGTTGCTTTGAAGACACCAACGTCACCGATGACACACAA  
CTCTTGACCTACTGGATTGTCTTTTCATTTTTGAGTGTCATTGAAATCTGGTCCAAGGCA  
ATTCTATATTTGATTCCATTCTACTGGTTTTTGAAAACCGTTTTCTTAATCTACATTGCC  
TTGCCTCAAACCTGGTGGCGCTAGAATGATCTATCAAAGATCGTAGCCCCATTGACCGAC  
AGATATATCCTAAGAGATGTTAGCAAGACAGAAAAGGATGAAATTAGAGCTTCCGTCAT  
GAGGCTTCTAAGGCTACAGGTGCTTCTGTTCATTAA

&gt;YPR028W, 180 aa (SEQ ID NO 394)

MSEYASSIHSQMKQFDTKYSGNRILQQLNKTNLPKSYLVAGLGFAYLLLIFINVGGVGE  
ILSNFAGFVLPAYLSLVALKTPTSTDDTQLLTYWIVFSFLSVIEFWSKAILYLIPFYWFL  
KTVFLIYIALPQTGGARMYQKIVAPLTDRIYLRDVSKTEKDEIRASVNEASKATGASVH

YDR145W, 2120 bp, CDS: 501-2120 (SEQ ID NO 99)

AAGTGATTATCTGAATAATGAAAGATGGTAGGAAATAAGGTATTGAAACA  
GGTTCAAACCTTTAAAAGAAAAC TGCCAAATAAACTTTCTCGATGCGTAG  
CTGAAATTTCAACTTCAAAAAAAAAAAAAACGCGTGTAACTTTCTACGTGC  
AAAACGATGTGTATGAATCCCGTCTTAATTAGTAAATAGGGTCTAGTAAG  
CGTAGCGAGGATGAATTAAATGCATTGTTGAATATGAAGAGCACCTTATG  
GTATATAAATGTACAATCTTGATTGATGACAGCTTTGCAAGTAAACGTAT  
CAAATGAATATCACGATTTTGGCTGTATTACCCGGGCAGTATACGCGGCG  
AATTTTGTTAAAAAATGTGTTAGACTTAAGTCGGAGCAAATGAATAATGG  
GCATATATAGCGCATAGGTTGCTAGTGTAAAGACAGGAGACTGTCCAATA  
GCATTGCAATCATAACCGAATCTTTGCCAGTGTGTGTATAAAATACGACA  
ATGTCTTCCAATCCAGAAAATCTGGTGTAAATGCGAATAATAATACGGG  
CACTGGTAACGCTGATGCGATCACAGGAGCTCAGCAAATATGGTACTGC  
AACCAGAGACAGTTGCAAGAAATGGCCGCTAAGTTTCAAGACATTACTGACT  
GAAGCAAGAAATGTAGGTGAAACTACTCCTAGGGGCAAGGAATTGATGTT  
CCAAGCCGCAAGATCAAACAGGTATATGATGCCCTTACACTGAATAGGA  
GAAGACAACAGGCTGCGCAAGCCTACAATAATACTTCAAATTCAAATTCA  
AGCAATCCAGCTTCTATTCTACTGAAAATGTCCCTAATTCATCACAGCA  
ACAACAACAACAACAACAACAGACAAGAAACAACAGTAACAAATTTAGCA  
ATATGATAAAACAGGTTCTCACCCTGGAAGAGAACCAAGAATATGAAAAG  
CTATGGCAGAATTTCCAAGTCCGTATACGAGTATAAAGGAGAAAGAGAC  
CTACTTGAAACAAAATATTGATAGGTTAGAACAAGAAATAAATAAACAGA  
CGGACGAAGGGCCCCAAGCAGCAGCTACAAGAAAAGAAAATTGAACTGCTT  
AACGATTGGAAGGTGCTAAAAATTGAGTATACCAAGCTGTTCAATAATTA  
TCAAAACAGTAAAAAACATTCTATGTAGAGTGTGCAAGACACAATCCGG  
CTTTACATAAATTTTGCAAGAAAGCACTCAACAGCAACGAGTGCAGCAA  
CAAAGGGTACAACAACAACAACAACAACAGCAGCAGCAGCAACAGCA  
GCAACAGCAACAGCAACAGCAACAGCAACGCCAGGGTCAAACCAAAGAA  
AGATTTCTAGTTCTAATTCTACTGAAATACCCTCTGTAACCGGCCCTGAT  
GCACTGAAATCGCAGCAGCAGCAGAGAATAACAATACTGCCACCAATAA  
TCCCAGGGGCAATGTTAACTTCACTTACAGACTGAACAATCGAAAGCTAAGG  
TAACCAATGTAAATGCAACGGCATCTATGTTGAATAATATAAGTTGAGC  
AAATCGGCAATATTCAAACAACAGAGCCTGCCATACCCATATCGGAAAA  
TATATCTACCAAAACACCAGCACCGGTAGCTTATAGATCCAACAGACCTA  
CAATAACTGGAGGTTCTGCTATGAATGCCAGTGCTTTGAATACACCAGCA  
ACAATAAATTACCACCCTATGAAATGGATACTCAGAGAGTTATGTCAA  
GCGTAAATTAAGAGAGTTAGTGAAGACTGTCGGAATTGATGAGGGTGACG  
GTGAAACTGTCATTGACGGTGATGTTGAGGAATTACTATTGGATCTTGCC  
GACGATTTTGTTACTAATGTTACAGCTTTTTCTTGTTAGATTGGCAAAACA  
CAGAAAATCGGACAATTTGGAGGCAAGAGACATTCAATTACATTTGGAGA

37/251

GAAATTGGAATATTAGGATTCTCTGGTTATTCCGCAGACGAAATAAGAAGT  
ACAAGAAAATGGAATCCCTCTCAAATTATAACCAGAAATTGCAGAGTAT  
CACATCAGATAAGGTAGCAGCTGCAAAAAACAATGGAAACAATGTTGCAA  
GCTTGAATACAAAAAATAA

YDR145W, 539 aa (SEQ ID NO 100)

MSSNPENSGVNNANNNTGTGNADAITGAQONMVLQPRQLQEMAAKFRTLTLT  
EARNVGETTPRGKELMFQAAKIKQVYDALTLNRRRQQAQAYNNTSNSNS  
SNPASIFTEVPNSSQQQQQQQQQTRNNSNKFNNMIKQVLTPEENQEYK  
LWQNFQVRHTSIKEKETYLKQONIDRLEQEINKQTDEGPKQQLQEKKIELL  
NDWKVLKIEYTKLFNNYQNSKKTFFVECARHNPALHKFLQESTQQQRVQQ  
QRVQQ  
ALKSQQQQQNTITATNNPRGNVNTSQTEQSKAKVTNVNATASMLNNISS  
KSAIFKQTEPAIPISENISTKTPAPVAYRSNRPTITGGSAMNASALNTPA  
TTKLPPYEMDTQVRMSKRKLRELVKTVGIDEGDGETVIDGDVEELLLDLA  
DDFVTNVTAFCRLAKHRKSDNLEARDIQLHLERNWNIRIPGYSADERS  
TRKWNPSQNYNQKLQSITSDKVAAAKNNGNNVASLNTKK

YDR216W, 4472bp, CDS: 501-4472 (SEQ ID NO 109)

CAAAGAACAACGCCTTAAAAATAGGAAAACGTTTTTCGCTACAGGTGTTGT  
TATTATTGTTGTTGTGCTGTTGTTTATTGTGCTATACTTGTGGTATTTAT  
TCTGGACTTCCGATCGGAAATTTTCTTCCCTTGAAGACCTTTTGAAGACA  
ACAGTTATATATCATTTGATCTGAATTTCTCAGGCTATTTTCAAATTTCCA  
TACCTCCTTATTCCAACATTTGCTCGACTACTATAGAAAAGCCTTATTCT  
TTTATCTTTGAAAGAAAGAAAAGGTGTCATAGCAAAGTTTATTTGTACT  
CTGTTTTGATATACTCCCTCTTATTCTGTTGGAAGTATAAGATTGATTTGC  
ATAAATTAACCAATCATTTTGCTACTTTCCCGGTTCTCCCTTTATTATAA  
ACACTTCAGAAAAATATTCTGCTACTATTCTTACTTTACTATAAGAATT  
TTGTTTTCCAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAA  
ATGGCTAACGTAGAAAAACCAAACGATTGTTTCAAGGCTTTCCCGTTGTTGA  
CTTGAATTCGTGCTTTTCTAACGGCTTCAATAATGAGAAACAAGAAATAG  
AAATGGAAACGGATGATTCACCGATTTTATTAATGTCATCATCAGCTTCC  
AGAGAAAACCTCAAACACTTTCTCTGTGATACAGAGGACGCCAGATGGAAA  
GATCATTACCACAAATAATAATGAAGTCCAAGATTAACAAGCAACTGG  
ACAAGTTGCCCCGAAAATTTAAGGCTTAATGGTAGAACCCCAAGTGGGAAA  
CTAAGGTCAATTTGTTTGCAGGTTTGTACGAGAGCGTTTCGCAAGACAAGA  
GCACTTGAAAAGACATTACAGATCGCATACAAATGAAAACCTTATCCCT  
GTGGCCTCTGCAACAGATGCTTTACTAGGAGGGACTTACTGATCAGGCAT  
GCTCAAAAAATCCATAGTGGTAATTTAGGGGAAACGATTTCCCATACCAA  
GAAAGTGTGAGAACTATAACTAAAGCTCGGAAAAATTTCTGCATCCTCAG  
TCAAGTTTCAAACCTCAACCTATGGTACTCCAGATAATGGTAATTTTGTG  
AATCGCACTACTGCCAATACAAGAAGAAAAGCAAGCCCTGAAGCTAATGT  
TAAACGTAAGTACTTGAAAAAAGTACGCGCAGGGCTTCATTTAGCGCAC  
AATCAGCATCCAGCTATGCTTTGCCCGACCAATCTTCGCTAGAACAACAT  
CCAAAGGATCGTGTTAAATTTTCTACGCCTGAATTAGTTCCACTTGACTT  
GAAGAATCCTGAACCTTGACTCTTCGTTTGACCTGAATATGAATCTAGATT  
TAAACCTAAATCTAGATTCCAATTTCAATATAGCATTAACCGTTCTGAT  
TCTTCTGGATCAACAATGAATTTGGATTATAAATTGCCCGAATCAGCAAA  
TAACTACACATATTCTTCCGGCTCACCAACCCGCGCATATGTCGGCGCTA  
ACACGAATTCTAAGAACGCTTCATTTAATGACGCAGACTTATTGTGCTCG  
TCGTACTGGATAAAAGCCTATAATGATCATTTGTTTTAGTATCTGAAAG  
TGATGAAACTTCTCCAATGAAGTCTGAATTAAACGACACTAAATTAATCG  
TCCCAGATTTTAAATCGACTATACATCATTTGAAGGATTCAAGGTCCTCC  
TCTTGGACTGTTGCTATAGATAATAATAGCAATAACAATAAGGTATCAGA  
CAACCAACCTGATTTGCTCGATTTTCAAGAACTGCTGGATAATGATACTT  
TAGGTAATGATTTGTTAGAGACCACTGCCGTTTTAAAGAATTTGAAGT

38/251

TTACATGATGATAGCGTAAGTGCTACCGCCACGTCAAATGAGATTGACCT  
TTCCCATTTGAACCTATCAAACCTCTCCAATTTCTCCTCATAAGTTAATTT  
ATAAGAATAAAGAGGGGACCAATGACGATATGTTGATTTCTTTCGGACTC  
GATCATCCTTCCAATCGCGAAGATGATCTGGATAAGCTATGTAATATGAC  
CAGAGATGTTCAAGCCATATTCAAGTCAATATTTGAAAGGAGAAGAGTCTA  
AACGATCCCTGGAAGACTTTTTATCAACGTCAAACAGGAAAGAAAAGCCA  
GATAGCGGCAACTATACTTTTTATGGGTTAGATTGTTTAAACGTTATCGAA  
AATATCAAGAGCTCTGCCGGCCTCCACTGTGAACAACAATCAGCCATCGC  
ATTCCATAGAATCAAAGCTATTTAATGAACCAATGAGAAATATGTGCATT  
AAAGTGCTTAGATACTATGAAAAGTTCAGTCATGATAGTAGTGAGAGTGT  
CATGGACTCTAATCCAAACTTGCTGTCCAAAGAATTGTTAATGCCAGCTG  
TGAGTGAATTGAACGAATATTTAGATCTTTTCAAGAATAATTTCTTCCC  
CATTTCCCTATTATTCACCCAAGCTTGCTTGATTGGATTGGATAGCTT  
GCAACGATATACTAATGAGGATGGGTATGATGACGCTGAAAACGCGCAGT  
TGTTTGATCGATTAAAGTCAAGGGACAGATAAAGAATATGATTACGAGCAC  
TATCAAATCTTGTCATTTCGAAAATCGTTTGTTTACCCTTATTTATGGC  
CACATTTGGTTCTTTGCATAAGTTCGGTTACAAATCTCAAACAATAGAAT  
TGTATGAGATGAGTAGAAGAATTCTACATTCTTTTTTGGAGACTAAAAGA  
AGGTGTGCGAGTACAACAGTAAATGACAGTTATCAGAACATTTGGTTGAT  
GCAATCCCTAATATTGAGCTTCATGTTGCTCTAGTTGCTGATTATTTGG  
AGAAAATTGACTCCTCTTTGATGAAAAGGCAATTGTCCGCATTATGTTCA  
ACGATCAGATCAAACCTGTTTACCGACAATTTCTGCAAATCTGAGAAGAG  
TATCAATAATAACAATGAACCTTTAACATTTGGTTCTCCTCTTCAATACA  
TCATTTTTTGAGTCAAAAATTAGATGCACCTTAATGGCTTATGATTTTTGT  
CAGTTCTTGAAATGTTTCTTCCATATTAAATTCGATTTGTCTATAAAGGA  
AAAAGATGTTGAAACCATTTATATTCCCGACAATGAGTCAAAATGGGCCA  
GTGAATCGATAATATGTAATGGGCATGTTGTGCAAAAGCAAAATTTTTAT  
GATTTTAGAACTTTTATTACAGTTTCACGTATGGACACTTACACTCAAT  
ACCAGAATTTTAGGGTCATCTATGATTTATTATGAATACGATTTAAGAA  
AAGGAACCAAATCACATGTGTTTTTGGATCGAATCGATACGAAAAGGCTA  
GAGAGGATCTTGACACTTCTTCTATGGCAATGATAATATGGCAGCAAC  
CAATAAAAAATTGCGATCTTAATTGATGACACCATAATTTTGAAAAAT  
ATTTAATGTCAATGAGATTCAACAGATTGATCGCTCGTTTACTGAG  
AAGGTTAGAAAAGGACAAATAGCAAAGATATATGATTCCTTTTTGAACTC  
TGTGAGGTTGAATTTTTTGAAGAATTATTCAGTTGAAGTATTGTGTGAAT  
TTTTAGTAGCGTTGAACTTTTCAATCCGTAATATTTGCTCTTTATACGTA  
GAAGAAGAAAGTGATTGCTCCCAAAGAATGAATCTCCAGAGCTGCCAAG  
GATCCACCTGAATAATCAAGCGCTTCTGTCTTCAATTTACAAGGCTATT  
ACTATTGCTTCATCCTAATTATCAAATTTTTATTGGATTTTGAAGCAACT  
CCAAATTTTAAGTTACTGAGAATTTTTATTGAGTTGAGAAGCCTTGCGAA  
TTCTATTTTACTTCCCACACTTTCAAGATTGTATCCGCAAGAGTTTTCTG  
GATTTCCCTGATGTTGTATTTACGCAACAATTTATAAATAAAGATAATGGT  
ATGCTTGTCCCTGGTTTATCCGCAAATGAACACCATAATGGTGCAAGTGC  
AGCTGTTAAGACTAAGTTAGCCAAAAGATCAATGTTGAAGGGCTTGCAA  
TGTTTTATTAATGAAATCCTAGTTAACTCTTTTAAAGATACTCTTTTTTG  
AATATGGAGGATCCTATTTCGAAATGAATTTTCTTTGATAATGGGGACAG  
GGCAGTGACAGACTTGCCCTCGTTTCAGCACATTTCTATCGGATACCGGCC  
TAGAAGGTATTAACCTTCAGCGGCTTAAATGATTTCGCATCAAACATGTTTCT  
ACTTTGAATCTTTTACGTTACGGGGAAAATCATTTCATCAAACATAAAAA  
TGGTGGAAGGGGCAAGGATTTGCCGAAAAGTACCAATTATCTCTGAAAT  
ATGTTACTATTGCCAAGTTATTTTTTACCAATGTTAAAGAAAACATACATT  
CATTGTACATGTTAGATAAGATGGCAAGTGATTTCACACTTTGGAAAA  
TCATCTAAAGGGAAACAGTTGA

39/251

YDR216W, 1323 aa (SEQ ID NO 110)  
MANVEKPNDCSGFPVVDLNSCFNNGFNNEKQEIEMETDDSPILLMSSSAS  
RENSNTFSVIQRTPDGKIITNNNMNSKINKQLDKLPENLRNLNGRTPSGK  
LRSFVCEVCTRAFARQEHKLRHYRSHNTNEKPYPCGLCNRCFTRRDLLIRH  
AQKIHSGNLGETISHTKKVSRTITKARKNSASSVKFQTPTYGTPDNGNFL  
NRTTANTRRKASPEANVKKYLKKLTRRASFSQAQSASSYALPDQSSLEQH  
PKDRVKFSTPELVPLDLKNPELDSSFDLNMNLDLNLNLDNLFNIALNRS  
SSGSTMNLDYKLPESANNYTYSSGSPTRAYVGANTNSKNASFNADLLSS  
SYWIKAYNDHLFSVSEDETSPMNSELNDTKLIVPDFKSTIHHLKDSRSS  
SWTVAIDNNSNNKVSNDQPDFVDFQELLDNDTLGNDLLETTAVLKEFEL  
LHDDSVSATATSNEIDLHLNLSNPSIPHKLIYKNKEGTNDMDLISFGL  
DHPSNREDDLDKLCNMTRDVQAI FSQYLKGEESKRSLEDFLSTSNRKEKP  
DSGNYTFYGLDCLTLKISRALPASTVNNNQPSHSIESKLFNEPMRNMCI  
KVLRYYEKFSHDSSSEVMDSNPNNLSKELLMPAVSELNEYLDLDFKNFLP  
HFPIIHPSLLDLDLDSLQRYTNEGDYDDAENAQLFDRLSQGTDKKEYDYEH  
YQILSISKIVCLPLFMATFGSLHKFGYKSQTIELYEMSRRLHSFLETKR  
RCRSTTVNDSYQNIWLMQSLILSFMFALVADYLEKIDSSLMKRQLSALCS  
TIRSNCLPTISANSEKSINNNEPLTFGSPLQYIIFESKIRCTLMAYDFC  
QFLKCFHFIKFDLSIKEKDVETIYIPDNESKWASESIICNGHVQKQNFY  
DFRNFFYYSFTYGHLSIPEFLGSSMIYYEYDLRKGTKSHVFLDRIDTKRL  
ERSLDTSSYGNDNMAATNKNIAILIDDTIILKNNLMSMRFIKQIDRSFTE  
KVRKGQIAKIYDSFLNSVRLNFLKNYSVEVLCEFLVALNFSIRNISSLYV  
EEESDCSQRMNSPELPRIHLNNQALS VFNLQGYCYCFILIIKFLLDFEAT  
PNFKLLRIFIELRSLANSILLPTLSRLYPQEFSGFPDVVFTQQFINKDNG  
MLVPGLSANEHNGASAAVKTAKKINVEGLAMFINEILVNSFNDSFSL  
NMEDPIRNEFSFDNGDRAVTDLPRSAHFLSDTGLEGINFSGLNDSHQTVS  
TLNLLRYGENHSSKHKNGGKGQGF AEKYQLSLKYVTIAKLFFTNVKENYI  
HCHMLDKMASDFHTLENHLKGNS

YBR112C, 3401 bp, CDS: 501-3401 (SEQ ID NO 51)  
GGGTGCCGTATCGGCTCTAATTATTTTATCTCTCTATTTTCTTTCTTTTC  
TCTGCGCTACTCCTTTCTCGATCGTTGCTACTCCCGTCGCTAGCCACTGG  
TCTCCCGCGTACTGTACTCCATCTTTTTTTGGCGTTTTTCCCCTATCCAA  
CTCGAACAAGGTTTGTAAATTTATTTTATTTTCTTTTCTTCGGTCGG  
TCGTTCTTTTCCCTTCCGATTATCAAAGCAAAGCGCATTTTTTCTTTG  
TCTTTTTGTTTTTTGTTCCTGTTCTCTGTTTTTTTACAAACCACGTCAG  
GAGTTCAATTGAGAGAACTAGAATCAACAAAGCCAAATACGACAACGTCA  
CTAGTCTTTGAACCAGAGGCGTATTCCCGTTACCTCTTTTCCCATATTTT  
TGTTTTTCTTTTTTCACTGCTATAAGCCTTTAGACTAGTACTACAAC TACA  
ACAGCAACAACAACAACAAAACACGACTGGAAAAAAAAAATTAGGAAAA  
ATGAATCCGGGCGGTGAACAAACAATAATGGAACAACCCGCTCAACAGCA  
ACAACAACAGCAACAACAACAGCAGCAACAGCAACAGCAGGCAGCAGTTC  
CTCAGCAGCCACTCGACCCATTAAACAAATCAACTGCCGAAACTTGGCTC  
TCCATTGCTTCTTTGGCAGAAACCCTTGGTGATGGCGACAGGGCCGCAAT  
GGCATATGACGCCACTTTACAGTTCAATCCCTCATCTGCAAAGGCTTTAA  
CATCTTTGGCTCACTTGTACCGTTCCAGAGACATGTTCCAAAGAGCTGCA  
GAATTATATGAAAGAGCACTTTTGGTAAATCCCGAATATCAGATGTGTG  
GGCTACTTTAGGTCAATTGTTATCTGATGCTGGATGATCTGCAAAGAGCTT  
ACAATGCCATATCAACAGGCTCTTACCACCTCAGTAATCCCAACGTACCG  
AAATTATGGCATGGAATCGGCATTCTTTATGACAGATATGGTTTCGCTCGA  
CTATGCCGAAGAAGCTTTTGCCAAAGTTTGGAAATGGACCCTCATTTTG  
AAAAGGCAAACGAAATTTACTTCAGACTAGGTATTATTTATAAACATCAG  
GGTAAATGGTCTCAAGCTTTGGAATGCTTCAGATACATTCTCCCTCAACC  
TCCTGCTCCCTTGCAGGAGTGGGACATATGGTTTCAGTTGGGTAGTGTTC  
TGGAGAGTATGGGAGAGTGGCAAGGTGCGAAGGAAGCCTACGAGCATGTC  
TTGGCTCAAAATCAACATCATGCCAAAGTATTACAACAATTAGGTGTCT

40/251

TTACGGTATGAGTAAACGCTACAATTTTATGACCCCTCAAAGGCCATTGGGATT  
ATCTTCTTAAAGTCGTTAGAAGCAGATCCCTCCGATGCCACTACATGGTAC  
CATCTCGGTAGAGTGCATATGATTAGAACAGATTATACTGCCGCATATGA  
TGCTTTTCCAACAAGCTGTTAATAGAGATTCAAGAAACCCCTATCTTTTGGT  
GCTCAATCGGTGTTTTATATTACCAAATTTCTCAATACAGAGACGCCTTA  
GACGCGTACACAAGAGCCATAAGATTAAATCCTTATATTAGTGAAGTTTG  
GTACGATCTAGGTACTCTTTACGAAACTTGTAACAACCAATTATCTGACG  
CCCTTGATGCGTATAAGCAAGCTGCAAGACTGGACGTAAATAATGTTTCA  
ATAAGAGAAAAGATTAGAAGCTTTAAACAAAGCAGTTAGAAAACCCAGGCAA  
TATAAACAAATCGAACGGTGCGCCAACGAATGCCTCTCCTGCCCCACCTC  
CTGTGATTTTACAACCTACCTTACAACCTAATGATCAAGGAAATCCTTTG  
AACACTAGAATTTTACGCCAATCTGCCAATGCTACTGCTTCAATGGTACA  
ACAACAGCATCCTGCTCAACAAACGCCTATTAACCTTCTGCAACAATGT  
ACAGTAATGGAGCTTCCCTCAATTACAAGCTCAAGCTCAAGCTCAAGCT  
CAAGCACAAGCTCAAGCACAAGCACAAGCTCAAGCACAAGCACAAGCACA  
AGCGCAAGCACAAGCACAAGCACAAGCGCAAGCACAAGCACAAGCACAAG  
CACAAGCACATGCACAAGCGCAAGCACAAGCACAAGCACAAGCACAAGCA  
CAAGCACAAGCGCGCAGGCACAACAACAACAACAACAACAACAACAACA  
ACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACA  
AGCAGCAGCAATTACAGCCCCCTACCAAGACAACAGCTGCAGCAAAAGGGA  
GTTTCTGTGCAAATGTTAAATCCTCAACAAGGGCAACCATATATCACACA  
GCCAACAGTCATACAAGCTCACCAACTGCAACCATTTTCTACACAAGCTA  
TGGAACATCCGCAAAGCTCTCAACTGCCACCTCAACAGCAACAACCTACAA  
TCTGTTCAACATCCACAACAACCTTCAAGGCCAGCCTCAAGCCCAAGCTCC  
CCAACCTTTAATCCAGCATAACGTGGAACAGAACGTTTTTACCTCAAAGA  
GATACATGGAAGGTGCAATCCACACTTTAGTAGATGCCGCCGTATCCAGT  
AGCACCCACACAGAGAATAACACAAAGTCTCCTCGTCAACCAACCCATGC  
CATTTCCAACGCAAAAGTCTCCCGCAACGGAATAACGAACGCTGAACCAAGG  
TAAAGAAGCAAAAAGTTGAAGTCTCCAAATTCAAAACATCAACAAATTAGTA  
AATACTGCTACTTCCATTGTAAGAAAATGCAAAATCTGAGGTAGCAACCA  
ATCGCCAGCAGTAGTGGAGTCTAATACCAATAATACTTCAACAAGAAGAAA  
AACCCTGTAAAAGCAAACTCAATACCTTCAGTAATTGGCGCACAGGAACCT  
CCACAGGAAGCTAGTCCTGCTGAAGAAGCTACCAAGCAGCTTCTGTTTC  
TCCTTCTACAAAACCGCTTAATACGGAACCAGAGTCATCTAGTGTCCAAC  
CAACTGTATCATCAGAAAGTTCAACAACAAAAGCAAATGACCAAAGCACT  
GCTGAGACCATAGAACTTTCTACTGCTACTGTTTCTGCAAGCAAGCCC  
TGTAGAAGACGAAGTAAGACAGCATTTCTAAAGAGGAAAACGGCACAACCTG  
AAGCATCTGCACCTTCTACTGAAGAGGCGGAGCCAGCAGCTTCCAGAGAT  
GCTGAAAAACAACAAGATGAAACCGCTGCTACAACGATAACTGTAATCAA  
ACCTACTTTGGAAACAATGGAAACAGTGAAAGAGGAGGCCAAAATGCGTG  
AGGAAGAGCAAACATCTCAAGAAAAATCCCCACAGGAGAACACACTTCCA  
AGAGAAAATGTTAGTAAGGCAAGTGGAAGAAGATGAAAACCTACGACGACTA

YBR112C, 966 aa (SEQ ID NO 52)

[illegible]

41/251

QAQAQAQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQLQPLPRQQLQQKG  
VSVQMLNPQQGQPYITQPTVIQAHQLQPFSTQAMEHPQSSQLPPQQQQLQ  
SVQHPPQLQGQPQAQAPQPLIQHNVEQNVLPQKRYMEGAIHTLVDAAVSS  
STHTENNTKSPRQPTHAIPTQAPATGITNAEPQVKKQKLNSPNSNINKLV  
NTATSIENAKSEVSNQSPAVVESNTNNTSQEEKPVKANSIPSVIGAQEP  
PQEASPAEEATKAASVSPSTKPLNTEPESSSVQPTVSSESSTTKANDQST  
AETIELSTATVPAEASPVEDEVQRHSKEENGTEASAPSTEEAEPAASRD  
AEKQQDETAATTTITVIKPTLETMETVKEEAKMREEEQTSQEKSPQENTLP  
RENVVRQVEEDENYDD

YMR043W, 1361 bp, CDS: 501-1361 (SEQ ID NO 305)  
AAGCTGTGCCAAACAAGGTCATCTCCAAATACTTACCAAAAAGCTAGGGC  
GTACTGTACTGGAATCTCTGCTTTTTTCTTTACCTTACTTCAATTTGCCCT  
TGCTGCTTTTTTACGTGTGTTTTGGCGTTTCTGCTTTTCTTTTTTATTA  
CTCGTTGTTGATAAATCATTTTTCTAAGTATTATACATACTATATCATCGCA  
TACCAATACGGTTTCCATTCTCACCACCTTTTTTCTGGAAAAATACATAG  
CCTAACAAAGCAATTTTTATTTTACGTTTGTAAATTCATTATACTGATAATA  
TTTTTGAATTTTTTTTTTTTTTTTTGATACATTTTTTTTAATCGCTGTTTTGT  
CTGTTTTTTTTTCGATTTCAGTTATAGGGAAAAAACGGGAAAGGAAAGAGAA  
AAAAAATTAGTGCAGAGCAATAAGAAGCGAAAAATCAAAAAAAGTTTTG  
GATCTGCAAGACTTGTCTGTCACGCAACAATATTATAGCCACCCAGCAAAA  
ATGTCAGACATCGAAGAAGGTACGCCACTAATAATGGGCAACAGAAAGGA  
GAGAAGAAAGATAGAAATTAAGTTCATCGAGAATAAAACAAGGCGCCATG  
TGACATTTTTCCAAAAGGAAGCACGGTATCATGAAAAAGGCGTTTGAGCTT  
TCTGTTCTAACGGGGACCCAGGTCCGTGTGCTAGTCGTTTCAGAAACAGG  
TTTGGTATATACTTTTCAGCACGCCGAAGTTTGAACCTATAGTCACGCAGC  
AGGAAGGTAGAAACCTGATCCAGGCCGTGTCTTAACGCCCCCTGATGATGAG  
GAAGAAGACGAGGAGGAAGACGGTGATGATGATGATGATGATGATGACGATGA  
TGGTAATGATATGCAACGCCAGCAACCACAACAACAGCAACCGCAACAAC  
AGCAACAAGTATTGAATGCACACGCAAAATAGCTTAGGCCATCTAAATCAA  
GATCAGGTACCGGCAGGCGCGCTGAAACAAGAGGTGAAGTCACAATTGCT  
AGGCGGTGCCAATCCTAATCAAACTCAATGATTCAACAGCAGCAACATC  
ACACGCAGAAATTCACAACCACAACAGCAACAGCAACAACAACCACAGCAG  
CAAATGTCACAGCAACAATGTCACAGCATCCTCGACCACAGCAAGGAAT  
ACCACATCCGCAACAATCGCAGCCACAGCAACAGCAACAACAACAACAAC  
AATGCAACAGCAGCAACAGCAGCAACAACAACAACCCCTCACCGGCATT  
CATCAGCCTCACCAACAGGCTTTTGCCAACGCTGCCTCCCCCTATCTGAA  
TGCTGAACAGAATGCTGCCTACCAACAATACTTTCAAGAACCGCAACAAG  
GCCAATACTAA

YMR043W, 286 aa (SEQ ID NO 306)  
MSDIEEGTPTNNGQKERRKIEIKFIENKTRRHVTFSKRKHGIMKKAFEL  
SVLTGTQVLLLVVSETGLVYTFSTPKFEPVITQQEGRNLIQACLNAPDDE  
EEDEEEDGDDDDDDDDGNDMQRQQPQQQQPQQQQQVLNAHANSLGHLNQ  
DQVPAGALKQEVKSQLLGGANPNQNSMIQQQQHHTQNSQPQQQQQQQPQQ  
QMSQQQMSQHPRPQQGIPHPPQSQPQQQQQQQQQLQQQQQQQQQPLTGI  
HQPHQQAFANAASPYLNAEQNAAYQQYFQEPQQGQY

YPL089C, 2531 bp, CDS: 501-2531 (SEQ ID NO 385)  
TTCCACGTTTCGCAAAAATACTTCCACGGTGACGAAGTCTGTCTCAGTCG  
TATATTAAATGCAGAAATCGTCTTATCATTATTGGGCTCTCTTAACGGCG  
CAGCATCACCGGGTGATGAATGCCAAGCCGAGAAAGAAAGAAAAAATT  
TACTTCAGATTTCTGATAAAAATAAAACGGAAGAGATGAAAGCTAATAAT  
AGAAACAGCTCGATCTTCTCTGAACAATAATAATTAAAGGACAGACAAA  
AAGAAACGTAAGAAAGAAGCGAGCCTGTTCTAAAGTGTTCAACGACTGAT  
TCAATTAGAACTGCCTACTCCTGATAGCCAACCTCACTTTTGACTCGTTA

42/251

AAGTAATTGAAAGCTGGCAAGCAGAATTATTCTTTTTTTTTTCAAGGTT  
TCTATCACGTTGTGAGGTTAATATCCCCCGAGCAAACAGGCTGAAGCGT  
GAAAAAACTTAAATATTAAAGTGTGCGAAAACCTATACTATAGATACAAC  
ATGGGTAGACGGAAGATTGAAATCCAGAGAAATTTCTGATGACAGAAATAG  
GGCTGTCACGTTTATAAAACGTAAAGCTGGCCTTTTTAAGAAGGCCCATG  
AACTATCCGTTCTTTGTCAAGTAGACATAGCCGTCATTATACTGGGGTCC  
AATAACACGTTCTATGAGTTTTCTCTGTGGATACGAATGATTTAATCTA  
TCACTACCAAATGACAAAACCTTGCTTCACGAAGTGAAAGATCCTTCCG  
ATTATGGAGACTTTCACAAAAGTGCATCCGTTAACATAAATCAAGACCTA  
CTCAGGTCGTCATGTCAAATAAGCCTTCGAAATCAAATGTTAAAGGAAT  
GAACCAGTCAGAAAATGATGATGATGAGAACAATGATGAGGACGACGATG  
ATCATGGCAATTTTGAGAGGAATTCAAATATGCATTTCGAATAAAAAAGCC  
TCTGATAAAAAATATACCGAGTGCACACATGAAGTTGTTATCCCCGACCGC  
ACTCATTTCAAAGATGGATGGTAGTGAGCAAAAATAAACGTCATCCTGAGA  
ACGCGCTGCCGCCTTTACAACATTTGAAAAGATTGAAACCGGATCCTTTG  
CAAATAAGTAGAATCCGCAACAGCAACAGCAGCAAAATATATCGAGACC  
ATACCATAGTAGCATGTACAATCTTAACCAGCCTTCATCCAGTTCATCTT  
CTCCTTCCACGATGGATTTTCCAAAATTACCAAGCTTTCAAACTCTTCC  
TTTAATGGTCGTCCTCCACCCATTTCCATTTACCGAACAAAGTTCAGTAA  
GCCATTTACAAATGCATCCTCAAGGACCCCTAAACAGGAGCACAAAATTA  
ACAATAGTGGCAGCAATAATAATGACAACAGCAACTACACTCAGTCACCA  
TCTAATTTCTTTGGAAGACTCTATTTCAGCAGACTGTCAAAGCAAGAAGGAA  
ATTGTCCGCCAGACCGGTACTTCGTGTGAGAATTCGGAACAACAATTTCA  
GCAGTAATTCCGCTATTCCAAGTGAACCCCTCCTCTGCCTCCTCCACATCG  
GCCAACGGCAATAGTATGGGCTCTTCGCAGATAATGAAAGAAAACAAAAC  
AAGTAGGTCCTAGCAAAATTTCTCCACTATCCGCATCTGCCCTCAGGCCCT  
TAACCTCTCCAAAAGGTAATAATGGCAGAATGGTAATAAAATTGCCAAAT  
GCAATGCGCCTAACGGTTCTAACAATGGTAATGGCAGTAACAATAACAA  
TCACCCTTATCCTTTTCGGAAGTGGGTCTTCACCTCTTTTTTCTGCAACAC  
AGCATACATTTGCCACTCCCTTGCAACCATCGAATATTCCTGGCGGACCT  
TTCCAACAAAATACATCTTTTTTTAGCTCAAAGACAAACCCAGCAATACCA  
ACAAATGTCTTTCAAAAAACAGAGCCAAACAGTACCATTAACACAACAT  
TAACCGGACGCCCCCTTCAACTTTTTTCGGCCCTGAAACCAGCAATGGC  
CCTCCAATGGTTCACTGCCATCGAAGTTCGTACATGATTTGATGAGTAA  
TTCTCCAAATGTTTCTTCTATATCGATGTTTCCAGACTGGTCAATGGGAC  
CCAACAGTGCCAAGCCGGGAAACACAACAATCCTGGTACTTTCCCTCCC  
GTACAGACGGCCGTAAACAACGGCAACTCCAGCAATATCAGCAGCACTAA  
CAACACTAACAACAACAACAATAACAACAACAACAGCAGCAACAACA  
ACAGCAACAACGGCAACGACAATAACAGTAACAATAGCAATAACAGTTAC  
TATAGTAATAATGAAGATGCACCCGTAAATGGAGCTGCTATTTTCAAGAACA  
TACTACCGATGGTGACTCGAACAATCAGTCCAACCTCAAGTACATATGATG  
CTGCTGCCACCGCATATAATGGAATACCGGGCTGACTCCATACATAAAT  
ACTGCTCAAACACCACTAGGCACATAAATCTTTAATTTTTTCGACTGATAT  
TTCAGGAGAAAAAATTCAAGCAAAATATAA

YPL089C, 676 aa (SEQ ID NO 386)

MGRRKIEIQRI SDDNRNAVTFIKRKAGLFKKAHELSVLCQVDIAVIIIGS  
NNTFYEFSSVDNDLIYHYQNDKNLLHEVKDPSDYGDFHKSASVNIQDL  
LRSSMSNPKSKSNVKGMNQSENDDDENDEDDDDHGNFERN SNMHSNKKK  
SDKNIPSAHMKLLSPTALISKMDGSEQNKRHPENALPPLQHLKRLKPDPL  
QISRTPQQQQQNI SRPYHSSMYNLNQPSSSSSSPSTMDFPKLPSFQNSS  
FNGRPPPI SISPNKFSKPF TNASSRTPKQEHKINNSGNNNDNSNYTQSP  
SNSLED SIQQT VKARRKLSARPVLRVRI PNNNFSSNSAIPSEPSSASSTS  
ANGNSMGSSQIMKENKTSRSSKISPLSASASGPLTLQKGNNGRMVIKLPN  
ANAPNGSNNNGNSNNNNHPYPFGSGSSPLFSATQPYIATPLQPSNIPGGP  
FQQNTSFLAQRQTQYQYQMSFKQSQT VPLTTTLTGRPPSTFSGPETSNG

43/251

PPTGSLPSKFVHDLMSNPVSSISMFPDWSMGPNsAKPGNTNPGTFPP  
VQTAVNNGNSSNISSTNNTNNNNNNNNNNSSNNNSNNGNDNNSNNSNNSY  
YSNNEDAPVNGAAI SEHTTDGDSNNQSNSSYDAAATAYNGNTGLTPYIN  
TAQTPLGTFKFFNFSTDISGEKNSSKI

YOR372C, 2165 bp, CDS: 501-2165 (SEQ ID NO 371)

AAAATCGTGGTTACTTTTCATATTCCTTAAACACTTTACCACGTGTACTGT  
GCGCGTTTCGAGCGTAGCTTTTCGTGGTGAATTTATTGTAAGATTCTCCAGC  
TGGCTCGATAGTTCTGCCTCCTGCGTATCCATATCCATTTCCGGTATGCTT  
TTACTATTCAACCTAGTCGGCAATTTTTTCACCTGAATATTGTTGAACAC  
TTCTGGCATCCTAGATACTCATCTGTATTTATTTCATTATCTGTTGTGCAT  
CGTTAATAGCATTCCAGTAAACAAGTTTAGGTCACTACCCGCATAAGCCT  
TTTGGCGTTTGGCGTAACCTCCTCGCGAAAAGAAACGGGACGCAAAAA  
AAAAACAACAAAACAAGAACAACAAAACAACAAATAGGACAGAGCCTTAA  
GGAGCTGCAAGGATCTTCTGAATATTTGGCATCGGCATTGTGGGTGGAAA  
AAGTGTCCAAATTGGAATAAATTGGTCAGAATAGAGCATTGATTCCAAC  
ATGGACAGAGATATAAGCTACCAGCAAAATTATACCTCAACTGGGGCAAC  
TGCAACTTCTCAAGACAGCCCTCTACGGACAATAATGCAGATACAAATT  
TTTTGAAGGTAATGTCAGAATTCAAATATAATTTTAACAGTCCGTTACCT  
ACAACGACTCAATTCCCCACGCCCTATTCTTCTAATCAGTATCAACAGAC  
TCAAGATCATTGTTGCCAATACAGACGCTCACAACAGTTCGAGCAACGAAT  
CGTCGTTGGTAGAGAACAGTATATTACCGCATCATCAGCAGATACAACAG  
CAACAACAACAACAACAACAACAACAACAACAGCAAGCTCTAGGTTTC  
ACTTGTACCTCCTGCTGTACAAGGACAGATACAAGTGAGACTTTGGACG  
ATATCAACGTTCAACCTTCTTCTGTTTTGCAGTTCGGCAACTCTTTACCC  
AGCGAATTTTTGGTTGCATCCCCAGAGCAATTCAAAGAATTTTTGTTGGA  
CTCTCCGTCACCAATTTCAATTTCTTTTCAAAAACCTCCGGCAAAGACAC  
CACTTCGATTTGTAACAGATTCTAACGGTGCTCAGCAAAGCACCACAGAG  
AACCCAGGTCAACAACAGAATGTTTTTAGCAATGTCGATTTGAACAATCT  
TTTGAAGAGTAATGGAAAAACACCTCATCTTCATGCACCGGCGCATTTT  
CACGCATCCTCTGAGTAAGATTGACATGAATCTCATGTTCATCAACCG  
CTGCCGACTCTCCATCAAAAAGGTTCTCCTCCCTGTCGTTGACACCATA  
TGGAAGAAAAATTCTGAATGACGTCGGTACACCTTATGCAAAAGCATTGA  
TATCGTCTAACAGCGCGTTAGTGGATTTTCAGAAGGCAAGAAAGGATATT  
ACCACTAATGCAACATCCATAGGGCTGGAAAATGCCAACAACATCTTACA  
GAGAACGCCGCTAAGATCTAACAATAAAAAATTATTTATTAACCCCCC  
AGGATACCATCAATAGCACTAGCACACTAACTAAGGACAACGAAAATAAA  
CAGGACATATACGGCTCTTCACCGACTACCATCCAATTAAATTCATCAAT  
AACTAAATCTATCTCAAATTGGATAACTCTAGAATTCCTTGTTAGCTT  
CGAGATCAGATAACATTCTGGATTCCAATGTGGATGACCAATTGTTTGAT  
TTGGGGTTGACAAGATTACCTTTATCACCAACACCAAATTGTAATCTTT  
GCATAGTACAACCACAGGTACATCTGCCTTACAAATTCCTGAGCTACCCA  
AGATGGGGTCTTTTAGAAGTGATACGGGAATCAATCCAATTTCAAGTTCA  
AACACAGTTTCTTTTAAGAGCAAATCAGGCAATAATAATTCAAAGGGTCG  
AATCAAAAAAATGGGAAGAAACCTTCAAATTTCAAATTATTGTGGCAA  
ATATTGATCAATTTAACCAGGATACATCATCGTCATCTTTATCATCATCA  
TTGAATGCAAGTTCGAGTGCAGGGAATTCAAATTCAAACGTAACAAAGAA  
AAGAGCAAGTAAGTCAAAAGATCACAGTCTTTACTTTCTGATTCCGGAT  
CGAAATCACAAGCAAGGAAAAGCTGTAATCTAAATCTAATGGAAATTTA  
TTCAATTCACAGTAA

YOR372C, 554 aa (SEQ ID NO 372)

MDRDISYQQNYTSTGATATSSRQPSTDNNADTNFLKVMSEFKYNFNSPLP  
TTTQFPPTYSSNQYQQTQDHFANTDAHNSSNESSLVENSILPHHQIQQ  
QQQQQQQQQQQALGSLVPPAVTRTDTSETLDDINVQPSSVLQFGNSLP  
SEFLVASPEQFKEFLLDSPSTNFFHKTPAKTPLRFVTDNNGAQOSTTE



44/251

NPGQQQNVFSNVDLNNLLKSNGKTPSSSCTGAFSRTPLSKIDMNLMFNQ  
LPTSPSKRFSSLSLTPYGRKILNDVGTPYAKALISSNSALVDFQKARKDI  
TTNATSIGLENANNILQRTPLRSNNKKLFIKTPQDTINSTSTLT KD NENK  
QDIYGSSPTTIQLNSSITKSISKLDNSRIPLLASRSDNILD SNVDDQLFD  
LGLTRLPLSPTPNCNSLHSTTTGT SALQIPELPMG SFRSDTGINPISS  
NTVSFKSKSGNNSKGRICKNGKKPSKFQIIVANIDQFNQDTSSSSLSS  
LNASSAGNSNSNVTKKRASKLR SQSLLSDSGSKSQARKSCNSKSNGL  
FNSQ

YDR224C, 896 bp, CDS: 501-896 (SEQ ID NO 111)  
TTTCTTCAACAACGACGAGTTAACTATTGTGCTCTTTTTTTGAGCCACCA  
AATACACTCCATTCCAATAGCTTCGCACAGTGAGGCGAAAAATTTTGGAAC  
AGCGCTAATGAATTATTTGTGAGCTCGGCGAGTTCAAATTTGAAGAAAAC  
GCGGTGGGTTCGTTAACTATGGTTAGACGCTCAATGTGCGCCGAAAGGGA  
AGGCTGTTCTCACTTTTTCGCGCGTTGCACCTTTCTTCCGCGAAAAAT  
GAGAACGATGGATTTAAAATCAAGAGAATTGGCCTTAGTAGTGGCAAATA  
CTACCTTGGTTGGTTATCTTGTAAACGATTGGTAAGAAAGGGGCATCTCTG  
TTTTCTTGATGTATATAAACAACATGATTTGATCATCTCAGATGGTCAGA  
TTTATTAAAGACGTTTCTCTTTCCGCATTTTCGATTATTGTTATATTAAA  
TTTATCCTATATAGACAAGTCAAACCACAAATAAACCATACACACATACA  
ATGTCTGCTAAAGCCGAAAAGAAACCAGCCTCCAAAGCCCCAGCTGAAAA  
GAAACCAGCCGCTAAAAGACTTCCACTTCCACTGATGGTAAGAAGAGAA  
GCAAGGCTAGAAAGGAAACATACTCTTCTTACATTTACAAAGTTTGAAG  
CAAACCTCACCTTGACACTGGTATTTCCCAAAGTCCATGTCTATCTTGAA  
CTCTTTTCGTTAACGATATCTTTGAAAGAATCGCTACTGAAGCTTCTAAAT  
TGGCTGCGTATAACAAGAAGTCTACTATCTCTGCTAGAGAAATTCAAACC  
GCTGTTAGATTGATCTTACCAGGTGAATTGGCTAAGCATGCTGTCTCTGA  
AGGTACTAGAGCTGTTACCAAGTACTCTTCTCTACTCAAGCATAA

YDR224C, 131 aa (SEQ ID NO 112)  
MSAKAEKKPASKAPAEKKPAAKKTSTSTDGKKRSKARKETYSSYIYKVLK  
QTHPDTGISQKSMSILNSFVNDIFERIEATEASKLAAYNKKSTISAREIQT  
AVRLILPGELAKHAVSEGTRAVTKYSSSTQA

YLR294C, 830 bp, CDS: 501-830 (SEQ ID NO 281)  
ACCAACCAACTTCTTCCTTTGTCTCAATATCAAAGAAAAAAAAAAAAAC  
CCACTGCTCAGATGTTATAAGGAAGGGGTGTTAACTTATATACAGGTTCA  
TCTACCAGTCACCAGTCCATACAAACTTGAACCGTCTGCGTACCAGTCCT  
AATCAAAATGTTCCCTATCGCTTCCAGAAGAATACTGCTCAATGCTTCAG  
TTCTGCCATTGAGACTGTGCAATAGAAATTTCACTACCACAAGAATATCC  
TACAACGTCAACAAGATTTGTATTTGAGGGAAC TAAAAGACACCAAAC  
GGCTCCAAGTACCTTGCAAGATGCTGAAGGTAATGTTAAGCCTTGGAACC  
CACCACAAAAACCAAATCTACCAGAATTGGAAC TCAAGGCCCAGAGGCT  
TTAAAGGCTTACACCGAGCAAAATGTAGAAACTGCTCATGTTGCTAAAGA  
GTCTGAAGAGGGTGAGTCAGAGCCAATTGAAGAGGATTGGCTAGTTTGG  
ATGATGCTGAGGAAACCAAAGAAAGTCATTGAACTTTTCATAGCATCCTC  
CTTGTCGAAGAAAAACAAACAGAACCAAGCTGAACAAGATCATTATT  
TTTGGCTTTCTTCTCTCATCTTTTATATTTCGAATCCAGTACAATAAAG  
AAAAAGCAAAATACACTACGCACTCTTTGTAATCAGCCACACAAATGCA  
GAATTTATTTTTTAAACAAAAAATACAATTGTACATAGACACGCTTTTAT  
CTTCTCTATTACTACTATTCTTTTATTTCAATAACTATTACTTTCTAAGT  
ATGACCTACGCTTCTTTGGTAAATAAATAA

YLR294C, 109aa (SEQ ID NO 282)  
MMLRKPKKVIELFIASSLSKKKQTEPQAEQDHYFWLSSSHLFIFESSTIK  
KKQNTLRLTLCNQPHKMQLNFFKQKIQLYIDTSLSFLLLFFYFNYYFLS

45/251

MTYASLVNK

YMR256C, 683 bp, CDS: 501-683 (SEQ ID NO 319)  
CTTTTCAGTTATTTACCTTTCCTTCTCTCACGTGTAATATTTGTGTGTC  
ATACACACCGCTAAAAACCTTTGCATCAACTTATACCCTACATTTCTATA  
GACGCTATTTGGAAACAAGATGTAACCCTTTTTTTCTTTTAGTTTTGAGA  
TTTGTACTCGTAAAGAGTACGTTTATTTATTTATTCAAATTTTATTTCTC  
ATACCATGTAAATATAAGCGCATATAATCACTACGATCTTAGTACAGCTA  
GAATTGCTGACGCTTACAATTGCTTTTATTGTTTGATTATATGCACGTATA  
CATATAGTGTCTAGCAAAAAAAAAAAGGCAGTACTTGATTGGCTACGCC  
GCGCATCGTCCGAGAAATCCGGCCTGGTAGGGGCAGGTTTGAAAAGGCGG  
ATAGAAATAAAAGATGATATTATTTATTCATCCCATGAATAGTAGAACTC  
GATATAAGATTCTAAACCAACAAGTACAGAAAGCAAAACAATAATAAATA  
ATGGCTAATAAAAGTTATTCAACTACAGAAATCTTCCAATCTTCCACTAA  
ACCTCTATGGTGGAGACATCCAAGGTCAGCTTTATACCTGTATCCATTTT  
ATGCTATTTTTGCGGTAGCCGTCGTTACACCACCTCTATACATTCCAAAT  
GCTATTAGAGGTATCAAAGCCAAGAAGGCATAG

YMR256C, 60 aa (SEQ ID NO 320)  
MANKVIQLQKIFQSSTKPLWWRHPRSAlylypfyaifavavvtpllyipn  
AIRGIKAKKA

YLR327C, 761 bp, CDS: 501-761 (SEQ ID NO 287)  
TTCTCATACGTATGTTTTTTTAGATTATGCACCTTCTTTGCCACAGTAAA  
TGTTGGCGGGGAAGATGTTGAGCTAGCGCCGTGCACAGTGAAGAGACGGA  
GGCGATTGTGGGGTTTCATCGGATTGTGCGGGAAGAAGGCCCTACACCGTG  
TTGAGCCACCCCCCCTCAGGAGTAAATTTACACAAACAGTGGTGGTGCC  
TATGGTGGTATACGAGATAGTGATAGAAGCTGCTGGATTGGGGTAGAAAT  
TTTGTAGGCGTTTATGGATATGGTATGGATATGGTATGGCTTGAGGTAGG  
TAATCCAGACACCACCTGGAATATATATAAGGAGAGAGTTCTGGCAGGTA  
GATTTGTACTCCTCTCTACCACCTTCTTCTACTCCTTTTATTATGTAATG  
TTTATTATAAGCACAGCAAAAACGTTAAATAAACTTAATAAGATTTCATT  
ATAACATAACATTAAAGCACACAAATTTCTAACACAAACACAAATTCAAAC  
ATGACCAGAACTAGCAAATGGACAGTCCACGAAGCAAAGTCTAACCCAAA  
GTATTTTACCCATAACGGCAACTTTGGGGAGTCTCCCAACCACGTCAAGA  
GAGGAGGCTATGGGAAAGGCAATTGGGGCAAGCCTGGCGATGAGATTAAT  
GACTTAATCGATTCTGGCGAAATTAAGACAGTCTTCAACAAGACCAGAAG  
GGGCTCTAACTCCCAAAACAATGAAAGAAGGCTTTCTGATTTGCAACAAT  
ACCACATCTAA

YLR327C, 86 aa (SEQ ID NO 288)  
MTRTSKWTVHEAKSNPKYFTHNGNFGESPNHVKRGYgkgnwgkpgdein  
DLIDSGEIKTVFNKTRRGSNSQNNERRLSDLQQYHI

YHR161C, 2414 bp, CDS: 501-2414 (SEQ ID NO 211)  
GTCATGCGCGCAATAGGAAAGCGCACGAAACAAATGAGTAATTCGTAGGA  
AACAAATGCAGCCCCAGGGTCAGCAACTGACGTGACTCAGCCTGGCTTTT  
GTAGAAAAAGATGACGCCCTGGCAGAGAGGTGGGGGAATTGAGGGGTCTT  
CGCTACCCACCTTAAAGTATGGAAGAATATGATGAAGAATATGATGATAAC  
TCTTGGAAGCGAGCGGGGTTCCATCACTTTTTACGGATTGGTAACACA  
GGGGCCTCAGTTGATACCTTGGTATTCAGGCTTCCAGCGTTGGTGAGTTT  
AGTTAGCGGTATGGTATGCACATGGTGTGATGCTTGGTGGTAATCATTC  
GTTAGGTGAATTGAGCAGTAGCGATATTAGATATATTTAGTATTTTATAG  
CGTCTTTTTTGGTGGGGGAGGAAGGACAAAACCTGTCTCGTAAATATAAAG  
GGACTGTTTCGATATCGCAGATACTAGAGTATAAATTTTCGATTGAGGCGAG  
ATGACAACATATTTCAAGTTGGTAAAAGGTGCTACCAAGATCAAGTCAGC

46/251

CCCGCCCAAACAGAAGTATCTGGATCCGATACTGTTGGGGACCAGCAATG  
 AAGAGGATTTCTATGAGATCGTGAAGGGTTTGGATTTCCCGAATTAATGAC  
 ACGGCGTGGACTATTTGTGTATAAATCGCTGTTGGTGGTTTCAATTTGATGAT  
 AAGGGAGGGTTCCAAAGATGTTGCATTGCGGTACTACTCTAGGAACCTGG  
 AGTTTTTTTACATTTGAAAACATACGTGGCTCCAATGGCAGTGCGTCTGGA  
 GACATGAGGGCACTTGATAGATACGATAATTATCTGAAGGTGAGATGCAG  
 GGAGTTTGGTAAAAATCAAAAAGGACTATGTGAGAGACGGCTATCGAACAC  
 TGAAGCTGAACAGTGGCAATTACGGAAGCTCCAGAAACAAGCAACACTCT  
 ATCAATATAAGCAGTAGATCATGTGGAGTCCCAGAGGTACAAATACAAGC  
 CCTGATTAAAAACAAGTATACACAATATGATTTGAGTAACGAATTGATCA  
 TATTTGGTTTCAAGCTGCTTATTCAAGACCTGCTAGCGCTATATAATGCT  
 CTAACGAAGGTATCATAACTCTGCTGGAGTCTTTTTTTCGAACATCTCA  
 TCATAATGCAGAGAGAACTCTAGACCTGTACAAGACGTTTGTGATTTGA  
 CCGAGCACGTTGTCAGGTACTTGAAGAGCGGGAAGACTGCGGGCTTGAAA  
 ATACCCGTCATCAAGCATATCACTACCAAACGGTCAGATCGCTAGAAGA  
 ACATCTGATAGAGGATGATAAGACGCACAACACTTTTGTGCCCGTTGACA  
 GTTCTCAAGGAAGTGTGGGGCCGTAGTAGCCAAATCTACTGCACAGGAA  
 AGGTTGGAGCAAATCCGGGAACAAAAAGGATACTAGAGGCACAAATTGAA  
 AAACGAACAAGTAGCGATTTCCCTGCTCTAACTACTGTACGCGCGCTC  
 AATCTTACAACCCGTTTGGAACAGACTCTTCTATGCATACTAACATTTCCA  
 ATGGCTGTGGCTAATCAAACGCAACAGATCGCAAATAACCCATTTGTATC  
 TCAAACTCAGCCACAGGTGATGAATACACCAACCGCTCATACAGAGCCCG  
 CAAATTTAAACGTTCCTGAATATGCAGCGGTCCAACACACAGTGAACCTC  
 AACCTGTACAAGATGCTGGCGTAAGTGCCCAACAAACGGGGTACTATTTC  
 GATTAACAACCATTTAACACCCACATTTACAGGTGCAGGGTTTGGAGGAT  
 ACTCCGTTTTCACAGGATACAACCTGCCGCTTCTAATCAACAAGTCTCTCAT  
 TCACAAACTGGTTCTAACAACCCGTTTCGATTCACAAACGCCGCGACGAT  
 CGCAACAGGGAATCCTGCACACGAAAATGTCTTAAATAACCCATTTTCAC  
 GACCAAACCTTTGATGAACAAAATACCAATATGCCGCTACAACAACAGATA  
 ATAAGTAACCCCTTTTCAAAACCAAACGTACAATCAACAACAATTTCAACA  
 AAAAAAATGCCCTTTGAGCTCGATCAATAGCGTTATGACAACCCCTACTA  
 GCATGCAGGGATCGATGAATATTCCTCAGCGTTTGTATAAATGGAATTT  
 CAGGCTCACTACACTCAGAATCATCTCCAACAACAGCAACAACAGCAACA  
 GCAACAACAGCAACAGCAACAACAGCAACCACAACAGGGTTATTATGTGC  
 CTGCAACTGCAGGAGCCAACCCGTGTACAAATATAACTGGGACAGTTCAA  
 CCTCAAAATTTCCCTTTCTATCCACAACAGCAACCACAACCGGAACAGTC  
 TCAAACACAGCAACCAGTTTATAGGAAACCAATATGCTAACAACCTCAATT  
 TAATTGATATGTAA

YHR161C, 637 aa (SEQ ID NO 212)

MTTYFKLVKGATKIKSAPPKQKYLDPIILLGTSNEEDFYEIVKGLDSRIND  
 TAWTIVYKSLLVHLMIREGSKDVALRYYSRNLEFFDIENIRGSNGSASG  
 DMRALDRYDNYLKVRCREFGKIKKDYVRDGYRTLKLNSGNYGSSRNKQHS  
 INIALDHVESLEVQIQALIKNKYTQYDLSNELIIFGFKLLIQDLLALYNA  
 LNEGIITLLESFFELSHHNAERTLDLYKTFVDLTHEVVRYLKSGKTAGLK  
 IPVIKHITTKLVRSLIEHLIEDDKTHNTFVPVDSSQGSAGAVVAKSTAQE  
 RLEQIREQKRILEAQLKNEQVAISPALTTVTAAQSYNPFPGTDSMHTNIP  
 MAVANQTQQIANNPFVSQTQPQVMNTPTAHTEPANLNVPEYAAVQHTVNF  
 NPVQDAGVSAQQTGYYSINNHLTPFTGAGFGGYSVSQDTTAAASNQOVSH  
 SQTGSNNPFALHNAATIATGNPAHENVLNNPFSRPNFDEQNTNMPLQQQI  
 ISNPFQNTYNQQQFQQQKMLSSINSVMTTPTSMQGSMNIPQRFDKMEF  
 QAHYTQNHLLQQQQQQQQQQQQQQQQQQQQQYYPATAGANPVTNITGTVQ  
 PQNFPPYQQQPQPEQSQTQQPVLGNQYANNLNLIDM

YLR206W, 2342 bp, CDS: 501-2342 (SEQ ID NO 277)

TACACCCCTGACTTTCCCATCATACGACGATGCTCTAGTAAACTTGCACC

47/251

CGCACCTGTTAGATAAACAAGTGCGCCCAAGATCACAATACCGAAGGGGC  
GATATCACCCTCAGTATTCTACAGTCGAGCATAGCGTAGTCTGGCAGTA  
TCCCGCACGATCCATTGTATTGTTTGTCCAAACCGCATTATGTGTAAAC  
GATTAATCGTATATACATGGCCTACAAGAAATTACCCTGCGGCGAAGGGT  
GAAAAAAAAGTAGTGGAAGCTAAAGAAAGAAGAGTTTAGTTACGGACCC  
TTTCAAGGATTGACACACTCCCAATATTTTGCTACATTATTGACCTTTGT  
TGAAGGAGGCGTTTCGTTTATTTAATTATTTTGTCTGTTTTGCCTACAAC  
TGCGAATACGCTCACATTCTAGTTTGACCTTCACAAATCTTATCATCTT  
CTTTTGTATTATTTTGACACACCCCTATTAAGTGTATTTGTTTTGTAAGTA  
ATGTCTAAGCAGTTTGTTCGTTCTGCAAAGAACATGATGAAGGGCTACTC  
ATCCACACAAGTGCTTGTGAGAGATGCCACGGCGAACGACTCGAGGACTC  
CATCGATAGACACTCTCGACGATTTGGCACAGAGATCTTACGATTCCGGTG  
GACTTCTTCGAGATTATGGATATGTTAGACAAGAGGCTGAACGATAAGGG  
CAAATACTGGAGACACGTTGCCAAATCGCTGACCGTTTTGGACTATCTTG  
TTCGTTTTCGGGAGTGAGAACTGTGTGCTATGGTGCAGAGAGAATTTTAC  
GTAATTAAGACATTAAGGGAATTCAGACACGAAAATGAGTCCGGATTGTA  
CGAGGGACAAATTATCAGAGTAAAGGCTAAAGAACTCGTCTCTTTGTTGA  
ATGATGAAGAAAGGCTACGCGAAGAGAGGTCTATGAATACAAGAAACAGA  
AGGGCGAACAGAGCTGCTAGGCCAAGGCCAAGAAGACAAAGAACAAGGAG  
CAACCCACACGATTCTTCTCCCTCTTACCAGGACGATTTGGAAAAGGCC  
TAGAGGAGAGCAGAATTACTGCTCAAGAAGATGAACAACGTAGAAGAGAA  
CTGGCCAGTACGACGATGAAGATCCTGACTTCCAAGCTGCCTTACAAC  
AAGTAAAGAAGAAGAGGAGTTGAAGCAATTGCAGGAACACAGAGATTAC  
AGAAGCAACAACAGTCTCTGTCTCAATTTCAAGCTCCTTTACAACAACAA  
CAACCACAACAACACAGCGTACTACGACATTTTCGGTAATCCAATCTC  
CCAAGATGAATACTTACAGTATCAGTACCAACAGGACCAGGAACAAGCAA  
TGGCTCAGCAAAGATGGCTGGACCAGCAGCAAGAACAACAGCAGCTTGCT  
GAACAACAATATTTTCAGCAGCAACAACAAGCTGCGGCCCGCGCTTCTGC  
CTTGCAACAGCAACAACAACAGCCGCTAATATGCAACAACAACAACAGC  
CCGCTGATTTTCAACAACCTTTGCCTACAGGTTCTAATAATCCGTTTTTCC  
ATGGATAATCTTGAAAGACAAAAGCAGGAGCAACAGCATGCTCAATTGCA  
AAGACAACAAGAAGAAGCTAGACAACAACAAGAACAATTGAAGCTACAAC  
AATTGCAAAGACAACAACAAGAGGAAGCTCAATTACACCAGAAGAGGCAA  
GAAGAAGCCCAATTACAACAGCAGCAAGCCCAATTGCTACAACAGCAAGC  
CCAGTTCCAGCAACAACAACCTTGAAGCAAACAAGGACTGGGAACCAGT  
CTATATCGGATAAATACAGCGACTTGAATACCTTGTAGCAACTGGTACA  
GGGATAGATACTTTTGGTAACACTGGAGAGGCACGTATTCTGCACAACA  
TACAAAGACAGGCACATTTATAAATCTCAGGGTACAGGCTACAACAGG  
TTACTAATGAACCCAAGAACAACCTTTCTTAAGCAACCAATACACTGGT  
TTACCAAGCACAAATATCGTGCCACGCAACAGGGTACGGGTTTGGTAA  
CCAACCTCAAAGTCTCTCTACTAATCTCTCTCAGCAAAATCCTACTGGTA  
TAAGCTACTCTCAGCCACAACAGCAACAACAGCCACAGCAACAACCGCAA  
TACATGCAAAATTTCCAACAACAGCAACCTCAATACGCCCAAACTTCCA  
ACAACAACCACAATACACTCAAATTATCAACAACAACCACAATACATTC  
AACCTCATCAACAACAACAGCAGCAGCAGCAGCAGCAACAGCAGCAACAG  
GGATATACTCCTGACCAAGGTGTAAGCTTAATTGATCTTTGA

YLR206W, 613 aa (SEQ ID NO 278)

MSKQFVRS AKNMKGYSSTQVLVRDATANDSRTPSIDTLDDLAQRSYDSV  
DFFEIMDMLDKRLNDKGKYWRHVAKSLTVLDYLVRFGSENCVLWCENFY  
VIKTLREFRHNESGFDEGQIIIRVKAKELVSLNDEERLREERSMNTNRN  
RANRAARPRPRRQRTSRNPHDSSPSYQDDLEKALEESRITAQEDEQRRRE  
LAQYDDEDPDFQAALQLSKEEEEELKQLQELQRLQKQQQSLSQFQAPLQQQ  
QPQQQPAYYDIFGNPISQDEYLQYQYQQDQEQAMAQQRWLDQQQEQQQLA  
EQYFQQQQQAAAAASALQQQQTAAANMQQQQQPADFQQPLPTGSNNPFS  
MDNLERQKQEQQHAQLQRQQEEARQQQEQLKLQQLRQQQEEAQLHQKRQ

48/251

EEAQLQQQQAQLLQQQAQFQQQQPLKQTRTGNQSIDKYSIDLNTLLATGT  
GIDTFGNTGEARIPAQHTKTGTFINSQGTGYKQVTNEPKNNPFLSNQYTG  
LPSTNIVPTQTGYGFGNQPSPTNSPQQNPTGISYSQPQQQQPQQQPQ  
YMQNFQQQQPQYAQNFQQQPQYTQNYQQQPQYIQPHQQQQQQQQQQQQ  
GYTPDQGVSLIDL

YDR342C, 2213 bp, CDS: 501-2213 (SEQ ID NO 119)  
CACTTCTCAGAAATGCATGCAGTGGCAGCACGCTAATTCGAAAAATTCT  
CCAGAAAGGCAACGCAAAATTTTTTTTCCAGGGAATAAACTTTTTATGAC  
CCACTACTTCTCGTAGGAACAATTTCCGGCCCCCTGCGTGTTCTTCTGAGG  
TTCATCTTTTACATTTGCTTCTGCTGGATAATTTTCAGAGGCAACAAGGA  
AAAATTAGATGGCAAAAAGTCGTCTTTCAAGGAAAAATCCCCACCATCTT  
TCGAGATCCCCGTGTAACCTTATTGGCAACTGAAAGAATGAAAAGGAGGAAA  
ATACAAAATATATACTAGAACTGAAAAAAAAAAAAAGTATAAATAGAGACGATA  
TATGCCAATACTTCACAATGTTTCAATCTATTCTTCATTTGCAGCTATTG  
TAAAATAATAAAAACATCAAGAACAAACAAGCTCAACTTGTCTTTTCTAAG  
AACAAAGAATAAAACACAAAAACAAAAAGTTTTTTTAATTTTAATCAAAAA  
ATGTCACAAGACGCTGCTATTGCAGAGCAAACTCCTGTGGAGCATCTCTC  
TGCTGTTGACTCAGCCTCCCACTCGGTTTTATCTACACCATCAAAACAAGG  
CTGAAAGAGATGAAATAAAAAGCTTATGGTGAAGGTGAAGAGCACGAACCT  
GTCGTTGAAATTCCAAAGAGACCAGCTTCTGCCTATGTCAGTGTCTCTAT  
TATGTGTATCATGATCGCCTTTGGTGGTTTTCGTTTTTCGGTTGGGATACTG  
GTACCATTTCTGGTTTCATCAATCAAACCGATTTTCATCAGAAGATTTGGT  
ATGAAGCATAAAGATGGTACTAATTATTTGTCTAAGGTTAGAAGTGGTTT  
GATTGTCTCCATTTTCAACATTGGTTGTGCCATTGGTGGTATTATTCTTT  
CCAAATTGGGTGATATGTACGGTCTGAAGGTGGGTTTGATTGTGCTGTT  
GTCATCTACATCATCGGTATTATTATTCAAATTGCATCTATCAACAAATG  
GTACCAATATTTTCATCGGTAGAAATTATTTCCGGTTTGGGTGTTGGTGGTA  
TTGCCGTTTTATCTCCTATGTTGATTTCTGAAGTATCCCCAAAGCATTTA  
AGGGGTACTTTAGTCTCTTGTCTACCAATTGATGATTACTGCCGGTATTTT  
CTTGGGTTACTGTACCAACTTCGGTACTAAGAATACTCCAACCTCTGTGC  
AATGGAGAGTTCCATTAGGTTTGTGTTTTGCCTGGGCTTTGTTTATGATT  
GGTGGTATGACATTTGTTCCAGAGTCTCCACGTTATTTGGCTGAAGTCGG  
TAAGATCGAAGAAGCCAAACGTTCTATTGCCGTTTCTAACAAGGTTGCTG  
TTGATGATCCATCTGTTTTGGCTGAAGTCAAGCTGTCTTGGCTGGTGTA  
GAGGCAGAGAAATTAGCTGGTAATGCATCCTGGGGTGAATTGTTTAGTAG  
CAAGACAAAGGTCCTTCAGCGTTTGATCATGGGTGCTATGATTCAATCTC  
TACAACAATTGACAGGTGATAACTATTTCTTCTACTATGGTACTACTATT  
TTCAAGGCTGTTGGTTTGAGTGACTCTTTCGAAACCTCTATTGTCTTGGG  
TATTGTTAACTTTGCTTCCACCTTTGTTGGTATTTACGTTGTTGAGAGAT  
ATGGTCGTCGTACTTGTTTGCTATGGGGTGCTGCATCCATGACTGCTTGT  
ATGGTTGTCTATGCTTCCGTGGGTGTCAACAGATTATGGCCAAATGGTCA  
AGACCAACCATCTTCCAAGGGTGCTGGTAAGTGTATGATTGTCTTTGCCT  
GTTTCTATATTTTCTGTTTTGCTACTACATGGGCTCCAATTCCTTATGTC  
GTTGTTTCTGAACTTTCCCATTTGAGAGTCAAGTCTAAGGCTATGTCTAT  
TGCTACAGCTGCTAATTGGTTGTGGGGTTTCTTGATTGGTTTCTTCACTC  
CATTTATTACTGGTGCTATTAACCTTCTACTACGGTTACGTTTTTCATGGGC  
TGTTTGGTCTTCATGTTCTTCTATGTTTTGTAGTTGTTCCAGAACTAA  
GGGTTTGACTTTGGAAGAAGTCAACACCATGTGGGAAGAAGGTGTTCTAC  
CATGGAAGTCTGCCTCATGGGTTCCACCATCCAGAAGAGGTGCCAACTAC  
GACGCTGAAGAAATGACTCACGATGACAAGCCATTGTACAAGAGAATGTT  
CAGCACCAATAA

YDR342C, 570 aa (SEQ ID NO 120)  
MSQDAAI AEQTPVEHLSAVDSASHSVLSTPSNKAERDEIKAYGEGEEHEP  
VVEIPKRPASAYVTVS IMCIMI AFGGFVFGWDTGTISGFINQTD FIRRFG

49/251

MKHKDGTNYLSKVRTGLIVSIFNIGCAIGGIILSKLGDMYGRKVGLIVVV  
VIYIIGIIIIQIASINKWYQYFIGRIISGLGVGGIAVLSPMLISEVSPKHL  
RGTLVSCYQLMITAGIFLGYCTNFGTKNYSNSVQWRVPLGLCFAWALFMI  
GGMTFVPESPRYLAEVGKIEEAKRSIAVSNKVAVDDPSVLAEEVAVLAGV  
EAEKLAGNASWGELFSSKTKVLQRLIMGAMIQSLQQLTGDNYFFYYGTTI  
FKAVGLSDSFETSIVLGIVNFASTFVGIYVVERYGRRTCLLWGAASMTAC  
MVVYASVGVTRLWPNGQDQPSSKGAGNCMIVFACFYIFCFATTWAPIPYV  
VVSETFPLRVKSKAMSIATAANWLWGFLIGFFTFFITGAINFYGYVFMG  
CLVFMFFYVLLVVPETKGLTLEEVNTMWEEGVLPWKSASWVPPSRRGANY  
DAEEMTHDDKPLYKRMFSTK

YDR343C, 2213 bp, CDS: 501-2213 (SEQ ID NO 121)  
AAAAAATGTTTTTTTAGGCAACGGAGATTTCGTTTTATCCACGTTTACCCC  
ACAAAAAGTGCAGGTACATTGTGGGGCCCCGGCATCGAAAACCAGTTTTT  
TTCCTTTAAACGCTGGAaaaaaaggagaaattattggaactttgcagaga  
ATAGTCCGTAGGCAAATTGAAAATGTTCTTAAAAAATTCGTTTCTTAC  
TCATTGAGATTATTCAGATGCCCTCCGTGCCTTCATTGAAAAAATCCAA  
GAGATGTCTCGGATCTGTATGCAGATTTTGGCTTGCAGACAATGGAGAGC  
AAATGGGTATACAATATAGAAAGCACAGAAACATATAAAAAGAGCTCGAG  
AAAAGACATATGGTTTGTAACTATCTTCTTCTTTTTTCCAATTTTCTGT  
TTTAATAATAAAAAACAAGAACAACAAGCTCAACTTGTCTTTTCTAAG  
AACAAAGAATAAACACAAAAACAAGTTTTTTTAATTTAATCAAAAA  
ATGTCACAAGACGCTGCTATTGCAGAGCAAACCTCCTGTGGAGCATCTCTC  
TGCTGTGTGACTCAGCCTCCCACTCGGTTTTATCTACACCATCAAACAAGG  
CTGAAAGAGATGAAATAAAAGCTTATGGTGAAGGTGAAGAGCACGAACCT  
GTCGTTGAAATTCCAAAGAGACCAGCTTCTGCCATATGTCACGTCTCTAT  
TATGTGTATCATGATCGCCTTTGGTGGTTTCGTTTTCGGTTGGGATACTG  
GTACCATTTCTGGTTTCATCAATCAAACCGATTTCATCAGAAGATTGGT  
ATGAAGCATAAAGATGGTACTAATTATTTGTCTAAGGTTAGAAGTGGTTT  
GATTGTCTCCATTTTCAACATTGGTTGTGCCATTGGTGGTATTATCTTTT  
CCAAATTGGGTGATATGTACGGTCGTAAGGTGGGTTTGATTGTCTGTGT  
GTCATCTACATCATCGGTATTATTATTCAAATTGCATCTATCAACAAATG  
GTACCAATATTTTCATCGGTAGAATTATTTCCGGTTTGGGTGTTGGTGGTA  
TTGCCGTTTTATCTCCTATGTTGATTTCTGAAGTATCCCCAAAGCATTTA  
AGGGGTACTTTAGTCTCTTGCTACCAATTGATGATTACTGCCGGTATTTT  
CTTGGGTACTGTACCAACTTCGGTACTAAGAACTACTCCAACCTCTGTGC  
AATGGAGAGTTCCATTAGGTTTGTGTTTTGCCCTGGGCTTTGTTTATGATT  
GGTGGTATGACATTTGTTCCAGAGTCTCCACGTTATTTGGCTGAAGTCGG  
TAAGATCGAAGAAGCCAAACGTTCTATTGCCGTTTCTAACAAGGTTGCTG  
TTGATGATCCATCTGTTTGGCTGAAGTCGAAGCTGCTTTGGCTGGTGT  
GAGGCAGAGAAATTAGCTGGTAATGCATCCTGGGGTGAATTGTTTAGTAG  
CAAGACAAAGGTCCCTCAGCGTTTGATCATGGGTGCTATGATTCAATCTC  
TACAACAATTGACAGGTGATAACTATTTCTTCTACTATGGTACTACTATT  
TTCAAGGCTGTTGGTTTGAGTGACTCTTTCGAAACCTCTATTGCTTTGGG  
TATTGTTAACTTTGCTTCCACCTTTGTTGGTATTTACGTTGTTGAGAGAT  
ATGGTTCGTCGTACTTGTGTTGCTATGGGGTGCTGCATCCATGACTGCTTGT  
ATGGTTGTCTATGCTTCCGTGGGTGTCACCAGATTATGGCCAAATGGTCA  
AGACCAACCATCTTCCAAGGGTGCTGGTAACGTATGATTGTCTTTGCCCT  
GTTTCTATATTTTCTGTTTGTCTACTACATGGGCTCCAATTCCCTTATGTC  
GTTGTTTCTGAAACTTTCCCATTGAGAGTCAAGTCTAAGGCTATGTCTAT  
TGCTACAGCTGCTAATTGGTTGTGGGGTTTCTTGATTGGTTTCTTCACTC  
CATTTATTACTGGTGCTATTAACCTTCTACTACGGTTACGTTTTTCATGGGC  
TGTTTGGTCTTTCATGTTCTTCTATGTTTTGTAGTTGTTCCAGAACTAA  
GGGTTTGACTTTGGAAGAAGTCAACACCATGTGGGAAGAAGGTGTTCTAC  
CATGGAAGTCTGCCCTCATGGGTTCCACCATCTAGAAGAGGTGCCAACTAC  
GACGCTGAAGAAATGGCTCACGATGATAAGCCATTGTACAAGAGAAATGTT

50/251

CAGCACCAAATAA

YDR343C, 570 aa (SEQ ID NO 122)

MSQDAAI AEQTPVEHLSAVDSASHSVLSTPSNKAERDEIKAYGE GEEHEP  
VVEIPKR PASAYVTVSIMCIMIAFGGFVFGWDTGTISGFINQTD FIRRFG  
MKHKDGTNYLSKVRTGLIVSIFNIGCAIGGIILSKLGD MYGRKVGLIVVV  
VIYIIGIIIQIASINKWYQYFIGRIISGLGVGGIAVLSPMLISEVSPKHL  
RGTLVSCYQLMITAGIFLGYCTNFGTKNYSNSVQWRVPLGLCF AWALFMI  
GGMTFVPESP RYLAEVGKIEEAKRSIAVSNKVAVDDPSVLA EVEAVLAGV  
EAEKLAGNASWGELFSSSKTKVLQRLIMGAMIQSLQQLTGD NYFFYYGT TI  
FKAVGLSDSFETSIVLGIVNFASTFVGIYVVERYGRRTC LLWGAASMTAC  
MVVYASVGVTRLWPNGQDQPSSKGAGNCMIVFACFYIFCFATTWAPIPVV  
VVSETFPLRVKSKAMSIATAANWLWGFLIGFFT PFITGAINFYGYVFMG  
CLVFMFFYVLLVVPETKGLTLEEVNTMWEEGVLPWKSASWVPPSRRGANY  
DAEEMAHDDKPLYKRMFSTK

YGR192C, 1499 bp, CDS: 501-1499 (SEQ ID NO 183)

ACAGTTTATTCTCGCATCCACTAAATATAATGGAGCCCGCTTTT TAAGC  
TGGCATCCAGAAAAAAGAATCCCAGCACCAAATATTGTTTTCTTCA  
CCAACCATCAGTTCATAGGTCCATTCTCTTAGCGCAACTACAGAGAACAG  
GGGCACAAACAGGCAAAAACGGGCACAACCTCAATGGAGTGATGCAACC  
TGCCTGGAGTAAATGATGACACAAGGCAATTGACCCACGCATGTATCTAT  
CTCATTTTCTTACACCTTCTATTACCTTCTGCTCTCTCTGATTTGGAAAA  
AGCTGAAAAAAAAGGTTGAAACCAGTTCCTGAAATTATTCCTTACTTG  
ACTAATAAGTATATAAAGACGGTAGGTATTGATTGTAATTCTGTAAATCT  
ATTTCTTAAACTTCTTAAATTCTACTTTTATAGTTAGTCTTTTTTTTAGT  
TTTAAACACCAAGAACTTAGTTTCGAATAAACACACATAAACAAACAAA  
ATGGTTAGAGTTGCTATTAAACGGTTTCGGTAGAATCGGTAGATTGGTCAT  
GAGAATTGCTTTGTCTAGACCAAACGTCGAAGTTGTTGCTTTGAACGACC  
CATTCATCACCAACGACTACGCTGCTTACATGTTCAAGTACGACTCCACT  
CACGGTAGATACGCTGGTGAAGTTTCCCACGATGACAAGCACATCATTGT  
CGATGGTAAGAAGATTGCTACTTACCAAGAAAGAGACCCAGCTAACTTGC  
CATGGGGTTCTTCCAACGTTGACATCGCCATTGACTCCACTGGTGTTTTTC  
AAGGAATTAGACACTGCTCAAAAGCACATTGACGCTGGTGCCAAGAAGGT  
TGTTATCACTGCTCCATCTTCCACCGCCCCAATGTTTCGTCATGGGTGTTA  
ACGAAGAAAAATACACTTCTGACTTGAAGATTGTTTCCAACGCTTCTTGT  
ACCACCAACTGTTTGGCTCCATTGGCCAAGGTTATCAACGATGCTTTCCG  
TATTGAAGAAGGTTTGATGACCACTGTCCACTCTTTGACTGCTACTCAAA  
AGACTGTTGACGGTCCATCCCACAAGGACTGGAGAGGTGGTAGAACCGCT  
TCCGGTAACATCATCCCATCCTCCACCGGTGCTGCTAAGGCTGTCCGGTAA  
GGTCTTGCCAGAATTGCAAGGTAAGTTGACCGGTATGGCTTTCAGAGTCC  
CAACCGTCGATGTCTCCGTTGTTGACTTGACTGTCAAGTTGAACAAGGAA  
ACCACCTACGATGAAATCAAGAAGGTTGTTAAGGCTGCCGCTGAAGGTAA  
GTTGAAGGGTGTTTTGGGTTACACCGAAGACGCTGTTGTCTCCTCTGACT  
TCTTGGGTGACTCTCACTCTTCCATCTTCGATGCTTCCGCTGGTATCCAA  
TTGTCTCCAAAGTTTCGTCAAGTTGGTCTCCTGGTACGACAACGAATACGG  
TTACTCTACCAGAGTTGTCTGACTTGGTTGAACACGTTGCCAAGGCTTAA

YGR192C, 332 aa (SEQ ID NO 184)

MVRVAINGFRIGRLVMRIALSRPNVEVVALNDPFITNDYAA YMFKYDST  
HGRYAGEVSHDDKHIIVDGKKIATYQERDPANLPWGSSNVDIAIDSTGVF  
KELDTAQKHIDAGAKKVITAPSSAPMFVMGVNEEKYTS DLKIVSNASC  
TTNCLAPLAKVINDAFGIEEGLMTTVHSLTATQKTV DGP SHKDW RGGRTA  
SGNIIPSSTGAAKAVGKVLPELQGKLTGMAFRVPTVDVSVVDLTVKLNKE  
TTYDEIKKVVKAAAEGKLKGVLYTEDAVVSSDFLGDSHSSI FDASAGIQ  
LSPKFVKLVSWYDNEYGYSTRVVDLVEHVAKA

51/251

YOR374W, 2060 bp, CDS: 501-2060 (SEQ ID NO 373)  
CGACCCCTCTGGTTAGATGACACTCCTGCCCCAACTGCCACGAATCTGTAA  
CCCCATAACTATACCCGTACGCAGTACTAAAAATGTATGTAATTAGTAAA  
TGTATGTAACAATTTACCGTTTTGTGTAACAATTCATTCATTCATTCTT  
TTGATCCTTTTAGTACCGTCCGCACATGATGTCATTTCCCCCTCATTTTTG  
TTTGCTGGTATGATTCCCCGCCCCGGCGACGGTACGGCTGTTATCCAGCG  
ATGCGGGGACTTCCGTCCACAGGTATCTTTTTCTCCAACCTCCAACAGAGAT  
GGAAAAATGAGGGGCGGGTGTAGGTAAGCAGAATGAGGAGAAATTTGTAAT  
GAAAAATGGAAGTTCCGGCGGTTATATAAAATGGGGGGGGTTTTGTCGGTGACA  
ATTGACTTCACTCTCCTTTCTCAAAAATCTTGGGTGTTAGGATTAGAA  
GTATCTGGAAGCAACCAAGAACTACAATAACAAAAATAAATAAAGC  
ATGTTTCAGTAGATCTACGCTCTGCTTAAAGACGTCTGCATCCTCCATTGG  
GAGACTTCAATTGAGATATTTCTCACACCTTCTATGACAGTGCCTATCA  
AGCTGCCCAATGGGTTGGAATATGAGCAACCAACGGGGTTGTTTCATCAAC  
AACAGATTTGTTTCTTCTTAAACAGAACAGACCTTCGAAGTCATTAAACC  
TTCCACGGAAGAAGAAATATGTCATATTTATGAAGGTAGAGAGGACGATG  
TGGAAGAGGCCGTGCAGGCCGCCGACCGTGCCTTCTCTAATGGGTCTTGG  
AACGGTATCGACCTATTGACAGGGGTAAGGCTTTGTACAGGTTAGCCGA  
ATTAATTGAACAGGACAAGGATGTCATTGCTTCCATCGAGACTTTGGATA  
ACGGTAAAGCTATCTCTTCTCGAGAGGAGATGTTGATTTAGTCATCAAC  
TATTTGAAATCTTCTGCTGGCTTTGCTGATAAAATTTGATGGTAGAATGAT  
TGATACTGGTAGAACCCATTTTCTTACACTAAGAGACAGCCTTTGGGTG  
TTTGTGGGCAGATTATTCCTTGGGAATTTCCCACTGTTGATGTGGGCCTGG  
AAGATTGCCCCCTGCTTTGGTCAACGGTAACACCGTCGTGTTGAAGACTGC  
CGAATCCACCCCATTTGTCCGCTTTGTATGTGTCTAAATACATCCACAGG  
CGGGTATTCCACCTGGTGTGATCAACATTGTATCCGGGTTTGGTAAGATT  
GTGGGTGAGGCCATTACAAACCATCAAAAATCAAAAAGGTTGCCTTCAC  
AGGGTCCACGGCTACGGGTAGACACATTTACCAGTCCGCAGCCGACGGCT  
TGAAAAAGTGACTTTGGAGCTGGGTGGTAAATCACCAAACATTGTCTTC  
GCGGACGCCGAGTTGAAAAAAGCCGTGCAAAACATTATCCTTGGTATCTA  
CTACAATTCTGGTGAGGTCTGTTGTGCGGGTTCAAGGGTGTATGTTGAAG  
AATCTATTTACGACAAATTCATTGAAGAGTTCAAAGCCGCTTCTGAATCC  
ATCAAGGTGGGCGACCCATTTCGATGAATCTACTTTCCAAGGTGCACAAAC  
CTCTCAAATGCAACTAAACAAAATCTTGAAATACGTTGACATTGGTAAGA  
ATGAAGGTGCTACTTTGATTACCGGTGGTGAAAGATTAGGTAGCAAGGGT  
TACTTCATTAAGCCAACTGTCTTTGGTGACGTTAAGGAAGACATGAGAAT  
TGTCAAAGAGGAAATCTTTGGCCCTGTTGTCACTGTAACCAAATTCAAAT  
CTGCCGACGAAGTCATTAACATGGCGAACGATTCTGAATACGGGTTGGCT  
GCTGGTATTACACCTCTAATATTAATACCGCCTTAAAAGTGGCTGATAG  
AGTTAATGCGGGTACGGTCTGGATAAAACACTTATAACGATTTCCACCACG  
CAGTTCCTTTCCGGTGGGTCAATGCATCTGGTTTGGGCAGGGAAATGTCT  
GTTGATGCTTTACAAAATACTTGCAAGTTAAAGCGGTCCGTGCCAAATT  
GGACGAGTAA

YOR374W, 519 aa (SEQ ID NO 374)  
MFSRSTLCLKTSASSIGRLQLRYFSLPMTVPKLPNGLEYEQPTGLFIN  
NKFVPSKQNKTFEVINPSTEEIICHIEGREDDVEEAVQAADRAFSNGSW  
NGIDPIDRGKALYRLAELIEQDKDVIASITLDNGKAISSSRGDVLVIN  
YLKSSAGFADKIDGRMIDTGRTHFSYTKRQPLGVCGQIIPWNFPLLMWAW  
KIAPALVTGNTVVLKTAESTPLSALYVSKYIPQAGIPPGVINIVSGFGKI  
VGEAITNHPKIKKVAFTGSTATGRHIYQSAAAGLKKVTLELGGKSPNIVF  
ADAELKKAVQNIILGIYNSGEVCCAGSRVYVEESIYDKFIEEFKAASES  
IKVGDPEDESTFQGAQTSQMLNKKILKYVDIGKNEGATLITGGERLGSKG  
YFIKPTVFGDVKEDMRIVKEEIFGPVVTVTKFKSADEVINMANDSEYGLA  
AGIHTSNINTALKVADRVNAGTVWINTYNDFFHHAVPFGGFNASGLGREMS  
VDALQNYLQVKAVRAKLDE



52/251

YER177W, 1304 bp, CDS: 501-1304 (SEQ ID NO 151)  
AGATAGATAGATATAGATAGATAATGGACGTAGTTATAGAACAGAAAATC  
GGTAGATCGAAAACACAGGGGAAAAAGGGGGGGGGGGGGGGGAGACAGCG  
CAGCCACGTGACGGGCTTCCTCTTTGGAAAGTGGAGCGAAGTTTTGCGGA  
AGCTACTTTTATTCGGGCTGGAGTCAAAGAGGAAGCTCGGTGGCAAATA  
GCTTCCTCTTTGTGGCCGGGGCGCGGGGGGACGAGGCAAAAAGCAAAGAA  
AAGCAAAAAAATAAAAAAAAAAAAAACAAAAACAGGGGTATGAGAAAAAG  
ACACGCTTTTCCACGCGCAGCAAAAAGGAAAAAGGAAAAGGAAACTCTTT  
ATTATTGGACCTTAAACCTGAAAACGAGACGAACCGTAACATAAAACCGT  
GTAGTTTCTGCAAAAATAACTTAGTTTTTCTACTTTTCAAATTGAGAG  
CGCAAGCAAGTGAGAAGAAAAAGCAAGTTAAAGATAAACTAAAGATAAAA  
ATGTCAACCAGTCGTGAAGATTCTGTGTACCTAGCCAAGTTGGCTGAACA  
GGCCGAACGTTATGAAGAAATGGTCGAAAACATGAAGACTGTTGCCTCCT  
CTGGCCAAGAGTTGTCGGTCGAAGAGCGTAATTTGTTGTCTGTTGCTTAT  
AAGAACGTTATTGGTGCTCGTCTGCTCTTGGAGAATTGTTTCTTCTAT  
TGAGCAAAAGGAGGAGTCCAAGGAGAAGTCCGAACACCAGGTGAGTTGA  
TTTGTTCTGATACCGTTTGAAGATTGAGACCGAATACTAAGATCTCCGAC  
GATATTTTGTCCGTGCTAGACTCCCACTTAATTCATCAGCCACCACTGG  
CGAGTCCAAGGTTTTCTACTATAAGATGAAGGGTGACTACCACCGTTATT  
TGGCTGAATTTTCTAGTGGCGATGCTAGAGAAAAGGCCACAAACGCCTCT  
TTAGAAGCATACAAGACCGCTTCTGAAATTGCCACCACAGAGTTACCCCC  
AACTCACCCAATCCGTCTAGGTTTGGCTCTTAACCTTCTCTGTCTTCTATT  
ATGAAATTCAAACCTCTCCAGACAAAGCCTGCCATTTGGCCAAGCAAGCT  
TTTGACGACGCTATTGCTGAGTTGGACACTCTGTCTGAAGAATCATACAA  
AGATAGCACACTTATCATGCAACTGCTAAGGGACAATTTAACCTTATGGA  
CTTCAGACATGTCCGAGTCCGGTCAAGCTGAAGACCAACAACAACAACAA  
CAACATCAGCAACAGCAGCCACCTGCTGCCGCCGAAGGTGAAGCACCAAA  
GTAA

YER177W, 267 aa (SEQ ID NO 152)  
MSTSREDSVYLAKLAEQAERYEEMVENMKTVAASSGQELSVEERNLLSVAY  
KNVIGARRASWRIVSSIEQKESEKSEHQVELICSYRSKIETELTKISD  
DILSVLDSHLIPSAATTGESKVFYKMKGDYHRYLAEFSSGDAREKATNAS  
LEAYKTASEIATTELPPTHPIRLGLALNFSVFYIEIQNSPKACHLAKQA  
FDDAIAELDTLSEESYKDSTLIMQLLRDNLTLWTSDMSESGQAEDQQQQQ  
QHQQQQPPAAAEGEAPK

YOR267C, 2780 bp, CDS: 501-2780 (SEQ ID NO 363)  
TAGTTCTATTTGGCTATATATTTTCAGAGTGACAAATCTTTAAGAGAGACA  
AACTGAGAATTAGCATATAGAATCATTACATAACTGTTTACAAACAAGT  
AAGCCCAAGACAGTTCCCAACCGCTTAAAGAAGTTTTTCTTAGAGGGAGC  
AAAGTTCGTTTACATTTACACACACAGTTTTTTTTTCACTTTTTTGGGCC  
TCTTCCTTTTCCCGTTTTTTTCAAAAAGCTTAGAAATCTTCTCACCTCC  
TATTTTTCTAGAATCGTGAAGAATTTCCAGATTTAACAGTTTTCCACTTT  
TTCAATAAGGAAATAGTAGGAATAATAAAAAAAGGATAGTAGTAACGATA  
TACGTCGACTTTCCAGACTGGTCTCGAGCCGGAATTAAATACAATAGCAG  
CGTTTGACTACCAATTGTAGCTCCGCTAGAATTGATCGAAAAACAAAAT  
ATAACACTAATAATTATAATAATACGGTAGAATAATTTCTCGTATAAAG  
ATGCCTAATCTATTGTGAGAAACCCATTCCATGGTCATCATAATGACCA  
TCATCATGACCGTGAAAATTCGTCTAATAACCCGCCACAGTTGATCAGAA  
GTTCTAAATCTTTCTTAAACTTCATTGGTAGAAAACAAAGTAATGACTCA  
CTAAGAAGCGAGAAATCTACAGATTCCATGAAATCTACCACAACCACTAC  
AAATTATACTACAACAACCTTAATAACAACACCCATAGCCATTCTAATG  
CAACCAGTATCTCAACAACAACCTACAATAATAACTATGAAACAACAC  
CACCATAATATTTCTCATGGGCTCCATGACTATACTTCTCCCGCCTCTCC

53/251

AAAACAAACCCACTCCATGGCAGAATTGAAAAGGTTTTTCAGACCTTCTG  
TAAATAAAAAACTATCTATGTCTCAACTTCGTTCCAAGAAACATAGCACC  
CATTCACCCCCACCTTCAAAATCAACTTCTACAGTTAATTTAAATAATCA  
CTATCGTGCCAGCATCCTCATGGCTTTACAGACCACTATGCTCATACCC  
AGTCTGCTATACCGCCAAGTACCGATTCTATCCTATCTTTGTCCAATAAT  
ATTAATATATATCACGATGATTGTATTCTGGCTCAAAAAATACGGGAAATT  
GGGTAAGTTATTGGGTTCCGGTGCCGGTGGGTCCGTTAAAGTTCTTGTGA  
GACCAACTGATGGTGCTACTTTTGCCGTCAAAGAATTTCAGACCAAGGAAA  
CCGAATGAGAGTGTGAAAGAATATGCCAAGAAGTGCACCGCAGAATTTTG  
TATTGGTTCGACTTTACATCACCCAAATGTTATCGAAACTGTTGACGTTT  
TCTCTGATTCTAAACAAAATAAATACTATGAAGTTATGGAGTACTGTCCG  
ATTGATTTTTTTGCTGTGTTATGACAGGCAAGATGTCTCGTGCCGAGAT  
CAACTGTTGCTTGAAGCAATTGACTGAAGGTGTTAAATATTTACATTCTA  
TGGGATTGGGCACATAGAGATTTGAAATTGGATAATTGTGTCATGACTTCC  
CAGGGTATTTTGAAATTAATTGATTTTGGTAGTGCTGTTGTGTTTCAGATA  
TCCTTTTGAAGATGGCGTAACGATGGCTCATGGAATCGTGGGTAGTGACC  
CTTACTTAGCGCCGGAAGTGATTACCTCCACCAAATCTTATGATCCTCAG  
TGCGTCGATATATGGTCTATTGGGATCATATATTGTTGTATGGTGCTTAA  
AAGGTTTCCATGGAAAGCCCCTAGAGATTCTGACGATAATTTTAGATTAT  
ATTGTATGCCGGATGATATAGAACACGACTATGTTGAATCTGCCAGGCAT  
CACGAAGAGTTACTGAAGGAAAGAAAAGAAAAGCGTCAAAGGTTTTTGAA  
TCACAGTGACTGTTCCGCCATCAATCAGCAACAACCAGCTCATGAATCAA  
ACTTGAAAACAGTTCAAAATCAAGTTCCAAATACTCCAGCATCTATACAG  
GGTAAAAGCGATAACAAACCAGACATTGTGGAAGAAGAAACCGAAGAAAA  
TAAAGAAGATGATAGCAATAATGATAAAAGAAAGCACGCCAGATAATGACA  
AGGAAAGTACCATCGATATTAATAAAGCAAAATGAGAATAAAAGCACG  
GTAGTTTCAGCTAACCCAAAGAAAGTAGATGCCGATGCCGACGCTGATTG  
CGATGCTAATGGTGACTCTAACGGCAGAGTGGATTGCAAGGCTAACAGTG  
ACTGCAATGACAAAACGGATTGTAATGCTAACAAATGACTGCAGCAATGAA  
TCGGATTGTAACGCTAAAGTTGATACTAACGTCAACACTGCTGCCAACGC  
TAACCTTGATATGGTTCCCCAAAACAATCCACAACAACAACAACAAC  
AACAACAACAACAACAACAACAACAACAACAACAACAACACCATCAT  
CACCAGCATCAAAATCAAGACAAGGCCCATAGTATCGCTTCCGATAATAA  
ATCGAGTCAACAGCACAGAGGACCTCACCATAAAAAAATTATTCATGGCC  
CATACCGTCTATTACGTCTACTACCACATGCTTCAAGACCTATCATGTCC  
CGTATACTGCAAGTAGATCCAAAGAAAAGAGCAACCTTAGATGATATTTT  
TAATGATGAATGGTTTGCCGCCATTGCTGCCTGTACCATGGATTCAAAAA  
ATAAAGTTATTAGAGCGCCTGGCCATCACCATACATTGGTTAGGGAGGAA  
AATGCTCACTTAGAGACCTACAAGGTTTAA

YOR267C, 759 aa (SEQ ID NO 364)

MPNLLSRNPFHGHNDHHHDRENSSNNPPQLIRSSKSFLNFIGRKQSNDS  
LRSEKSTDSMKSTTTTTNYTTTNLNMNTHSHSNATSISTNNYNNNYETNH  
HHNISHGLHDYTSASPQKQTHSMAELKRFRPSVKNKLSMSQLRSKKHST  
HSPPPSKSTSTVNLNNHYRAQHPHGFTDHYAHTQSAIPPSTDLSLSNN  
INIYHDDCILAQKYGKLGKLLGSGAGGSVKVLVRPTDGATFAVKEFRPRK  
PNESVKEYAKKCTAEFCIGSTLHHPNVIETVDVFSKQNKYYEVMYCP  
IDFFAVVMTGKMSRGEINCCCLKQLTEGVKYLHSMGLAHRDLKLDNCVMTS  
QGILKLIDFGSAVVFRYPFEDGVTMAHGIVGSDPYLAPEVITSTKSYDPQ  
CVDIWSIGIIYCCMVLKRFPWKAPRDSDDNFRLYCMPDDIEHDYVESARH  
HEELKERKEKRQFLNHSDCSAINQQQPAHESNLKTVQNQVPNTPASIQ  
GKSDNKPDIVEEETEENKEDDSNNDKESTPDNDKESTIDIKISKNNENKST  
VVSANPKKVDADADADCDANGDSNGRVDCKANSDCNDKTDNANNDCSNE  
SDCNAKVDTNVNTAANANPDMVPQNNPQQQQQQQQQQQQQQQQQQHHH  
HQHQNQDKAHSIASDNKSSQQHRGPHHKIIHGYPYRLRLLPASRPIMS  
RILQVDPKKRATLDDIFNDEWFAAIAACTMDSKNKVIRAPGHHTLVREE

54/251

NAHLETYKV

YLR110C, 902 bp, CDS: 501-902 (SEQ ID NO 275)

TATTGGCGTCTGATTTCCGTTTTGGGAATCCTTTGCCGCGCGCCCTCTC  
AAAACCTCCGCACAAGTCCCAGAAAGCGGGAAAGAAATAAAACGCCACCAA  
AAAAAAAAAAAAATAAAAGCCAATCCTCGAAGCGTGGGTGGTAGGCCCTGGA  
TTATCCCGTACAAGTATTTCTCAGGAGTAAAAAAACCGTTTGTTTTGGAA  
TTCCCCATTTTCGCGGCCACCTACGCCGCTATCTTTGCAACAACCTATCTGC  
GATAACTCAGCAAATTTTGCATATTCGTGTTGCAGTATTGCGATAATGGG  
AGTCTTACTTCCAACATAACGGCAGAAAGAAATGTGAGAAAAATTTGCAT  
CCTTTGCCTCCGTTCAAGTATATAAAGTCGGCATGCTTGATAATCTTTCT  
TTCCATCCTACATTGTTCTAATTATTCTTATTCTCCTTTATTCTTTCTTA  
ACATAACCAAGAAATTAATCTTCTGTCATTTCGCTTAAACACTATATCAATA  
ATGCAATTTTTCTACTGTCGCTTCTATCGCCGCTGTCGCCGCTGTCGCTTC  
TGCCGCTTAACGTTACCACTGCTACTGTCAGCCAAGAATCTACCACTT  
TGGTCACCATCACTTCTTGTGAAGACCACGTCTGTTCTGAAACTGTCTCC  
CCAGCTTTGGTTTCCACCGCTACCGTCACCGTCGATGACGTTATCACTCA  
ATACACCACCTGGTGCCCATTTGACCACTGAAGCCCCAAAGAACGGTACTT  
CTACTGCTGCTCCAGTTACCTCTACTGAAGCTCCAAAGAACACCACCTCT  
GCTGCTCCAACCTCACTCTGTCACCTCTTACACTGGTGCTGCTGCTAAGGC  
TTTGCCAGCTGCTGGTGCTTTGTTGGCTGGTGCCGCTGCTTTGTTGTTGT  
AA

YLR110C, 133 aa (SEQ ID NO 276)

MQFSTVASIAVAVAASAAANVTTATVSQESTTLVTITSCEDHVCSETVS  
PALVSTATVTVDVITQYTTWCPLTTEAPKNGTSTAAPVTSTEAPKNNTTS  
AAPTHSVTSYTGAAAKALPAAGALLAGAAALLL

YLR109W, 1031 bp, CDS: 501-1031 (SEQ ID NO 273)

TGTCTATTAGTAATCAAGAAAAGAACCCTAAATCATCGGCGTCCCCTGTG  
GGGCTCTCGGAAAAACCGGTCCTGACGTCAC TGAAAAGATTTTCGGCACAT  
GGTCATGGGACCAGAGAAAAATTAATCCGACATGTGGAATATTTCCCTTCC  
GTTAAGGTAGTGAGCGCGGATTTTTTCTGATTTGTAATTATACGGGGAGC  
TCTGGCCAAAAAGGTCAGTATTTGGTGATGAAGTTGAATATCATCTTTTG  
ATTTTCTTCTGTATCATTCTTTTTCTTTTTCCACACCCCTTCCGGACGGT  
ATTACATATTTGTTGAGAGGTTAAATGAAAAATAAAGGGGTGGAAAATTA  
AGGACGAGATGTAAGGGAAAAGCATAAACGAAACATTATATAAAGGAGCA  
CAATTTCCCTCTCCCTTGCCAATTGTGCATATACCGTTTCTTTATAACGAA  
ATTTCAACAAACCAGAACAACACAAGTACTACCAATAACCACAACAAAAC  
ATGTCTGACTTAGTTAACAAGAAATCCCAGCTGGCGACTACAAATTCCA  
ATACATTGCTATCAGCCAAAGTGATGCTGACAGTGAATCTTGTAAGATGC  
CACAAACAGTTGAATGGTCCAAATTAATTTCTGAAAACAAGAAGGTTATC  
ATTACCGGTGCTCCAGCTGCTTTCTCCCCAACCTGTACTGTCAGCCATAT  
TCCAGGTTACATCAACTACTTGGATGAATTAGTTAAGGAAAAGGAAGTTG  
ACCAAGTGATCGTTGTTACTGTTGACAACCCGTTTCGCTAACCAAGCGTGG  
GCTAAGAGTTTAGGTGTTAAGGACACCACACACATCAAGTTTGCCCTCCGA  
CCCAGGCTGTGCTTTCACCAAATCCATTGGTTTCGAATTAGCCGTCGGTG  
ACGGTGTTTACTGGAGTGGTAGATGGGCCATGGTTGTTGAAAACGGTATC  
GTTACTTACGCTGCCAAGGAAACCAACCCAGGTACCGATGTGACCGTTTC  
CTCAGTCGAAAGTGCTTTGGCTCATTTGTAG

YLR109W, 176 aa (SEQ ID NO 274)

MSDLVNKKFPAGDYKFQYIAISQSDADSESKMPQTVESKLI SENKKVI  
ITGAPAAFSPTCTVSHIPGYINYLDLVKEKEVDQVIVVTVDNPFANQAW  
AKSLGVKDTTHIKFASDPGCAFTK SIGFELAVGDGVYWSGRWAMVVENGI  
VTYA AKETNPGTDVTVSSVESVLAHL

55/251

YBL081W, 1607 bp, CDS: 501-1607 (SEQ ID NO 29)  
TTGTTGCAACAATTTTGGGATGCTTCTGCGTCGTACGACCCTGTATTTAC  
CTTCTCTAGCTCATCGCTTCCCAGGGTCCACGTTAATTTTCAATTTTTT  
CTTGCGTGTGCAAGATTTCAGGTCTCGAGAAATTTGTCAAAAATTTTTCAC  
TAGATATTAAGAACTATATACATCGAATAAGATGCCAGCACAGAAGAGAT  
AGGCAATCAGTTTAGATACTACAGACACTATCCAATAGTGCAAAGCAAAA  
GCAGCATAGAAAAAAGAGAATCCCGTTTCCAGCTTTTTCTCTTTTTCCCA  
TTCGTTTTTTCCTGATCTTTTTTCTGCATCGTGGCACCTAGAACAAGAGG  
TACCTTCCATCCTTCGCTTAATATTTGATACGACTTTTTTGATTTCATT  
ATTATTATTTGTTACTATTATTATTTATCATTTGGGTTTCGGTTTTTTGT  
AATAATTTTCTTTTTTTTTTTTGGCTCTATTTCACTAAGACATCGTATAT  
ATGCCAGGCCAGATAATCAGCATTCGTTTTTTGTGCGAGAACGAGGACAT  
GGATAAATCCTTGTGGAGTACCGCAGTTTGAAGCTCCTTCATCAGTCCA  
GTAATTCCTTCCAGTCTCACAATGCGCCCTCCACCAGTCGAACACCAC  
CCCCATTACAATCAGTGAATACAACAACACTGGTAGCTATTACTATTA  
CAACAACAACAATAACAGCAGTGTAACCCACATAACCAAGCTGGTCTAC  
AATCCATTAAACAGATCTATTCCATCGGCCCGTACGGGGCTTACAACCAG  
AACAGAGCTAATGACGTACCATATATGAATACCCAAAAGAAACACCACAG  
ATTTAGCGCTAACAATAATTTGAACCAGCAAAAATACAAGCAATATCCCC  
AGTATACGTCCAATCCAATGGTTACTGCACATCTGAAGCAAACGTACCCT  
CAACTGTACTACAATAGCAACGTCAATGCTCACAACAACAACAACAG  
CAACAACAACAACAACAACAACAACAGCAACAACAACAACAATCTTT  
ACAACCAGACGCAGTTCTCCACGAGGTACTTCAACTCGAACTCCTCTCCC  
TCGTTGACTTCTTCCACTTCTAACTCATCTCTCCATACAACCAAAGCAC  
CTTCGAATACATTTTGCCGTCAACTTCGGCAGCTTCCACAAATTTATCGT  
CGTCATCATCAAACAACCTCTATGCACACCAACCCAACTGCAACATCG  
ACATCCGCCGATTTAATCAATGATTTACCCGTGGGCCCCACGTCCAGTTC  
GCTTATCTCGGATCTACATTCTCCACCAACTGTATCTTTCTACCAGCAA  
GCCAAACCCCTGCTCATGTCTCTCCACCACATCTAGCTCTATTGGCACCAC  
ATAAACCCACCGCAACATTCACCATCCCCATCGCAAAGGGAGGATTTTTC  
GACGGCACCAAGTGAACATGTCTTCGTCCGCATCACTCTTGATGAATGATT  
CTTCTTTAGGATGGGGGTCTAACCACATGAACGTATCTTCATCCTCTCAA  
CCAGCATCATCAAGACCCTTTGGCATTTTGGAATACTGACATGAGCGTTTG  
GAGTTGA

YBL081W, 368 aa (SEQ ID NO 30)  
MPGQIISIPFLSQNEDMDKYLLEYRSLKLLHQSSNSFQSHNAPSHQSNYH  
PHYNHMKYNNNTGSYYYNNNNNSSVNPQNAGLQSIINRSIPSAFYGAYNQ  
NRANDVPYMNQKKHHRFSANNNLNQKQYKQYPQYTSNPMVTAHLKQTYF  
QLYNSNVNAHNNNNNSNNNNNNNNNNNNLYNQTFSTRYFNSNSSP  
SLTSSTSNSSSPYNQSTFEYILPSTSAASTNLSSSSNSNMHTNPPTATS  
TSADLINDLPVGPTSSSLISDLHSPPTVSFLPASQTLMSSTSSSIGTN  
INPPQHSPSPSQREDFSTAPVNMSSSASLLMNDSSLGWGSNHNMVSSSSQ  
PASSRPFGIWNTDMSVWS

YDR366C, 899 bp, CDS: 501-899 (SEQ ID NO 125)  
CTGTCGATATTGGGTTACTTTGTAGTGCATTATTTCCATCAATATTAGCA  
GTGTCTTCCAAGGTGAACCATTCGCTGGTAAACCATAGAGTAAAAAACA  
AGTGGAATGGTATCGATTGTATAAAGTACGCAGATTTGCGAAAATACCA  
GCAAGTTTGGCTTATGAATCAAATACAGCCCTTGTGAGAATACGATTAAT  
GTAAATACCGACCAAAGATATGCTATCCATTGCATAAAATCCAACGGATG  
ACCCGTGAACAATGCTAAATACCATAAGCACCCTGCATTTGTTTAGAA  
TGGAATACCTAAGACAATCTCAACTGCAAGGTATAGCGGCATAAACCCC  
AAAAAGACTATGAAAAAAAATATGTTTGAGAACAGGTTAGTAAATTG  
TGCTTTGCTTCGAATCCTTACAAGTTAACAAAAATTTATAGCGTTTGCCG  
GAAACATACTTTTGAAGGGTTAGAAGAGATGATCTCATAACTAAGGTTA

56/251

ATGGTTACAATTGGTAGTTCCTCCCTGGTATTATTTCTTTTCTTCGTAGT  
TTTTGTACAGATCACTTATACAGCTTTACACAGATTTTCCCGCTTGTTGT  
GCACTTTTTTTTCGAAGATTATTGAAGAGGGATGCGTTTGGTACAATAAA  
AAACATAGGTTCCCAAACCTATATAAATATATATATGTATATGTATATAT  
ACTACATATATGCTTTGAGAAATATGTGAATGTTGAGATAATTGTTGGGA  
TTCCATTGTTGATAAAGGCTATAATATTAGGTATACAGAATATACTAGAA  
GTTCTCCTCAAGGATTTAGGAATCCATAAAAGGGAATCTGCAATTCTACA  
CAATTCTATAAATATTATTATCATCATTTTATATGTTTATATTCTATTGA

YDR366C, 132 aa (SEQ ID NO 126)  
MVTIGSSSLVFLFFVVFVQITYTALHRFSRLCTFFSKIIEEGCVWYNK  
KHRFPNLYKYIYVYVYILHICFEKYVNVEIIVGIPLLIKAILGIQNILE  
VLLKDLGIHKRESAILHNSINIIIIILYVYIH

YDR154C, 851 bp, CDS: 501-851 (SEQ ID NO 101)  
TAGACGGGCTTCCACGCGCTTCCACTCATTTCTGTCTCTGGTAATGGCCG  
TGGCCCTTCTCACTTTGGTTGGGCTTACGCTGACAAGTGTCTGTTTCGATT  
CCCTGTATAAATATAAACGTATTCTCTTGAGCCTTCTATCCTTTTGCCAC  
TGTCGTCATCATTTGTTCTCTCTTTTTCGCTAGATAGGTTATATTAAGAT  
TTGTCTTGAATTTAATATCTCAACTCAATCCAACTCAACCGCTAATACT  
ACCATGTCCCAAGTCTATTTTGATGTGCAAGCTGATGGCCAACCAATTGG  
CCGTGTCTGTTTTCAAGTTGTACAACGACATAGTCCCAAAGACTGCAGAAA  
ACTTCAGAGCTCTATGTACCGGTGAAAAGGGATTCTGGCTACGCTGGCTCT  
CCATTCCACAGAGTTATTCCAGACTTCATGTTGCAAGGTGGTGACTTCAC  
TGCTGGTAACGGTACCGGCGGTAAGTCTATCTACGGTGGCAAATTCCCAG  
ATGAAAACCTTCAAGAAGCACCACGACAGACCAGGTTTGTGTCCATGGCC  
AACGCCGGTCCAAACACCAACGGTTCTCAATTCTTCATCACCACCGTTCC  
ATGCCCATGGTTGGACGGTAAGCATGTTGTCTTTGGTGAAGTTGTTGACG  
GTTACGACATCGTTAAGAAGGTTGAGTCCTTGGGTTCTCCTTCCGGTGCC  
ACCAAGGCTAGAATTGTTGTTGCCAAGTCCGGTGAATTATAACCGCTCTG  
CCTGGAACAATACAGCAAAAATTGAAACGAACATATTCTCTCTTAAATTAT  
ATGTATATGTATAAGGTATGTGTATGTATGACAATCAATTCTTATAACTA  
A

YDR154C, 116 aa (SEQ ID NO 102)  
MKTSRSTTTDQVCCPWPTPVQTPVLNSSSPFFHAHGWTVSMLS LVKLLT  
VTTSLRRLSPWVLLPVPPRLELLLSPVNYNRSAWNNTAKIETNYSLLNY  
MYMYKVCVCMTINSYN

YHR162W, 890 bp, CDS: 501-890 (SEQ ID NO 213)  
CGCTCGCTTCCAAGAGTTATCATCATATTCTTCATCATATTCTTCCATAC  
TTAAGGTGGGTAGCGAGGACCCCTCAATTCCCCCACCTCTCTGCCAGGGC  
GTCATCTTTTTCTACAAAAGCCAGGCTGAGTCACGTCAGTTGCTGACCCT  
GGGGGCTGCATTGTTTCTACGAATTACTCATTTGTTTCGTGCGCTTTCC  
TATTGCGCGCATGACTAGGATGGAAAAAAGAGAAAAAAGAAAGCGT  
TGAGTATATAATAAGAAAGAAAGAAAGTCCGAGAGAAAAAGAACACAAA  
GGTTTTTCTCGAGGAAAACAGTAAAGTTTGATACGCACATCGTTGACAT  
CGCTGACTGCAATAGGAACTGAAATAGACGGCAAACCATTAGTTCATT  
GAAAGAACGTATTGTCGAGAATTATCACTCACTATATCAGAAAATTGACA  
CACGAATTATATAAACGAAGTTATACAGAAAAAGATTAAAGAAAAAGAAA  
ATGTCTACATCATCCGTACGTTTTGCATTTAGGCGGTTCTGGCAAAGTGA  
GACAGGCCCAAGACGGTGCATTTCTGGGCTCCTACTTTGAAATGGGGTC  
TGTTTTTTCGCTGGATTCAGCGATATGAAGAGACCGGTGAAAAAATTTCT  
GGTGCTCAAATTTGTCTGCTGCTATCTACTGCGCTGATTTGGACTCGTTG  
GTCCTTTGTTCATCAAGCCAAGAAACATCTTGTTGGCTTCTGTCAACTCGT  
TTCTTTGTCTGACCGCTGGCTATCAATTGGGTAGAATTGCCAACTACAGG

57/251

ATACGGAATGGCGACTCTATATCGCAATTGTGTAGCTATATTCTCAGCGG  
CGCCGACGAAAGCAAAAAGGAAATTACTACGGGCAGATAA

YHR162W, 129 aa (SEQ ID NO 214)  
MSTSSVRFAFRFRWQSETGPKTVHFWAPTLKWGLVFAGFSDMKRPVEKIS  
GAQNLSLLSTALIWTRWSFVIKPRNILLASVNSFLCLTAGYQLGRIANYR  
IRNGDSISQLCSYILSGADESKKEITTGR

YGR243W, 941 bp, CDS: 501-941 (SEQ ID NO 189)  
CCTCCACCAAAGCAAAATGAAAACAAAGCCATACTGGGAAAAATCTGAAA  
AAAAAATGGTAGGAGTAAAAGAAAAGAAAAATAAAGGTTACCCCTGCAG  
TTTGGATAGTCGGGTAACATTTGGCCCTTTTCCTCCTTGATTGGATATTA  
TTACCCCGATTACCCCTCATCTTGGGAGTGCCCGCTTTTATTTCTCCCG  
CCAATCGGCTATTAACGGCTTTACGTCATTCCGTGGGCGGGTCAAGCGAG  
CCGCTCCCTGGTTTGGTCACGCAAAACCGAAAGGCTCAAACAAAATAAG  
GCCATCATATATATATATGCGGCTGCGTGCGTGATTCTCCCGGATAATA  
TGGTGCGTTGCAATTGGAGTATTGGAGAAAATTTCTTTTCCCTTTTCATT  
ACGGCGGAAATACTTCATATAAAAAAAGAATACAATCAGTCTTTAAGA  
CTATACGCATAAGCATTCAAGACACATAGAAACACAAACCTATATTTTAA  
ATGTCAGCATCAGCTTTTAATTTTGCCTTTAGAAGATTTTGGAATAGTGA  
AACAGGCCCTAAACAGTACACTTCTGGGCCCCAACTTTGAAGTGGGGGC  
TGGTCTTCGCAGGGCTAAATGATATTAAGAGGCCTGTTGAGAAGGTATCA  
GGAGCACAAAATTTATCTTTATTAGCGACGGCACTGATTTGGACGCGTTG  
GTCGTTTGTTCATCAAGCCCAAGAACTATCTGTTAGCTTCCGTCAATTTTT  
TCCTGGGTTGCACTGCAGGCTACCATCTAACAAGAATTGCTAACTTTAGG  
ATACGGAACGGTGATTCTTTTAAACAGGTTATTCATACATAATAAAGG  
GGAGACTCCTGCAGCCGTCGCAGCAAAGCAAAGTGCATCCACATCGATGA  
ACAAAGGTGTGATCGGTACTAATCCGCCAATAACGCACTGA

YGR243W, 146 aa (SEQ ID NO 190)  
MSASAFNFAFRFRWNSSETGPKTVHFWAPTLKWGLVFAGLNDIKRPVEKVS  
GAQNLSLLATALIWTRWSFVIKPKNYLLASVNFFLGCTAGYHLTRIANFR  
IRNGDSFKQVIHYIIKGETPAAVAAKQTASTSMNKGVIQTNPPITH

YBR050C, 1517 bp, CDS: 501-1517 (SEQ ID NO 43)  
AAGTACGATATGGTATAACTGTAACATTGAAGGACTGAAGGACTGAAGGA  
CTGAAGGACTATAGTCAAGGGCCAATGGGGAAGGTCCCTTCCAGGCCATT  
TGCCCGATAGTTTGTCTTCTCTTGCTTTTCCGACGGCCCGATTGCATGT  
GGCGGGGCAGCACTGGATAAAAAACGTGGGGGGAGTGATTAAATTTATA  
CGCTTATTGTGTCAACACGGAAACCTTATAGTTATCATTACTAACATCGC  
AACAAGCTGCTTTTTTACTCGTTTTTAGCCACACCATACCCCTTTAATT  
AACTAATAATGCATAAAATAGTTATTGCTTCTTGAGTTGCAGCTTCTTCC  
TGGACGTACTGTTATATATGGCATGTCTTCGCATGTCCGTCAAATTTAGC  
GTTGTCTCGAAACTTAGGCTGTCGTTCTTGCTGTCTGTCTTCTGATAAAA  
TAATATATTGGAATAAGAAAAAATAGGAACAAGAAAGTGTGTGAGA  
ATGACTTTGAGTAATTGCGACTCTTTGGATAACTTATTCAGGACCCCTCC  
AGAGGAAGAAGAAAGTAGTAAATTCGTTGAGGCGGTGAGAACTTTGATGA  
ATAGAAACGATATGGGATATCCTCCCGCCGCTGCAAATGGTACGTATTGC  
TTAAAAAATCAAGTCTTTGAATGCCAAACAGTGGAAAAATAACAAGAA  
AAGAATGTGCATGTTGCCAGCAGTAAAGAAGAAAAATTCGACTTTCACG  
AGCAAAGAAGTTAATCTTGAATTTAAATTTATGGAAATTCATCAAGTTT  
ATCAATTGTAGTAGTAAAAACAATTACAATAAAAAATAAAGCATGTGAG  
AAGCTCGAACAACACTGTAAAAATGAAATGTTTTACCGTTACAAAAAC  
ACAAGAAAGTGGACAATGATCAAAGATTGGAGAACCTTTTTTGGAGAAGC  
TGGTTTAAGGCACGCAAAAGGAGAGATATAATGGGCAAGCCACGAGAGAG  
GCATATCAAATTTAACGATAACGTTGAACAGTGTATTATAACTGATGAGC

58/251

ATTTTCATACAAAGGCTTCCTTCTACACGGTTGAATTCGACTGATGAACAG  
CGCCCTTGTTCAAAGTCTGAACTAGATCCCTGTATTGGCAACGCAGCAAG  
TAAGCGAAGTTTCTATGATTATAACAGCGTTTACGTCGCGAGTGACGCAA  
TTATTACGACTGCCGCTGCCACTGCCATTATCAGTAGTAATAGTGGAGAC  
TATCAGCGTGGGCACGATGTTCCGCGATGTTCCAAGAAATGTTTTGTTACA  
GGCAGGAGAAACAGATTTTCAGTAGTGTGCTTCGGGTTGACTCCGATCTCA  
AGTTATCCAACATAAGTCATCATTTCCCCCGTAAACCTTCGTCAACTTCA  
AGTCATTTCGACCTTCATTTTCGAGTCGGAAACTGACACTGATACTGATAC  
TGACGCTGAAACAGAAAATGACATTGACGCTTACATAGACACCAGTATAC  
CCAACCTGCTCCTATAA

YBR050C, 338 aa (SEQ ID NO 44)

MTLSNCDSLDNLFDPPPEEESSKFVEAVRTLNRNDMGYPAAANGTYC  
LKKIKSLNAKQWKINKKRMCM LPAVKKKNFDFHEQRS LILNLNLWKFIKF  
INCSSKNYNKNKHNKVRSSNNTVKNENVLP LQKHKVDNDQRLNLFWRS  
WFKARKRRDIMGKPRERHIKFNDNVEQCIITDEHFIQRLPSTRLNSTDEQ  
RPCSKSELDPCIGNAASKRSFYDYNVYVADAIITTAATAIISNSGD  
YQRGHDVDRDVRNVLLQAGETDFSSVLRVDSDLKLSNISHSPVKPSSTS  
SHSTFIFESETD TDTDTDAETENDIDAYIDTSIPNLLL

YEL071W, 1991 bp, CDS: 501-1991 (SEQ ID NO 143)

TAGCTTGACCTGGTCAGATTAATCAGCTTCCAACGTTACTTCCCTTTTCGC  
AAGAATCTACCCAAAATGTCTCGAGCATCTTGATAATTACAGTATCGTTC  
GTCCCGACTTGGCATTGTGTTAAATTTCTAAGATGCTTCTATAGGAACA  
TAATTGTCAAGAAAGCACAACAAATTGTCTGCAATGTCAACAGGAGTGGC  
GCATTTTATGTTTTTTCATTTTTTTTTTTTTGTGCGTGATCATTAAGCGG  
GATATTGTCCACAGTCATCTAAAAGAATGACCATTTTCGACGACTTAGTTC  
GGAAAATATTTCCAGCGGATGACACCACTTGCCACAGTTGGTGACCGCCA  
AATCTAAGTCACGCGCGGAAACTGAAAGGTTGTGAGTATATAAGTGATCA  
CTCGCTTATATAACTGACGAGGCAGAACAGGGTGCCAAAATGCTCCTCAA  
TATTTTATTCATTTGAGATTC AAGGCTTAAAGACAGCATATATAAGAATT  
ATGACGGCGGCACATCCTGTGCTCAGTTAACTGCCGAGGCATACCTTAA  
AGTCAAGAGAAAACCCAAATTTCAAAGTTCTCGACTCGGAAGATTTGGCGT  
ACTTTTCGTTTCGATTTTGTCAAATGATGAAATCTTAAACTCTCAAGCTCCA  
GAAGAGCTTGCTTCGTTTFAACCAGGACTGGATGAAAAAATATAGAGGCCA  
GTCCAATTTAATTCTCTTGCCAAACTCCACTGATAAAGTGTTCAAGATTA  
TGAAATACTGTAAACGATAAAAAAGTTGGCAGTAGTACCACAAGGTGGTAAC  
ACCGACTTGGTCGGAGCCTCTGTTCCGGTATTTGATGAGATTGTTCTTTC  
TCTAAGAAATATGAACAAAGTCAGAGATTTTGATCCAGTTAGCGGGACTT  
TCAAGTGTGACGCGGGTGTGCTTATGCGTGATGCGCATCAATTTTACAC  
GACCATGACCATACTTCCCATTGGATCTGCCCTCTAGAAACAACGTGTCA  
AGTGGGCGGTGTAGTTTCAACAAATGCAGGTGGTTTGAACTTTTTAAGAT  
ATGGGTCTCTACACGGTAATGTTTTGGGTTTGGAAAGTGGTGCTACCCAAC  
GGTGAGATTATCAGCAATATCAATGCCCTAAGGAAGGACAATACTGGTTA  
TGACTTGAAACAATTATTCATCGGTGCAGAGGGTACTATCGGTGTGCTTA  
CTGGTGTATCCATAGTTGCAGCAGCAAAGCCAAAAGCCTTGAATGCCGTA  
TTTTTTGGTATTGAGAAATTCGATACCGTTCAGAAATTATTTGTCAAGGC  
TAAAAGTGAATTATCTGAGATTTTATCTGCTTTTGAATTCATGGACCGTG  
GCTCCATTGAATTACGATAGAATACTTGAAGGACTTGCCTTTCCCTCTG  
GAGAACCAACACAACCTTTTATGTTCTTATTGAAACGTCAGGGTCCAATAA  
GAGACACGACGATGAGAAGCTGACTGCTTTCCCTCAAAGATACCACAGATT  
CTAAATTAATTTTCGGAGGGTATGATGGCTAAGGACAAAAGCCGATTTTGAT  
AGACTTTGGACCTGGAGAAAAATCTGTTCCAACAGCTTGTAATTTTACGG  
TGGTATGTACAAGTATGACATGTCACTTCAATTGAAAGATTTATATTCCG  
TATCTGCGGCTGTGACGGAGAGATTAAACGCAGCCGGTTTGATTGGTGAT  
GCACCAAAACCAGTTGTTAAATCATGTGCTTATGGTCATGTCCGTGACGG

59/251

AAACATCCATTTAAATATCGCGGTAAGAGAAATTTACAAAACAGATTGAGG  
ACTTACTAGAACCATTGTATTATGAATATATTGCATCAAAGAAAGGTTCC  
ATCAGTGCTGAGCATGGGATCGGTTTCCATAAGAAAGGTAAGTTACACTA  
CACCAGAAGTGATATTGAAATTAGATTTATGAAGGATATCAAAAATCACT  
ACGATCCAAATGGAATCTTAAACCCATACAAGTACATTTGA

YEL071W, 496 aa (SEQ ID NO 144)

MTAAHPVAQLTAEAYPKVKRNPVFKVLDSEDLAYFRSILSNDEILNSQAP  
EELASFNQDWMKKYRGQSNLILLPNSTDVKVSKIMKYCNDKKLAVVPQGGN  
TDLVGASVPVFDEIVLSLRNMNKVRDFDPVSGTFKCDAGVVMRDAHQFLH  
DHDHIFPLDLPSRNNCQVGGVSTNAGGLNLFYRGSLSHGNVLGLEVLPN  
GEIISNINALRKDNTGYDLKQLFIGAEGTIGVVTGVSIVAAAKPKALNAV  
FFGIENFDTVQKLFVKAKESEILSAFEFMRGSIECTIEYLKDLFPPL  
ENQHNFYVLIETSGSNKRHDDEKLTAFLKDTTDSKLISEGMMAKDKADF  
RLWTWRKSVPTACNSYGGMYKYDMSLQKDLYSVSAAVTERLNAAGLIGD  
APKPVVKSCGYGHVGDGNIHLNIAVREFTKQIEDLLEPFVVEYIASKKGS  
ISAEHGIGFHKKGKLHYTRSDIEIRFMKDIKNHYDPNGILNPFYKYI

YDR133C, 836 bp, CDS: 501-836 (SEQ ID NO 95)

GTGCAGAGGGTGAATCAACGGCCCCCTTCACAGAAACCGCGCAGGAATTTT  
TCTGGTGTTTGTATTTTTTTTTTCTTGTACTTATCTCACTTTTCTTTTT  
CTAACTATTTTTTTTGCAATTTTTTTGTGTACACTTCCACAACATATAG  
GATGGTTTAGTCATCTCTCGAAGTATATAAACCCTTGCTGGATCGTGGTT  
GTTCTTCATCGACTTCTCTCTGCTAGACTCTCTTTTTTAAAATTTTTTCA  
TAGAATAAAAAACCAAGGATAACAAACATCTTCTTTCGTTTCGCTTCAAAA  
TAACTACAAATTAATAATGCAATTTCTTACCGTCGCTTCTATCGCTGCTA  
TTGCCGCTGTTGCCCTCCGCCGCTTCTAACATTACCCTGCTACTGTCACA  
GAAGAATCTACCCTTTGGTCACTATCACTTCTTGTGAGGACCACGTTTG  
TTCTGAAACAGTTTCCCCAGCTTTGGTTTCCACTGCTACCGTCACCGTAA  
ATGACGTTATCACTTAATACACCACCTGGTGTCCATTGCCAACCCTGAA  
GCACCAAGAATACCCTTCTCCAGCTCCAAGTAAAAGCCAAACCGAAAA  
GCCAAGTAAAAGCCAAACCAACAAGGTTCTAGCACTCAAACCTGTTACCT  
CCTACACTGGTGCCGCTGTTAAGGCTTTGCCAGCTGCCGGTGCTTTGTTG  
GCTGGTGCTGCCGCTTTTATTGTTGTAATTTACTCAACCTTTTCTTTAATA  
TATTTTTTAGAAAAATGGTTAAGTACTTTTCCGTCAATACAGCTTCCACAA  
AATCGTTTTATTTCAATTAATAAGATATTTCTGGTAA

YDR133C, 111 aa (SEQ ID NO 96)

MTLSLNTPPGVHCQPLKHQRIPLLQLQLKSQPKSQLKSQPNKVLALKLLP  
PTLVPLRLCQLPVLCLWLVLPLYCCNLLNLFNIFLEKWLSTFPSIQLPQ  
NRFISINKIFW

YHL021C, 1898 bp, CDS: 501-1898 (SEQ ID NO 193)

GGTAAAAGAAATGATCAGGGAGCGTTTCTTGCAACAGCAGCAACAGTACA  
GGCAGCAACAGCAGAAGGATGGCAATTACGTAAAGCCCTCTCAGGACAAC  
GTGGATAGCAAGGACTAACCAGACAGATTGAGGTCTTTCATGCATTACC  
ACCAGTAATAATATTATACGGAATAATATAGTTTATATAATATCCATAAT  
CATAATCATAATCATAATCATAATCGTGATATTGTACCAGCCCC  
GCTTCTCCCCCTTTTGAACACCATTATTATCGGACCCTCTTTACCTTTGA  
ATGGCTCAGTAAGGACCTTTGCGCAGCCGTAAGGGGGTCGGGAATACATT  
TCCGGGGTTGATCCTCGAGGAAAAGTGCTATCTATATAAGGAGAAGCCCT  
TCTAGATCCAAATATCAGGGGTAACCTTTCACAACCTGGCCAGGAACATAT  
TCCAAGTTAAAAGAAAAAATAATTATTAGAAACCAATTACCAACACAAG  
ATGCTAAGATCAAATTTATGCAGAGGATCTCGAATCCTTGCAAGACTGAC  
CACTACACCAAGGACATACACATCTGCGGCGACAGCTGCGGCTGCGAATC  
GGGACATATCATCAAAACATACTTCAATAGAGATTCTACGACAATTACG



60/251

TTCTCCATGGAGGAGTCCAGCAAGCCGGTTTCCGTTTGCTTTAACAACGT  
TTTTCTTAGAGATGCCTCCCATAGTGCCAAGCTGGTGACCACGGGAGAAC  
TGTATCATAACGAGAAATTGACCGCTCCTCAGGACATTCAAATTTCTGAG  
GACGGAAAATCTCTAGTGGTGAAATGGAAAGATGGCGGTATCACCAGTT  
CCCTTTACAATTTCTTATCGACTATAAAGGTTCCAGTTTGTTCGCCAG  
CAACAAGAAAACAAGAATCCAGATATAGACCCAGTTATGGAATAAGCGC  
ATCCTGAAAGATAACGTCAAGGACTTACTTTCTGTGAGCTACAACGAGTT  
TATTGATCCTAAGGATGACTCCAAGCTTTTCCAAACGCTGGTCAACCTAC  
AAAAGTTTGGTATCGCTTTCATTTCCGGTACTCCTTCATCCTCCTCTGAA  
GGCCTTACCATACAAAAGATCTGTGAAAAGGATCGGACCCATAAGATCGAC  
TGTACATGGTGAAGGTACATTTGACGTGAATGCATCCCAAGCGACAAGTG  
TTAATGCCCATATGCCAATAAAGACTTGCCGCTACATACGGATTTACCA  
TTTTTAGAAAATGTGCCAGGTTTCAGATTCTACAATCTCTACCTGCTAC  
AGAAGGGGAAGATCCCAATACTAGACCCATGAATTACTTCGTGGACGCAT  
TTTATGCTACCCGTAATGTTAGAGAATCGGATTTTGAGGCTTATGAGGCT  
TTACAAATTTGTTCTCTGTAAATTATATATATGAAAACGGCGATAAGAGGTA  
CTACCAATCCAAACCTTTAATCGAACATCACGACATTAACGAGGACAATA  
CTCTTCTGGGTAATTATGAGGCCCTTGATTAAATGCATTAACTACTCTCCA  
CCATACCAAGCACCTTTCACTTTCGGAATTTATGATAAGCCCTCAGATCT  
AAATAATAATCTGGACTTGAATTTAATTACCACCCAGCAAACTAACAG  
AGAGATTTTGTTTAAGTCTTTCATTAGGGGGTTGAACTTGTTCGAGAGT  
CATATCAATGACTTCAACAATCAATTTAGATTGCAGTTGCCCGAAAACCTG  
TTGTGTTATCTTTAACAACAGGAGAATTTTGCATGCTAACTCTTTAACAA  
GCTCAAACCAGCAATGGTTAAAGGGTTGCTATTTTCGATTCTGATACTTTC  
AAGAGTAAATTAAAGTTCTTGAAGAGAAGTTTCCTCATGACAAATAA

YHL021C, 465 aa (SEQ ID NO 194)

MLRSNLCRGSRLARLTTPRPTYSAATAAAANRGHIIKTYFNRDSTTIT  
FSMEESSKPVSVCFMNVFLRDASHSAKLVTGELYHNEKLTAPQDIQISE  
DGKSLVVKWKDGGHHQFPLQFFIDYKGSSFVSPATRKQESRYRPQLWNKR  
ILKDNVVDLLSVSYNEFIDPKDDSKLFQTLVNLQKFGIAFISGTPSSSSE  
GLTIQKICERIGPIRSTVHGEFTFDVNASQATSVNAHYANKDLPLHTDLP  
FLENVPGFQILQSLPATEGEDPNTRPMNYFVDAFYATRNVRSDFEAYEA  
LQIVPVNYIYENGDKRYQYQSKPLIEHHDINEDNTLLGNYEALIKCINYS  
PYQAPFTFGIYDKPSDLNNLDLNLITTPAKLTERFLFKSFIRGLNLFES  
HINDFMNQFRLQLPENCCVIFNNRRILHANSLTSSNQWLKGCYFDSDTF  
KSKLKFLKFKPHDK

YKL054C, 2717 bp, CDS: 501-2717 (SEQ ID NO 237)

CCTGCTCTAGACGAAGCTAGGGAGGAGGCGCCGTTTGAAAATGGCGGCAA  
ACTAAAAGAAGTTGACAAATGAAGTATATATTTTAGCACAGAATGTGCAT  
TATTCAACATGTAAATACTAATACTGCAATATCGACTTATAATAATGTAT  
AGTGATCCGTATATTAATAGATCTGTTTCAATTCCTTTACCTTTTTAGGAT  
ATCCGTCACCCGTGATTCCGTCGGAGGTGAGCACTCGCCCAAATAAAATAA  
CGGGAAATGGTGGCAAAAAGTAGTGGCGGGAAAAGGAAAAATTTTCGTTT  
TCTCCCATATAAACGTTTCATTCCTTTTCCTAAGTCTTTTACAGTAATTT  
CAGAAACATTCGTATTTTATATTTGATCTTTTGAAGCTACAAGAAAACT  
CTTACCAATTACCCCAAAAAATCACCATCATAAAGTACTTACATATTTA  
TTTTTGTATTGGTTCGTTTCTCAATATAATCTACATCATCATATATATA  
ATGTTCTACACAATTTAGGAAGTCTAATCATATAGTCATAGTAGTAAAAA  
ACTAAATCCTGCGCTAAAGTCCAAAATAGATACGCTTACAGAATTGTTCC  
CTGACTGGACGAGTGATGATTTAATTGATATAGTTCAAGAATATGATGAT  
TTGGAACTATAATTGATAAAATTACTTCCGGCGCAGTGACAAGATGGGA  
TGAAGTAAAGAAACCTGCTAAGAAGGAAAAATATGAAAAAAGGAGCAAC  
AACACTCATATGTCCCTCAACAACATTTGCCAAATCCAGAAGATGATATT  
ACATATAAGAGTTCTAATAATAGCAATTCTTTTACTTCTACAAAGCATAA

61/251

CAGTAGTAACAATTATACTCAAGCCAGAAATAAGAAGAAGGTACAAACAC  
CACGAGCTCATACAACCGGGAACATGTTAATCTCGACAAGGGGAAGCAC  
GTACCATCCAAGCCTGTTTCAAACACTACATCGTGGGCAGCAGCTGTTTC  
TGTAATACTAAACATGACGTTCTCAAGATTCAAATGATAACAATAATG  
AAGAATTAGAAGCACAAGGGCAACAAGCGCAGGAGAAAAATCAAGAAAA  
GAGCAAGAAGAGCAACAACAGCAGGAAGGGCATAATAACAAAGAAGAACA  
CAAACAAATAGAGCAACCTTCTTTATCTTCAAAGAAAACTTCTAGGA  
CATCTGCTTCACAACCAAAGAAAATGTCGTGGGCTGCAATTGCTACACCA  
AAGCCAAAGGCTGTTAAAAAGACCGAGTCTCTCTTGAAAACGTTGCTGA  
ATTGAAGAAAGAAATAAGCGATATTAAGAAGGATGACCAAAAGTCTGAAG  
CTAGTGAAGAAAAAGTTAATGAACAAGAAACATCTGCACAAGAACAAGAG  
GAGGAGACTGCTGAACCTTCTGAAGAAAATGAAGACAGAGTCCCTGAAGT  
GGACGGAGAAGAAGTCCAAGAAGAAGCTGAAAAAAGGAACAAGTAAAG  
AAGAGGAACAGACAGCGGAAGAGCTGGAACAAGAACAAGATAATGTTGCT  
GCTCCAGAAGAAGAAGTTACAGTTGTTGAAGAAAAGGTTGAAATTAGTGC  
TGTTATTTTCAGAGCCTCCAGAAGATCAAGCTAATACTGTACCTCAACCAC  
AACAACAATCCCAACAACCACAGCAACCACAGCAACCACAGCAACCACAG  
CAACCACAGCAACCACAGCAACAACAACAACCACAGCAACCACAACAACC  
ACAACAACAACACTACAACAGCAACAGCAACAGCAACAACAACCAGTACAAG  
CTCAAGCTCAAGCCCAAGAAGAACAATTATCTCAAACTACTATACTCAA  
CAACAGCAGCAACAATACGCTCAACAACAGCATCAGTTACAGCAACAGTA  
TTTGTCCCAACAACAACAATATGCTCAGCAACAGCAACAGCATCCACAAC  
CTCAATCACAACAACCTCAATCACAGCAAAGTCCACAAAGTCAAAAACAA  
GGGAACAACGTGGCTGCCCAACAGTACTACATGTATCAAAACCAATTTCC  
TGGATATTCTTATCCAGGTATGTTTGATTACAAAGGATACGCTTACGGTC  
AACAATATCAGCAACTTGCTCAAAACAACGCTCAAACTAGTGGTAATGCT  
AACCAATATAATTTCCAACAAGGTTATGGTCAAGCAGGCGCGAACACTGC  
TGCTGCTAATTTGACTAGTGCTGCCGCTGCTGCTGCCGCTTCTCCAGCTA  
CAGCTCACGCCCCAACCTCAACAACAACAGCCATACGGTGGCTCATTTCATG  
CCATACTACGCCCCTTTTACCAACAGTCATTCCCATATGGTCAACCTCA  
ATACGGTGTAGCTGGTCAATATCCATACCAGTTACCAAGAACAATTACA  
ACTATTACCAAACTCAAAACGGTCAGGAACAGCAAAGTCCAAATCAAGGT  
GTTGCCCAGCATTCTGAAGACTCTCAACAGAAGCAATCACAACAGCAACA  
GCAACAGCAACCTCAAGGTCAACCCCAACCTGAAGTTCAAATGCAAAATG  
GCCAACCTGTTAACCCACAACAACAATGCAGTTCCAACAATACTATCAA  
TTCCAACAACAACAGCAACAAGCTGCTGCCGCTGCCGCTGCTGCTGCCCA  
ACAAGGTGTACCATATGGCTACAACGGTTATGATTACAATTCTAAAAATT  
CAAGAGGTTTCTACTAA

YKL054C, 738 aa (SEQ ID NO 238)

MSTQFRKSNHNSHSSKKLNPALKSKIDTLTELPDWTSDDLIDIVQEYDD  
LETIIDKITSGAVTRWDEVKKPAKKEKEYEKKEQHSYVPQQHLPNPEDDI  
TYKSSNNSNSFTSTKHNSNNYTQARNKKKVQTPRAHTTGKHNLDKGKH  
VPSKPVSNNTTSWAAVSVDTKHDVPQDSNDNNNELEAQGQQAQEKQEK  
EQEEQQQEGHNNKEEHKQIEQPSLSSKKTTSRTSASQPKMSWAAIATP  
KPKAVKKTESPLENVAELKKEISDIKKDDQKSEASEEKVNEQETSAQEQE  
EETAEPSEENEDRVPEVDGEEVQEEAEKKEQVKEEEQTAELEQEEDNVA  
APEEEVTVVEEKVEISAVISEPPEDQANTVPQPQQQSQQPQQPQQPQ  
QPQQPQQQQQPQQPQQPQQQLQQQQQQQQPQVQAQAQAQEEQLSQNYTQ  
QQQQQYAQQQHQLQQQYLSQQQQYAQQQQQHPQPQSQQPQSQQSPQSQKQ  
GNNVAAQQYYMYQNQFPGYSPGMFDSQGYAYQQYQQLAQNNAQTSQNA  
NQYNFQQGYGQAGANTAAANLTSAAAAAASPATAHAQPQQQPYGGSFM  
PYYAHFYQQSFYGPQYGVAGQYPYQLPKNNYNYQTQNGQEQQSPNQG  
VAQHSEDSQQKQSQQQQQQQPQGPQPEVQMONGQPVNPQQMQFQQYYQ  
FQQQQQAAAAAQAQGVYPGYNGYDYNKNSRGFY

62/251

YLR311C, 848 bp, CDS: 501-848 (SEQ ID NO 283)

ACAAAACAGACTTAGTTATTTTATGGTATACAACAAAAGCTCGAATGAAA  
GACGGTTGGCACAAGAGAATTAACAAAATAAACGGAGGAAGAATAAAGTT  
ACACCTATTTCTCAAGAATTCTTTTAAATCCGCTCAAGAAAGTTTAAGGG  
TATTGCATAAAGAACAGAAACGCCGCTGGAAAAGGCTCTTTGTGCTACTT  
CATAATAAATACAGGCAATTTTCTCCACATATTAAGGTATTTTCGATCA  
TTCTTGCCAAAAAGCAAAACAATGTTGGTCGGGATCCAGATTGCAGTTGC  
GCAAGCTTCGTTTCAAGTCAATGAAACCATTCCGAGTTTTCAGTTTAAG  
GTTTCGCAAAGATACCAACTGGTTTGTAAGCAGCTGAAACGGTTCGGATT  
GAAATTACAGCATTTCGAGGATGTATAAGCGATGTCAGAATGCAGGAAAA  
AAAATTATTTAAGTGCAACACTAGATCATCCAAAACCCAGCATGAAGA  
ATGAAATTAACAAAAGAAAAAAAACGACTGCTTAGTAGGAGTGTCATA  
TATCCCTCCTTTAAATTTTTTACACTTACTTTCTTTTTTTTATTGAGAA  
TAGAAAAGGTGCATCTCTCTCTCTCTCTCTCTATCTCTATCTCTAAGG  
TTTTATTACTTTTATAACGTATGCTATCCATCTCTTTTCTTTTTTTTTTG  
TTTTGTTATTCCCTTTTTTACTCAGTTAGATTCTACTACTATATTTAC  
ATATTCTTCGAAGCTTTTATGAGTTAAATATTTTGTGTGCTTTATGGGGCA  
GAAAATAGTCGACGTCAGTCACCTCCAGGTTATTATGTAATTCGCTAA

YLR311C, 115 aa (SEQ ID NO 284)

MKLTKEKKNDCLVGVSYPPLNFFTLTFLFLLRIEKVHLSLSLSLSLR  
FYFHNVCYPSLFLFFCFVIPPFFYSVRFILLYLHILRSFYELNILLLYGA  
ENSRRQSPPGYYVIR

YMR107W, 848 bp, CDS: 501-848 (SEQ ID NO 309)

AGAGCAGAAATGATGAAGGGTGTTAGCGCCGTCCACTGATGTGCCTGGTA  
GTCATGATTTACGTATAACTAACACATCATGAGGACGGCGGCGTCACCCC  
AACGCAAAAGAGTGACTTCCCTGCGCTTTGCCAAAACCCCATACATCGCC  
ATCTGGCTCCTGGCAGGGCGGTTGATGGACATCAGCCGCTCCCTTAATT  
GCTAAAGCCTCCACAAGGCACAATTAAGCAATATTTTCGGGAAAGTACACC  
AGTCAGTTTGCGCTTTTATGACTGGGTTCTAAGGTACTAGATGTGAAGTA  
GTGGTGACAGAATCAGGGAGATAAGAGGGAGCAGGGTGGGGTAATGATGT  
GCGATAACAATCTTGCTTGCTAATCACCCCATATCTTGTAAGTAT  
ATAAATAGGAGCCTCCCTTCTTATGCAACTCCATAAAATTTTTTTTGT  
AGCCACTTCTGTAAACAAGATAAATAAAACCACTAATCGAGATATCAAAT  
ATGGGTAGTTTTTGGGACGCATTTCGAGTATACGACAAGAAAAAGCACGC  
AGATCCAAGTGTATATGGAGGAAACCATAACAACACAGGAGACAGTAAAA  
CGCAGGTTATGTTTTCGAAAGAGTACCGTCAACCTAGGACACATCAGCAA  
GAGAACTTGCAGAGCATGAGAAGATCTTCCATAGGATCACAGGACAGTTC  
CGATGTTGAGGACGTTAAGGAAGGGAGATTACCCGCAGAAGTAGAAATAC  
CAAAGAATGTTGACATCTCTAACATGTCGAAGGTGAGTTTTTAAGACTT  
TACGAAAGTTTGAGGAGGGGGGAACCCGACAATAAAGTAAATAGATAA

YMR107W, 115 aa (SEQ ID NO 310)

MGSFWDFAFVYDKKKHADPSVYGGNHMNTGDSKTQVMFSKEYRQPRTHQQ  
ENLQSMRRSSIGSQDSSDVEDVKEGRLPAEVEIPKNVDISNMSQGEFLRL  
YESLRRGEPDNKVNR

YKL066W, 944 bp, CDS: 501-944 (SEQ ID NO 243)

GAAAAACATCTCATAAATCATCCCTGGAAAAATGTCTAGTCAAACAGAAA  
GAACTTTTATTGCGGTAAAACCAGATGGTGTCCAGAGGGGCTTAGTATCT  
CAAATTCTATCTCGTTTTGAAAAAAAAGGTTACAACTAGTTGCTATTAA  
ATTAGTTAAAGCGGATGATAAATTACTAGAGCAACATTACGCAGAGCATG  
TTGGTAAACCATTTTTCCCAAAGATGGTATCCTTTATGAAGTCTGGTCCC  
ATTTTGGCCACGGTCTGGGAGGGGAAAAGATGTGGTTAGACAAGGAAGAAC  
TATTCTTGGTGCTACTAATCCTTTGGGCAGTGCACCAGGTACCATTAGAG

63/251

GTGATTTTCGGTATTGACCTAGGCAGAAACGTCTGTCACGGCAGTGATTCT  
GTTGATAGCGCTGAACGTGAAATCAATTTGTGGTTTAAGAAGGAAGAGTT  
AGTTGATTGGGAATCTAATCAAGCTAAGTGGATTTATGAATGAATAACTT  
ATGGCATGGGAGGGTACATATGAGCGCCTTTTTTTTCTCGCTTTGGGCAG  
CTCATATCATGTTCCCTCACTAGCTAATAATATAATGAATTTTTTAGAAG  
GAGCACGATTATATAAAAAAATACCACTTATGTTGCTACCCTTATATAC  
GAATTTATAATACTTAATGACGCTTCAATGACGCCTGATGTCAAATGCTT  
TTGGCTCCCAGTGAAATTGCCACACTTCCTTCTTCTTTCCGAACCTTTATA  
GTATCATCGAAAAATACAAGTTGGCAAAGGTCTATTACAATCGCGGAACG  
TACGATGTTTCATACGGTTTCAGCGAATAGTCTTGTAAATATCCGGAAGCAT  
GCCTACCGGCATTATTATAGGTAGTTCATCGCCCTTGGACTATGTAGGGG  
TACAAGTAAATAGGCAACTTGAAATGGATCTCCCTATTGAATGA

YKL066W, 147 aa (SEQ ID NO 244)  
MAWEGTYERLFFLALGSSYHVPSLANNIMNFLEGARLYKKNNTTYVATLIY  
EFIILNDASMTDPVKCFWLPVKLPHPHLLSELYSIIIEKYKLAKVYYNRRGT  
YDVHTVSANSLVISGSMPGTIIIGSSSPLDYVGVQVNRQLEMDLPIE

YML053C, 1139 bp, CDS: 501-1139 (SEQ ID NO 295)  
GAGGCGACACCTGCTAATGTTTACAATTTTCCCGATTGGGGTGCTAGAGG  
CATACAGTGGGCTACATGGCACAGCACGGCAGTGCAGAGTGAGAAAATAT  
GACTTCACGCTCGAGGCGAGGCCACGCTTTCGAAGCTTCGAATGCCACTA  
CCTAGACCATTGCTGTTTTGTACCTTCACGGTCCCATTAGAGACATTTTA  
CTTAATGCAAGATTGCCATATCCGTTGTCATGGTACCAAACAGGGTAATA  
ATTTCTAGAAATCATGATACACGTATGACATCTGGGTAACCTAATCCATC  
TGGGTAACCGATTTTTCTCTCCCTTTGCTTTCTCTTTACCACTCAGCTGA  
CTTTATTATTTTTTTTATATTTTTCATTTTGACAAAATTATATAGTTAGG  
AAGAATACAATAGGACTGCGACAGAAACAGATAAGGGCTCTTTTTTCTTG  
GGGTGGCTGCTTTTATTCATTAATTTAAGACTCAAGTGTGCTGCGTGAA  
ATGCTCTCATACTATGAACACAATACTGCGTTCCAAACAAACAATTGCAA  
TTCCGGTAGCAATGCCGCCACTACATAACAACAGCGACGCCAATAATGATA  
CGATCATGAATAAAAGAAAAAATGACCATTTTCGAGTTTGATACACACACT  
TTCTACCAAAGATCGAAGAGAAACAAAACGAGATTCTGTAAGTACAAAGTT  
TTCGGTTCGGTTCCGGGTGTGCTAATCTTAATAACAACAACAACATCA  
TCATCAACAACAACAACAACAATAATAATAATAAACCATAATCAT  
AATAACAGCAATAATACTGCAACCTACAATAATATTATTATAAAAAAAA  
TATCGAAATATGTCCCCTGAAACCGGTTAGTATGCACCACACTATGAACA  
GCCGCTTACTGAACGAATCTGAATTTTATTCTGAAACAGAAGAGTACATG  
ATTTCATGGTTATTTTCGGTAACACTAATCGCGACATAACAGGCACGAGTCC  
TACTGGAAGTGCTAGTATTATACAACACCAGTATCATCTTCTACCATCCC  
AAAGTATAATTGCATCACAAGCACCCGGTACTGCCATGGCCGCGTTGACT  
AACAACAATATCGCTAACGATTACATGGATATAGATTAA

YML053C, 212 aa (SEQ ID NO 296)  
MLSYYEHNTAFQTNNCNSGSNAATTYNDSANNDTIMNKRKNDHFEFDHT  
FYQRSKRTRKDSVSTKFSVSGCANLNNNNNNNIIINNNNNNNNNNNNNHNH  
NNSNNTATYNNIHYKKNIEICPLKPVSMHHTMNSRLLNESEFYSETTEEYM  
IHGYFGNTNRDITGTSPTGSASIIQHQQYHLLPSQSIIASQAPGTAMAALT  
NNNIANDYMDID

YOR121C, 806 bp, CDS: 501-806 (SEQ ID NO 355)  
GGTGACGCTGTTTGGGCTACTTCTGGTGGCCTATCTTTGCAACCAAACGA  
AATTGGTGAAATTGTTCAAGGCTTCGACAATCCAGCTGGTTTGCAAAGCA  
ATGGTTTGATATTCAAGGCCAAAAGTTCATGTTGTTGAGAGCTGACGAT  
AGAAGTATCTACGGTAGACATGATGCTGAGGGTGTGTTTGTGTAAGAAC  
TAAGCAAACCGTTATTATTGCTCATTATCCACCAACCGTACAAGCCGGTG

64/251

AGGCCACCAAGATTGTCGAGCAATTGGCTGACTTGTGATTGGTGTTCAA  
TACTAATTTATGCAGGTAAAGTTTTCTTGCCTTATACACCACCTATTC TG  
GCATCTGCGGGATTTCGCTTCCATTTTACAAATATTTTATTGATTGACG  
CTAATTATCAGTGTAAAAGGCGCACTTTTTATATGTAGTCACATCCGGTA  
TTTAACATATTTACGAAACAGTCTTAAGAATATCGACATTGTGATATAC TT  
ATGTTTAATTTATCTACATATTACAATCATACGAGAAACACGCAAAAACA  
ATTACTTGAATACTTCGAAAGGAGACCAATTTGGATGTACAACCCTTTTT  
TCGCCCTTTTCCTTTCGATATGTTATTGATAGCTTCAAAGTCCTCAGTAGA  
CAAAGTAAATATTTTCCGTGTTTCGTTTGTGATTTCGATCGGGATTACAGATT  
TTGGCAAGACAACATAACCTCTTTGGACGTGCCAGCTAATAACAACGTGT  
CCGGGTGAACGTTATTTTCTTCGCAATTTCAAGGATAACCGGTTCCTT  
CAATAG

YOR121C, 101 aa (SEQ ID NO 356)

MFNLSTYYNHTRNTQKQLLEYFERRPIWMYNPFFALFLRYVIDSFKVL SR  
QSKYFPVRFDSIGIHRFWQDNITSLDVPANNNVSGLNVIFLRNFKDNRFL  
Q

YOL106W, 854 bp, CDS: 501-854 (SEQ ID NO 341)

ATATGGTTTTCATCATTTTGTCTCAATTGTTCTCCATTTGGGTTACCTTTTT  
TGCCAGTTGGTTCGTACTTGGAGTTTTCAGAACTTGCACCCTTGAATT  
GTCCCTCTTTGCCAACAAC TAATCTCAAGGTGGTCAGGAAATATTGGTC  
GGCGATGCATCTGATACTTTTCAATTGATTTACTTCTTTCCCTGATCTAAT  
TAAGCCGATTTTGGAGCCGATTTTCAATTTTCATTTATAATGTAGTTGTTG  
TAAATTTTAAAGTCATTAACCTTTTCATGATATTGATATAGATATTGGG  
AACACCATCGCAGAAAGTAGAGGCGCCAAAAAATTTATGACTGTAGAAGA  
AAGACGAAGACAGTTAGCTTTACAAGTTTGGGAAGAGCGTATGGTAAACC  
CTTGATATATGGATCTATATAACTTGAATATGCTCTATTATATCGTGAT  
TTAATGACGGCTGTTGGCATTTCGGTCTTTACCAAGGTAGTAGGATTTGT  
ATGCTGAATGTGCGCCAGTACTATCGAACCATAGAAACCCATATATTTCCC  
CAATATTAATAATTTCTACTGAGAAATGGGTGAATTTTGAAATAATTGTTG  
GGATTCCATCGTTGATAAAGGCTATAATATTAGGTATACAGAATGTACTA  
GAAGTTCTCCTCGATGATATAGGAATCCCCATAATGGAATCTATATTTCT  
ATGTACCAATATTACGATTATTCCTCATTCATTTCATATGTTTCATTAT  
CCTATTACATTATCGATCCTTGCAATTCAGCTTCTCTAACTTCGGTGAC  
AGCTTCTATAATAACTTATGTCACTATCTAACACCGTATATGATAATATA  
TTGA

YOL106W, 117 aa (SEQ ID NO 342)

MLNVRQYYRTIETHIFPNINNSTEKWNFEIIVGIPSLIKAILGIQNVL  
EVLDDIGIPIMESIFLCTNITIIPHSISYVLSYYIIDPCISASSNFGD  
SFYNNLCHYLTPYMIY

>YAL003W, 1487 bp, exon1: 501-580, intron1: 581-946, exon2:  
947-1487 (SEQ ID NO 17)

CCGATGGAACGTTCTGGAAAAAGAAGAATAATTTAATTACTTTCTCAACTAAAATCTGGA  
GAAAAACGCAAATGACAGCTTCTAAACGTTCCGTGTGCTTTCTTTCTAGAATGTTCTGG  
AAAGTTTACAACAATCCACAAGAACGAAATGCCGTTGACAATGATGAAACCATCATCCA  
CACACCGCGCACACGTGCTTTATTTCTTTTTCTGAATTTTTTTTTTCCGCCATTTTCAAC  
CAAGGAAATTTTTTTTCTTAGGGCTCAGAACCTGCAGGTGAAGAAGCGCTTTAGAAATCA  
AAGCACACGTAACAATTTGTCGACAACCGAGCCTTTGAAGAAAAAATTTTTTCACATTGT  
CGCCTCTAAATAAATAGTTTAAGGTTATCTACCCACTATATTTAGTTGGTTCTTTTTTTTT  
TTCCCTTCTACTCTTTATCTTTTTTACCTCATGCTTTCTACCTTTTCAGCACTGAAGAGTCCA  
ACCGAATATATACACACATAATGGCATCCACCGATTTCTCCAAGATTGAAACTTTGAAAC  
AATTAACCGCTTCTTTGGCTGACAAGTCATACATTGAAGGGTATGTTCCGATTTAGTTTA

65/251

CTTTATAGATCGTTGTTTTCTTTCTTTTTTTTTTTTCTCCTATGGTTACATGTAAAGGGAA  
GTTAACTAATAATGATTACTTTTTTTCGCTTATGTGAATGATGAATTTAATTCCTTGGTC  
CGTGTTTATGATGGGAAGTAAGACCCCGATATGAGTGACAAAAGAGATGTGGTTGACTA  
TCACAGTATCTGACGATAGCACAGAGCAGAGTATCATTATTAGTTATCTGTTATTTTTTT  
TTCCTTTTTTGTTCAAAAAAGAAAGACAGAGTCTAAAGATTGCATTACAAGAAAAAAGT  
TCTCATTACTAACAAGCAAAATGTTTTGTTTCTCCTTTTAAAATAGTACTGCTGTTTCTC  
AAGCTGACGTCACGTCTTCAAGGCTTTCCAATCTGCTTACCCAGAATTCTCCAGATGGT  
TCAACCACATCGCTTCCAAGGCCGATGAATTCGACTCTTTCCAGCTGCCTCTGCTGCCG  
CTGCCGAAGAAGAAGAAGATGACGATGTCGATTTATTCCGGTCCGACGATGAAGAAGCTG  
ACGCTGAAGCTGAAAAGTTGAAGGCTGAAAGAATTGCCGCATACAACGCTAAGAAGGCTG  
CTAAGCCAGCTAAGCCAGCTGCTAAGTCCATTGTCACTCTAGATGTCAAGCCATGGGATG  
ATGAAACCAATTTGGAAGAAATGGTTGCTAACGTCAAGGCCATCGAAATGGAAGGTTTGA  
CCTGGGGTGCTCACCATTATCCCAATTGGTTTCGGTATCAAGAAGTTGCAAATTAAC  
GTGTTGTGCGAAGATGACAAGGTTTCTTGGATGACTTGCAACAAAGCATTGAAGAAGACG  
AAGACCACGTCCAATCTACCGATATTGCTGCTATGCAAAAATTATAA

&gt;YAL003W, 206 aa (SEQ ID NO 18)

MASTDFSKIETLKQLNASLADKSYIEGTAVSQADVTVFKAFQSAYPEFSRWFNHIASKAD  
EFDSFPAASAAAAEEEEEDDDVDLFGSDDEEADAEAEKLKAERIAAYNAKKAAPAKPAK  
SIVTLDVKPWDETNLEEMVANVKAIEMEGLTWGAHQFIPIGFGIKKLQINCVVEDDKVS  
LDDLQQSIEEDEDHVQSTDIAAMQKL

&gt;YAL060W, 1649 bp, CDS: 501-1649 (SEQ ID NO 19)

AAAGACTACGAGAATCAATAAACGAGGCTAAACTGCGTCACACATGATTGTGATTGAGTA  
CTCACGTTCTCGTGTTAATCCCGCGGTCTTCTTGTTTTACTAACTTTTCTTTCTCTCATA  
GCATTCTCTTGACAGTGTTTTATATACATCATATGTACATTTATCGAGCCAATCGAGGGC  
AGCAGTTTAACATCAAGCCGGATTTGCTCACGCTACTTTGACCCCTTTTCGTTTCGACGG  
AGAGAAGAAACCGGTGTTTTCTATCCTTGCCCTATTCTTCTCCTTACGGGGTCCTAGC  
CTGTTTCTCTTGATATGATAATAGGTGGAACGTAGAAAAAAAATCGACATATAAAAGT  
GGGCAGATACTTCTGTGACAAATGGCCAATTCAAGCCCTTTGGGCAGATGTTGCCCTTC  
TTCTTTCTTAAAAAGTCTTAGTACGATTGACCAAGTCAGAAAAAAAAGGAAGT  
AAAAAAGTTTTAATTAATTATGAGAGCTTTGGCATATTTCAAGAAGGGTGATATTCAC  
TCACTAATGATATCCCTAGGCCAGAAATCCAAACCGACGATGAGGTTATTATCGACGTCT  
CTTGGTGTGGGATTTGTGGCTCGGATCTTCACGAGTACTTGGATGGTCCAATCTTCATGC  
CTAAAGATGGAGAGTGCCATAAATTATCCAACGCTGCTTTACCTCTGGCAATGGGCCATG  
AGATGTCAGGAATTGTTTCCAAGGTTGGTCTTAAAGTGACAAAGGTGAAGGTTGGCGACC  
ACGTGGTCTGTTGATGCTGCCAGCAGTTGTGCGGACCTGCATTGCTGGCCACACTCCAAAT  
TTTACAATTCCAAACCATGTGATGCTTGTGAGAGGGGCAGTGAAATCTATGTACCCACG  
CCGGTTTTGTAGGACTAGGTGTGATCAGTGGTGGCTTTGCTGAACAAGTCGTAGTCTCTC  
AACATCACATTATCCCGGTTCCAAAGGAAATTCCTCTAGATGTGGCTGCTTTAGTTGAGC  
CTCTTTCTGTACCTGGCATGCTGTTAAGATTTCTGGTTTCAAAAAGGCAGTTCAGCCT  
TGGTTCTTGGTGCAGGTCCCATTGGGTTGTGTACCATTTTGGTACTTAAGGGAATGGGGG  
CTAGTAAAATTGTAGTGTCTGAAATTGCAGAGAGAAGAATAGAAATGGCCAAGAACTGG  
GCGTTGAGGTGTTCAATCCCTCCAAGCACGGTCATAAATCTATAGAGATACTACGTGGTT  
TGACCAAGAGCCATGATGGGTTTGATTACAGTTATGATTGTTCTGGTATTCAAGTTACTT  
TCGAAACCTCTTTGAAGGCATTAACATTCAAGGGGACAGCCACCAACATTGCAGTTTGGG  
GTCCAAACCTGTCCCATTCCAACCAATGGATGTGACTCTCCAAGAGAAAGTTATGACTG  
GTTGATCGGCTATGTTGTGCAAGCCTTCGAAGAAGTTGTTTCGTGCCATCCACAACGGAG  
ACATCGCCATGGAAGATTGTAAGCAACTAATCACTGGTAAGCAAAGGATTGAGGACGGTT  
GGGAAAAGGGATTCCAAGAGTTGATGGATCACAAGGAATCCAACGTTAAGATTCTATTGA  
CGCCTAACAAATCACGGTGAAATGAAGTAA

&gt;YAL060W, 382 aa (SEQ ID NO 20)

MRALAYFKKGDIIHFTNDIPRPEIQTDDEVIIDVSWCGICGSDLHEYLDGPIFMPKDGEC  
KLSNAALPLAMGHEMSGIVSKVGPVKVTKVVGHDVVDAASSCADLHCWPHSKFYNSKPC  
DACQRGSENLCETHAGFVGLGVISGGFAEQVVSQHHIIPVPKEIPLDVAALVEPLSVTWH

66/251

AVKISGFKKGSSALVLGAGPIGLCTILVLKMGASKIVVSEIAERRIEMAKKLGVEVFNP  
SKHGHKSIEILRGLTKSHDGFDSYDCSGIQVTFETSLKALTFKGTATNIAVWGPVKPVFP  
QPMDVTLQEKVMTGSIGYVVEAFEEVVRaihngDIAMEDCKQLITGKQRIEDGWEKGFQE  
LMDHKESNVKILLTPNNHGEMK

>YBL058W, 1772 bp, CDS: 501-1772 (SEQ ID NO 23)

TTATTTACATAGTGCCATTGAACACTTTTCAAGCAAACCTACGCCAGCCGGACGCAGACAA  
TAACACACACACAAAAGAGTCTTGCAGGTTCTCTTTTAGCGGCAACGGGCATGACACTAG  
GTATATTTGGTATGGGCATCACAGGGACATGTTGGAGCTGGGATGTTTCATCATTTCAGG  
AACTAAAGCAACGTCTGGAAGGCGTGCCAACAACGAATTTGTAGTGACAAACATGCCTC  
TGGATAAAAGAAGCCAGCAAGTAGTGGACAGCTTAGTTAAGACACACAATTCATCTCTTT  
GTAAATAGTGTATACCATAGTAGTAGTTTCAATAATATATCCACTACTTATATGTGTT  
ACCCGCATTAGAACTCTTATTGGTGGCGAAAATCGATGGCAATAAAGAACGGAAGGGGTT  
TAATAGTTGTATGCTTAACATATTTTCGATTTAAATATATAAGAAACGTCGGTAGCACAA  
AATTAAGTTCATTATTTAGGTATGGCGGAAATACCTGATGAAACCATCCAGCAGTTTCATGG  
CATTGACCAATGTGTGTCGATACATAGCCGTTCAATATCTCTCTGAATTTGGAGATTTAA  
ATGAAGCACTAAATTCCTATTATGCTTCTCAAACGGATGACCAAAGGATAGAAGAGAGG  
AAGCACATTGGAACAGACAGCAGGAGAAGGCCCTCAAGCAAGAAGCCTTCTCCACCAACT  
CTTTCGAATAAAGCCATAAATACGGAGCACGTTGGTGGGTATGTCCAAAACAGGATCCT  
CACAAGGTAGCAACGAGTACTTGAAGGAAAGGTTCTACCTCTCCTGAACCAACCAAGG  
GTAGTAGCCGCTCTGGAAGTGGTAACAACCTCCAGGTTTATGAGCTTTTCGGATATGGTAA  
GAGGTCAAGCTGATGATGACGATGAAGATCAACCGAGAAATACTTTTGCTGGTGGTGA  
CATCCGGCTTAGAGGTTACAGATCCTTCAGATCCTAATTCATTACTGAAGGATTTGCTGG  
AAAAAGCGAGAAGGGGTGGTCAAATGGGCGCTGAAAACGGATTCCGTGATGACGAAGACC  
ATGAAATGGGTGCCAATAGGTTTACTGGAAGAGGTTTTAGATTAGGGTCAACCATCGACG  
CAGCAGATGAAGTCGTAGAAAGACAACACTTCACAATCACAACGTAGACCAGAAAAAGTCA  
CAAGAGAAATTACATTTTGAAGGAAGGTTTTCAAGTGGCCGATGGTCCGCTTTATCGCT  
ATGATGATCCTGCGAACAGTTTCTATTTGAGCGAGTTAAATCAAGGGAGGGCTCCATTAA  
AGCTCTTAGATGTGCAATTTGGACAAGAAGTTGAAGTTAATGTATATAAAAAATTAGATG  
AGTCTTATAAAGCTCCGACGAGAAAACTGGGCGGTTTTTCAGGCCAGGGCCAAAGACTAG  
GATCTCCTATCCCGGGTGAATCGTCACCTGCGGAGGTTCCAAAGAATGAGACACCCGCTG  
CTCAGGAACAACCCATGCCGGAATGAGCCAAAACAAGGCGACACCTCCATCCAAATTA  
GATACGCAATGGCAAAAGAGAAGTTTTGCACTGCAATTCACAGATACAGTAAAGTTTTT  
TGTATGAGCATGTGACATCAAATGCGAACACTGACCCATCGAGGAATTTACCTTGAATT  
ATGCCTTTCTATCAAACCAATAAGCAACGATGAGACAACATTGAAGGACGCTGATCTGC  
TGAACCTCCGTTGTCTGCGTCAAAGATGGGCATGA

>YBL058W, 423 aa (SEQ ID NO 24)

MAEIPDETIQQFMALTNVSHNIAVQYLSEFGDLNEALNSYYASQTDDQKDRREEAHWNRQ  
QEKALKQEAFTSNSSNKAINTEHVGGLCPKPGSSQGSNEYLKRKGSTSPPTKSSRSRGS  
GNNSRFMSFSDMVRGQADDDDEDQPRNTFAGGETSGLEVTDPSDPNSLLKDLLEKARRGG  
QMGAEENGFRDDEHHEMGAANRFTGRGFRLGSTIDAADDEVVEDNTSQSQRRPEKVTREITFW  
KEGFQVADGPLYRYDDPANSFYLSLNQGRAPLKLDDVQFGQEVENVYKKLDESYKAPT  
RKLGGFSGQGQRLGSPFPGESSPAEVPKNETPAAQEQPMPDNEPKQGDTSIQIRYANGKR  
EVLHCNSTDTVKFLYEHVTSNANTDPSRNFNLNYAFPIKPISNDETTLKDADLLNSVVVQ  
RWA

>YBR039W, 1436 bp, CDS: 501-1436 (SEQ ID NO 41)

TTGAGATTTTCCAAGTAGTAACCTCATCTTCTGAGTGTGCTATCAAATACATACTAAGGA  
GAATAAACTCTTGTTATTACGTATTCTTCATCCTTATGGGTAGAGAGCGCACTGTTTGTAG  
TACATTTTCTAGACGTCGAAACGTAGAGCAATTTGTCGATAAAACAAAAAAGTAAGAA  
GATATATGAATAGGACGTGTCGCTAGAACTAGTAAGTATATGATGGAGATATAATAAGTG  
AATTATTCGATATTTAATGAACGTTCTCATTTATTTGGAAGAAATGTTTATCACGTGATG  
GAGAACCAATGAGCGGCGAGTAACACGCGAGGAACCCGACCGCAATAACGATTAAAGA  
AGGCCCGGAAGGGAGATGCTTAAATGATTATCACTCAGTTAAAAAGACAAATAAGAAAC  
TATTGAGACTGAACCGTTTTGGTTAATTTACAGGTGGAACAATTGAAGACGAGCAGTAAA

67/251

CATTATTTTATTTAGTAGTCATGTTGTCAAGAATTGTATCAAACAATGCAACACGCTCCG  
TAATGTGCCACCAAGCGCAAGTGGGTATTCTTTATAAGACTAACCAGTGAGAACTTATG  
CTACTTTGAAAGAAGTGGAAATGCGTTTGAAATCTATCAAAAATATTGAGAAGATCACAA  
AAACTATGAAGATTGTTGCATCTACAAGATTGAGTAAAGCTGAAAAGGCTAAAAATTTCCG  
CAAAGAAGATGGATGAAGCAGAGCAGTTGTTTTACAAGAACGCCGAAACCAAAAATTTGG  
ATGTTGAGGCTACTGAAACAGGTGCTCCTAAAGAGTTGATTGTTGCTATCACCTCTGATA  
AGGGGTTGTGTGGTTCTATCCACTCTCAAATTGGCTAAAGCTGTGAGAAGACATTTGAATG  
ATCAACCAACGCCGATATAGTCACATTTGGTGATAAAAATTAATAATGCAGCTATTGAGAA  
CCCATCCTAACAACATTAAATTTGTCTATTAAATGGAATTGGTAAAGATGCCCCAATTTC  
AAGAATCTGCTTTGATTGCCGATAAGTTATTGAGTGTCATGAAGGCCGGCATTACCCAA  
AGATTTCCATTTTCTACAATGACCCAGTGCTTCCCTATCTTTTGAACCATCTGAAAAAC  
CGATCTTTAACGCCAAGACCATTTGAACAATCCCCATCATTCGGCAAATTTGAGATCGACA  
CGGACGCAAACGTTCCAAGAGATTTGTTTGAATATACTTTGGCTAACCAAATGTTGACAG  
CAATGGCTCAAGGTTATGCTGCTGAAATTTCCGCCAGAAGAAACGCTATGGATAACGCTT  
CCAAGAATGCCGGTGATATGATCAATCGTTACTCTATCTGTACAAACAGAACAAGACAAG  
CTGTCATTACTAATGAAC TGGTTGATATTATTACTGGTGCTTCCTCTTTGGGATGA

&gt;YBR039W, 311 aa (SEQ ID NO 42)

MLSRIVSNNATRSVMCHQAQVGILYKTNPVRTYATLKEVEMRLKSIKNIEKITKTMKIVA  
STRLSKA EKAKISAKKMDEAEQLFYKNAETKNLDVEATETGAPKELIVAITSDKGLCGSI  
HSQLAKAVRRHLNDQPNADIVTIGDKIKMQLLRTHPNNIKLSINGIGKDAPTFQESALIA  
DKLLSVMKAGTYPKISIFYNDPVSSLSFEPSEKPIFNAKTIEQSPSFGKFEIDTDANVPR  
DLFEYTLANQMLTAMAQGYAAEISARRNAMDNASKNAGDMINRYSILYNRTRQAVITNEL  
VDIITGASSLG

&gt;YBR062C, 848 bp, CDS: 501-848 (SEQ ID NO 45)

CCATTTTGGTGACCAACTCTCCTACCCGAATTACTGTGATGATATATACTCTTCGTTTTTC  
TAGTAATGGCTTCATTTTGCCTAAGTTGGTCAAATTTGTTGTGGGCGGCTTTTGTTTGCA  
CCGAGGAGCGCTCAGTTCGTTATAATACCAGTTTTGCCACTCCTAAACTACTAAAGAAAT  
AATAGAAAAGATATATTCATCAAACATAATCACAAATCAAAAAATGTCTACATATGAAGGT  
ATGTAATGATATATATGAAGTAAGTTCCCCAAAGCCAAATTAACCTAACCGAATTTTAATC  
TGCACCTCATCATTTAGATTAGAGGAACATGGAAATACAACAAAAC TCAAGGGATTACCAAGA  
AGTAGGAGGAAC TTCACAGGAGGAGCAGAGAAGACAGGTCAAGATCCCAACTGCAAGGTC  
TATTTCAAACCTTTGGTAACACCAGTGGTGAGGGTGATGCACATTCAGATTCAACACTAC  
TTTTACGATTATATCGCAAATGCTTCCAGAATCATTTACAGGAAGAATGGTTGCAAGAAA  
TGGATAAAGGCAAGAGTGCAGGCTGTCTTGATACTTTTGCAGCCTCTTTACCACGAATCA  
ATAAAAAAAGCTCAAAGCAACTGACAAC TGTCCATTTGTTACACTAATTATTTAGAAG  
ATGAGTACCCCTTAGTAGTTGAATTACCTCATTGCCATCATAAGTTCGACTTAGAGTGT  
TGTCTGTCTGGCTATCTCGAAGTACAACATGTCCATTATGCAGAGATAATGTTATGGGCC  
ACCGAATCATTAATGAGATTGATACAAC TGAAGCAGAACTGGAAGAAGATTGGGGTATGT  
ACGGTTAA

&gt;YBR062C, 115 aa (SEQ ID NO 46)

MLPESLQEEWLQEMDKGSAGCPDTFAASLPRINKKKLKATDNC SICYTNYLEDEYPLVV  
ELPHCHHKFDLECLSVWLSRSTTCPLCRDNVMGHR IINEIDTTEAELEEDWGMYG

&gt;YBR101C, 1373 bp, CDS: 501-1373 (SEQ ID NO 49)

AATGATGAAATGTTATCCCCAGGGTCCATTAAAGTCATCCAGAAAACAGATAGATGGATTG  
AAGGCCGTAGGTTTGGATTTTGTCTACAAATTTGGACGAGTTTATCAAAAAGAACAGTGAT  
AAAATTCGCTAAACAAGATCACAGAAAATAAACCTCACTTCAATATATATGATGTGTAGG  
TAGGGTATATACTTATACCACTGCTGTGACAGTGTACTAACCTATTTCTATTTTGTAG  
GTAAGCTTTTTCAGCTACTGGTTGGTCAAGTTGGGCCCTATTAAGGTTGTAATCAGCTTAT  
TCGTTTGAATGATATACCTCTTGGACTGGAATCTTCTGGAAGTTTTTTGGAGGTTAGAA  
AAGAGGAAGGCATCTCGCGCTGACAGAAATTTGCTTATAAACCAGCGATTGGCTATATCT  
AAAAGAGCACTCATCGTCAGTCAGAAAGCCATTACCTTTCAACGAAAGAGTAAAATAGAA  
AAAAAACACATACATAACTATGGAAAAGCTATTACAGTGGTCTATTGCGAATTCTCAAG



68/251

GGGACAAAGAAGCTATGGCTAGGGCCGGCCAACTGATCCTAAATTGCTACAGCAGTTAT  
TCGGTGGTGGTGGTCTGACGATCCAACCTTAATGAAAGAATCCATGGCTGTTATTATGA  
ATCCGGAGGTTGACTTAGAAACAAAACCTCGTTGCATTTGACAACTTTGAAATGTTGATTG  
AGAACTTAGATAATGCTAATAATATCGAAAATTTAAACTGTGGGAGCCATTGTTGGATG  
TTCTTGTTTCAGACGAAGGATGAAGAACTACGTGCTGCTGCTTTATCCATTATTGGAACGG  
CTGTGCAAAACAACCTTGGATTTCGCAAAATAATTTTCATGAAATACGACAATGGTCTGCGAA  
GCCTTATCGAAATAGCTAGTGACAAGACAAAGCCACTCGACGTGAGAACAAAAGCTTTTT  
ACGCACTATCTAATCTAATAAGAAACCACAAAGATATCTCAGAAAAGTTTTTCAAATTAA  
ATGGGCTCGACTGCATAGCACCTGTATTAAGTGATAACACCGCCAAACCAAACTGAAAA  
TGAGAGCCATTGCCTTATTGACCGCATATTTGTCATCTGTTAAGATTGATGAAAATATAA  
TCAGTGTGCTGAGAAAGGATGGAGTAATTGAAAGTACGATTGAGTGCCTGTCTGACGAGA  
GTAACCTGAACATCATAGATAGAGTTCTGTCTTTTCTCTCTCACCTGATATCTTCCGGAA  
TAAAATTTAATGAACAGGAATTGCACAAATTGAACGAAGGTTACAAACATATCGAGCCTC  
TAAAGGACAGACTTAATGAAGACGATTATTTAGCCGTAAAGTATGTATTATGA

>YBR101C, 290 aa (SEQ ID NO 50)

MEKLLQWSIANSQGDKEAMARAGQPDPKLLQQLFGGGPDDPTLMKESMAVIMNPEVDLE  
TKLVAFDNFEMLIENLDNANNIENLKLWEPLLDVLVQTKDEELRAAALSIIIGTAVQNNLD  
SQNNFMKYDNGLRSLIEIASDKTKPLDVRTKAFYALSNLIRNHKDISEKFFKLNLGLDCIA  
PVLSDNTAKPKLMRAIALLTAYLSSVKIDENIISVLRKDGVIESTIECLSDENLNIID  
RVLSFLSHLISSGIKFNEQELHKLNEGYKHIEPLKDRLNEDDYLA VKYVL

>YBR139W, 2027 bp, CDS: 501-2027 (SEQ ID NO 55)

GGAGGAGTCAAGGGCCTGGAAAGTACGGATCCTGTAGAAATATCACTGGCAATTATACTG  
AGTTTATTGTTGGTGTGCTATTTCATATTTGAGCTGGTATTGGACGAAAGCAAGGATAAT  
GAGTTTGTGTCTACTGACTCCAACACCCTAGGCTGGATTTGATCTTTCTCCATCCTTTAA  
TTTTAACCTTTTAATTAGTGGTTGGATCAAGTTTTTCGAGACTATTCCAATCTGTGACTTG  
TTGGATAAATAGTTTTTGAATCGTTTAGTATAATCCTTTTTTCTAAAAGTGCTTAGAGTT  
CTCTAAGATGTTCTTGTTTACAATGTGAGCGATTTAGGAAATTTCTAAAATGGCCGAG  
GCGGCGCTAGCATTCTACGAAAGGTGAGATAACGCTTCGTTATCGAAAATGTCAGGGGA  
CAGGGGTTATATAAGAACGAAAATTGTCATCCTGCATTTTTTCTTTAAAACAGCTATACA  
AAAAGTGATACCGACATACAATGAAGTATCTAAACTTAGTTTTCTGTGCTTCAGCTTCTTA  
TTAGCATCAAATACGCCTCATTTCGGCCGAGCCTTTTTCTCTTTTTGAAGATGATACCACCT  
TTGCCAATTTGGATAAACAGCTAAAGCTTCCACAGAATACACAGCAAACCTTAAATTGG  
ACCGTTTGAATCACGATGATCCGCTGTTTACAACCTTTTATTCTTCTGTGGACACAGATT  
ACAGTTTGAGACTTAGAACAGTAGATCCTTCTAAACTAGGAATTGACACCGTAAAACAAT  
GGTCGGGTTACATGGACTATAAGGATTCCAAACACTTTTTTTACTGGTTTTTTGAAAGTA  
GGAACGATCCTGCTAACGACCCAATTATTCTTTGGTTAAATGGTGGACCTGGTTGTTCCT  
CGTTTACTGGGTTGCTATTTGAACTAGGCCCTCATCAATTGGCGCCGATATGAAACCAA  
TCCACAATCCCTATTCTTGAATAATAACGCTTCAATGATCTTCTTAGAACAGCCACTCG  
GAGTCGGCTTTTTCTATGGTGATGAAAAAGTCTCCTCTACAAAATTAGCAGGCAAAGATG  
CGTACATTTTCTGGAATTGTTTTTTGAAGCTTTTCTCATTTACGCTCCAACGATTTCC  
ACATTGCAGGCGAATCCTATGCAGGACATTATATCCCTCAAATTGCACATGAGATCGTTG  
TCAAGAACCCTGAAAGAACGTTCAATTTAACTTCAGTTATGATTGGTAATGGTATCACAG  
ACCCTTTGATTCAAGCAGATTATTATGAACCAATGGCATGCGGGAAGGGGCTATCACC  
CTGTTCTCTCATCAGAAGAATGTGAGAAAATGAGTAAAGCTGCAGGTCGTTGTCTGAGGT  
TGAACAAGTTATGTTATGCTTCTAAATCAAGTTTACCATGCATAGTCGCCACTGCTTACT  
GTGACTCTGCACTTTTGAACCGTACATTAACACAGGACTCAACGTCTATGACATTAGAG  
GGCCCTGTGAAGATAATAGTACTGATGGTATGTGTTATACAGGTCTCCGCTATGTGACACC  
AGTATATGAATTTTCTGAAGTTCAAGAAACGCTAGGGTCCGACGTGCATAATTATTCTG  
GCTGTGATAATGACGTGTTACCGGATTTTTGTTTACGGGCGATGGAAGTAAACCATTTTC  
AACAATATATTGCTGAATTATTAATCACAACATTCCGGTATTAATATATGCGGGTGATA  
AGGATTATATTGTAATTGGCTGGGAAACCATGCTTGGTCCAATGAGTTGGAATGGATCA  
ATAAACGTAGGTATCAGAGAAGGATGTTAAGACCATGGGTGAGTAAAGAAACAGGTGAAG  
AGTTGGGACAAGTCAAGAACTATGGCCCTTTTACCTTTTTGAGAATATACGATGCCGGTC  
ATATGGTGCCCTATGATCAACCGGAGGCAAGTTTGGAAATGGTCAACAGTTGGATTTCG

69/251

GTAATCGTGCTTTTTTCGGATCTTCCACCTTGAAAATGCTAGTTAG

&gt;YBR139W, 508 aa (SEQ ID NO 56)

MKYLNLVFLVQLLLISIKYASFGRAFSLFEDDTTFANLDKQLKLPQNTQOTLKLDRNLHDD  
PLFTTFISSVDTDYSLRLRTVDPSKLGIDTVKQWSGYMDYKDSKHFFYWFFESRNDPAND  
PIILWLNGGPGCSSFTGLLFELGPSSIGADMKPIHNPYSWNNNASMIFLEQLGVGFSYG  
DEKVSSTKLAGKDAYIFLELFFFAFPHLRSNDFHIAGESYAGHYIPQIAHEIVVKNPERT  
FNLTSVMIGNGITDPLIQADYYEPMACGKGGYHPVLSSECEKMSKAAGRCRRLNKL CYA  
SKSSLPCIVATAYCDSALLEPYINTGLNVYDIRGPCEDNSTDGMCTGLRYVDQYMNFP  
VQETLGSVDVHNYSGCDNDVFTGFLFTGDGSKPQQYIAELLNHNIPVLIYAGDKDYICNW  
LGNHAWSNLEWINKRRYQRRMLRPWVSKETGEELGQVKNYGPFTFLRIYDAGHMPYDQ  
PEASLEMVNSWISGNRAFSDLSTLENAS

&gt;YCL052C, 1751 bp, CDS: 501-1751 (SEQ ID NO 67)

TGCACATGTTGAGTATGCGTATTGGGCATTTTCCTATTCTGAGAAGGAGTATGAAATAAT  
TGCCGAGGGTTT CAGAATGCTCTTTTAGAAAATAAAATGAATGTAAATAGTTGGAATGTAT  
CTTTAAGTAGACAAATGCAGGTAAGTTT TAGTGGCCTTTGCGGATTAACAGTATGCTCTT  
AGTGCAAAACACGAAAAGAGCTCCCAATCTTTGAACACAATCGACCACGGAGGAACAATA  
CACGTAGAAGGGGATAACTAAAACCTTTGTCGTGCAAGAGTATTGGAGGACACACTAACAG  
CAGAACTTTGCCTTCTTAACTCTTGTTTATGATTGCTTGAAGTATTACACATGTAATAAA  
AGATGATTATTTTTTTTTTCTTAAAAAAGTTCTTTCTTTGAAGATCCCCCTGATAAAA  
AAGATCAAATAATGGAAACGCTAATCATAATCAAATCGGGAGGAGAATAAACGCAAGAAG  
TGTGCGTTTTCTAGCTGAGTAATGGTGACAAGACATAGAGTGACTGTACTCTACAATGCCC  
CTGAGGATATCGGTAATCATATGCGCCAAAATGACACTCATTGACTGTTCGTGGAGGTT  
CTGGTGTGGTTTTACAACAAAGGTGGCTATTAGAGAGGACTGGAAGCTTGGATAAATCCT  
TTACGAGAATCACTTGGAGGCCCAGAGCGGACTTGGCTAGAAGTTTAAGCGTTATAGAAA  
ATGAACTGAGTGTCTGGCTTTT CAGTTTACTCAAATTCCTTCGGATGTGCCGAAAGGTTTA  
TTACTAACCCAGTCTACAATTCATTTACAGTGAGAAGTTTGACATAGAGCAGTACTTGC  
CTCCCGAAGTAGATTGAATCTGTCATGGAATCCAGAAGATTTTACATATGATATATCAG  
TGGAGCCACACAAATCCAAATTGTTGAATATCGTCTGTTGAAACAGGGTGAAGAATTTA  
CAATTGCAAGAGTGAAAGATGAGAACTCGAAGTAGGTGTATTCTTTGTGGATGCAAGTG  
ATGAAAGATGTGAGAAACATCCTTATTGTATATAAACAGGGCCATATCGCATACAATCACT  
CGACGACTACGACATCACTATATCTGAATGAACCTATCGGTTTGCATCCAAAAATCATGA  
TTGATCTCACAGATTTTGAAGAACGCCCTAAATGCATGTATCTAATGCACCTGCAATTGC  
CGTTAGAATTATTTATCGATAAATCCAATCCTCTCCCTTACTACTTTTTTGGAGAAGACG  
ACTTAGAATTACCAGAATACTCTCTTCGAGATAAGGCATGGGGTTCTGAAAGTATCTTTG  
AATTGAAAGCCGGCACAATGAATGAAGTGACATTCGATACTAGATATATTGAGCCTTCTA  
ATAATAAAGGGGATAAATTAGAAGTTTCATTTGATCCAGAAGTTATATTAGCCTGCGACA  
CAGGTGACAATAAAGTTTCCCGTAATCCATTTTATAAAAAAGGCTTAGGATATGAATCTC  
TCTTTACAGACGATACTACATTCGCCCATTTGAACTCGACAACCTTCTTAGTACCAATTC  
CAAGGCCTGACACAAAGGATTATTCGAAGATCAAAAATGGTACGTTACTATGCTTACTCA  
TCTCCATCATATACATTTTCTCCAAGGTATTTGGTAACAACAAGAAGAAAAGATCAGTAA  
AACGGGAATAA

&gt;YCL052C, 416 aa (SEQ ID NO 68)

MVTRHRVTVLYNAPEDIGNHMRQNDTHLTVRGGSGVVLQQRWLLERTGSLDKSFTRITWR  
PRADLARSLSVIENELSGFSVYSNSSDVPERFITNPVNSFHSEKFDIEQYLPPEVDLN  
LSWNPEDFTYDISVEPTQIQIVEYRLLKQGEFTIARVKDEKLEVGVFVDASDESVDVI  
GGIRCNRWMDGKMERCQKTSLLYKQGHIAYNHSTTTTSLYLNPEIGLHPKIMIDLTD  
FERPKMYLMHLQLPLELFDKFQSSPLLLFGEDDLELPEYSLRDKAWGSEIFELKAGTM  
NEVTLHTRYIEPSNNKGDKLEVSFDPEVILACDTGDNKVS RNPFYKKG LGYESLFTDDTT  
FRHLNSTLLVPIPRPDTKDYSKIKNGTLLCLLSIIYIFSKVFGNNKKKRSVKRE

&gt;YCR009C, 1298 bp, CDS: 501-1298 (SEQ ID NO 73)

GTACAAAAATGATTACGAAAATATAGATGATGTAAGCAAGGTACGGTTATAAACAGTTAA

70/251

CATATAAGTTTACTTCACTTTTTTGTGACTCCTTTACTTGTCTTCCCTGCACTTTGATT  
TTACTTCAGAAAAAATAAGATATATGTTTCTGATAAAACTTTTAGGTTAGCGGAGAAGAT  
GTTGCCACGAATATCATGTAATTGAAAGGCAACGAAAGGCTATCGTTTGCCATTCATAA  
TGTGATTGCACTTGTCTTTTTTCATTGTAACAGACATGAAACGTTTCCTTTACGTCCCTAT  
GAATTTTTTGTGGCTGAACTGGGCGCTGCAGGGGCTGGACGATCCAAATGCGCGGATTTT  
GAACAATTATGAGAATCCGAATTAAAAGAAAGGGAAAACAAATTTAATAACAGGCAGACG  
TGAGAGAAGAAAAGGAAACGCTGTGATATAGAAAACATACAAATCCTATTATAAGAAGC  
CAGAAGAAAGCTGATACAAGATGAGTTGGGAAGGTTTTAAGAAAGCTATCAACAGAGCTG  
GTCACAGTGTGATAATTAAGAATGTCGACAAGACCATTGATAAAGAGTATGACATGGAAG  
AACGTCGTTATAAAGTTCTTCAAAGAGCAGGTGAGGCATTACAAAAGGAAGCCAAAGGTT  
TCTTGGACTCATTTGAGAGCTGTGACAGCATCACAGACTACCATTTGCCGAGGTCATCTCTA  
ACCTCTATGACGATTCAAAATATGTTGCTGGTGGTGGTTACAACGTTGGTAACATATTATT  
TGCAATGTGTTCAAGATTTTGATAGCGAAACTGTTAAGCAATTAGACGGGCCCTTAAGAG  
AAACCGTACTAGATCCAATAACAAAGTTTTTCGACGTATTTCAAAGAAATTGAGGAGGCCA  
TAAAAAAGAGAGACCATAAGAAACAAGACTTCGATGCTGCGAAGGCAAAAGTTTCGTAGAT  
TAGTGGACAAACCTGCTAAAGATGCCTCTAAACTGCCAAGGGCTGAAAAAGAATTGAGCT  
TAGCTAAAGATATTTTCGAAAATCTTAATAACCAATTGAAAAC'TGAAC'TACCACAGTTAG  
TTTCATTAAGAGTACCTTACTTTGACCCAAGTTTTGAAGCTTTAATCAAGATTCAGCTAA  
GGTTCGTGACTGATGGTTACACTCGTTTAGCGCAGATTCACAATATTTGGACCAACAAT  
CAAGAGACGACTATGCCAATGGGTATTAGACACTAAAATCGAAGAATATTAGGACAAA  
TGACAAGCCTAGATATTTGTGCGCTCGGGATAAAATAA

&gt;YCR009C, 265 aa (SEQ ID NO 74)

MSWEGFKKAINRAGHSVIIKNVDKTIDKEYDMEERRYKVLQRAGEALQKEAKGFLDSLRA  
VTASQTTIAEVI SNLYDDSKYVAGGGYNVGNYYLQCVQDFDSETVKQLDGPLRETVLDPI  
TKFSTYFKEIEEAIKKRDHKKQDFDAAKAKVRRLLVDKPAKDASKLPRAEKELSLAKDIFE  
NLNNQLKTELPQLVSLRPVYFDPSEALIKIQLRFCTDGYTRLAQIQYLDQQSRDDYAN  
GLLDTKIEELLGQMTSLDICALGIK

&gt;YCR010C, 1352 bp, CDS: 501-1352 (SEQ ID NO 75)

GAGCTCCGTGGAATAGGCGAGCGGCTGAGTGGTTCTCCAAGCTACGGTTTTTACGTGTAG  
CCCCATGTGAGCAAGCCAAACAAGGGCCCTTAAAGGCGTGACTACAAAAGGGGCGGGTT  
GGAAGGTCATCTGCAGCGAGATACGAAAAGATTTTTTGCCAGATTTGCGGTTGGGCGGCT  
ATTTCCGGTATTGTTGGGGTAACAAACGTTGGGGAAGACTGCATTTTCTTACAGCTTTTTT  
TCGTTATCGCGGGTTGGGCGGCTATGGCGCCTTCTCCTCTGTACTCCAACCTGTCAGAGA  
CACCAAGCTGTATATAAAGCACCTTGGTTGGATCGTATTTCCCTGAGATCTTGCTATAGG  
TTCATTTTATATATCGTCCAATAGCAATAACAATACAACAGAACTACTAGCATCTGTTT  
ATAAGAAAAGGCAAATAGTCGACAGCTAACACAGATATAACTAAACAACCACAAAACAA  
CTCATATACAAACAATAATATGTCTGACAAGGAACAAACGAGCGGAAACACAGATTTGG  
AGAATGCACCAGCAGGATACTATAGTTCCCATGATAACGACGTTAATGGCGTTGCAGAAG  
ATGAACGTCCATCTCATGATTGCTTGGGCAAGATTTACACTGGAGGTGATAACAATGAAT  
ATATCTATATTGGGCGTCAAAAGTTTTTGAAGAGCGACTTATACCAAGCCTTTGGTGGTA  
CCTTGAATCCAGGGTTAGCTCCTGCTCCAGTGCACAAATTTGCTAATCCTGCGCCCTTAG  
GTCTTTCAGCCTTCGCGTTGACGACATTTGTGCTGTCCATGTTCAATGCGAGAGCGCAAG  
GGATCACTGTTCCCTAATGTTGTGCTCGGTTGTGCTATGTTTTATGGTGGTTTGGTGCAAT  
TGATTGCTGGTATTTGGGAGATAGCTTTGGAAAATACTTTTGGTGGTACCGCATTATGTT  
CTTACGGTGGGTTTTGGTTGAGTTTCGCTGCAATTTACATTCCCTTGGTTTGGTATCTTGG  
AAGCTTACGAAAGACAATGAATCTGATTTGAATAATGCTTTAGGATTTTATTTGTTGGGGT  
GGCCCATCTTTACGTTTGGTTTAAACGTTTGTAACCATGAAATCCACTGTTATGTTCTTTT  
TGTTGTTCTTCTTACTAGCATTAACTTTCTACTGTTGTCTATTGGTCACTTTGCTAATA  
GACTTGGTGTCAACAAGAGCTGGTGGTGTCTGGGAGTTGTTGTTGCTTTCATTGCTTGGT  
ACAACGCATATGCAGGTGTTGCTACAAAGCAGAATTCATATGTACTGGCTCGTCCATTCC  
CATTAACCATCTACTGAAAGGGTAATCTTTTAA

&gt;YCR010C, 283 aa (SEQ ID NO 76)

MSDKEQTSNNTDLENAPAGYYSSHDNDVNGVAEDERPSHDSLGIYTGDNNEYIYIGRQ

71/251

KFLKSDLYQAFGGTLNPG LAPAPVHKFANPAPLGLSAFALTTFVL SMFNARAQGITV PNV  
VVG CAMFYGGLVQLIAGIWEIALENTFGGTALCSYGGFWLSFAAIYIPWFGILEAYEDNE  
SDLNNALGFYLLGWAIFTFGLTVCTMKSTVMFLLFLLLALTFLLLSIGHFANRLGVTRA  
GGVLGVVVAFI AWYNAYAGVATKQNSYVLARPFPLPSTERVIF

&gt;YCR021C, 1499 bp, CDS: 501-1499 (SEQ ID NO 79)

ATCGAAAGCGTGCTTTGTAAAGATATTTGGTATGGCTAAAGTAAGCAAAGCCATATCCCG  
ATCCCGATCCCGACTCTTATTCGGATCCCTTCCGCCACATCCTGCATGTTTATTCGAATA  
CCAAATTAGCTCATCTTCGTTATTTTCATCATCCCTTTCTGCTATGGCAAGGACAAGTTTT  
TTTCTAGCATCTCATCGAAAACCTTCTCTCCCTAATTGGCCAAAGTTTTTCATATTCATC  
ATCAGTTAGAAAGTATAATATCAATCCCTTACCTCATTACAAGTTGTATCACACTAAAAA  
AATCATATATAAGTCTGTGAGAGTCTTCAATTATTTAGCGTAACACCTATTCACTTTCTA  
ATCTTGTTTCTTGTTTTTACATTCTGCAATACAACACAACAACAATATTAACCTCAATTA  
TTATTATTTATAATTACAAAAACAAAACAACAAGTTTGAGACTTTAATATCTTTTGATTA  
CTAAAAACAACAATTTCAAATGAACGATACGCTATCAAGCTTTTTTAAATCGTAACGAGG  
CTTTAGGGCTTAATCCACCACATGGCCTGGATATGCACATTACCAAGAGAGGTTCCGGATT  
GGTTATGGGCAGTGTTTGCAGTCTTTGGCTTTATATTGCTATGCTATGTTGTGATGTTCT  
TCATTGCGGAGAACAAGGGCTCCAGATTGACTAGATATGCCTTAGCTCCTGCATTTTGA  
TCACTTTCTTTGAATTTTTTGCTTTCTTCACTTATGCTTCTGATTTAGGTTGGACTGGTG  
TTCAAGCTGAATTTAACCACGTCAAGGTTAGCAAGTCTATCACAGGTGAAGTTCCCGGTA  
TTAGACAAATCTTTTACTCGAAATATATTGCCTGGTTCTTGTCTCGCCATGCCTTTTAT  
TTTTAATCGAGTTAGCCGCTAGTACTACTGGTGAGAATGACGACATTTCCGCCTTGGATA  
TGGTACATTTCGCTGTTAATTCAAATCGTGGGTACCTTATTCTGGGTTGTTTCGCTATTAG  
TTGGTTCAATTGATCAAGTCCACCTACAAGTGGGGTTATTACACCATTGGTGCTGTGCGTA  
TGTTGGTTACCCAAGGTGTGATATGCCAACGTCAATTCTTCAATTTGAAAACCTAGAGGGT  
TCAATGCACCTTATGCTGTGTACCTGCATGGTAATCGTTTGGTTGTACTTTATCTGTTGGG  
GTCTAAGTGATGGTGGTAACCGTATTCAACCAGACGGTGAGGCTATCTTTTATGGTGT  
TGGATTTATGTGATTTTGCCATTTATCCATGTTACTTGCTAATTGCAGTCAGCCGTGATG  
GCAAATTGCCAAGGCTATCTTTGACAGGAGGATTCTCTCATCACCATGCTACGGACGATG  
TGGAAGATGCGGCTCCTGAAACAAAAGAAGCTGTTCCAGAGAGCCCAAGAGCATCTGGAG  
AGACTGCAATCCACGAACCCGAACCTGAAGCAGAGCAAGCTGTCTGAAGATACTGCTTAG

&gt;YCR021C, 332 aa (SEQ ID NO 80)

MNDTLSSFLNRNEALGLNPPHGLDMHITKRGS DWLWAVFAVFGFILLCYVVMFFIAENKG  
SRLTRYALAPAF LITFFEFFAFFTYASDLGWTGVQAEFNHVKVSKSITGEVPGIRQIFYS  
KYIAWFLSWPCLLFLIELAASTTGENDDISALDMVHSLLIQIVGTLFWVVSLLVGLIKS  
TYKWGYTTIGAVAMLV TQGVICQRQFFNLKTRGFNALMLCTCMVIVWLYFICWGLSDGGN  
RIQPDGEAIFYGVLDLCVFAIYPCYLLIAVSRDGLPRLSLTGGF SHHHATDDVEDAAPE  
TKEAVPESPRASGETAIHEPEPEAEQAVEDTA

&gt;YDR073W, 1010 bp, CDS: 501-1010 (SEQ ID NO 91)

GTTAGCTTGCCCTGCATTTCCCATGCGTCTCGAATAGGAATTATTCAAGATGGATTATT  
GGCATTTACGAGTAACCAAGGATAACCCCGCTGTGCGTGAAACCACCCTCTTTTCACGTT  
TCTTCAAGGCCAGTGCAAACGCGAATAAACATATCTACGCTATATATAGATATGACGTTT  
CTCAAGCCAACAGAAGTAGATAAAGCAGCCAGGAGGGTAGAGAGTGTTCAAATTATAGCA  
AGCCTTCTTCTACCTGTTTTTTTTTGATGATTGTTTTGCCGGGTAACAATCGACTTTCGG  
GCAAATTTTTTTTCTTTTTTCTCCTAACAGTATATACGGAGTGAGAGAACAGACTTCCCA  
TAAAAGCATATTACGTGGGGTCGTAGTAAGATTGCCGTTTATGATACCTCTATTTCAGGG  
CTCAGAGCGCATCACGATCGGGAGTGTAATTCATGTGCATATAAGCAAAACACACAGA  
TTTCTTTTTTTCCAGAAAATGAGCAGTGAAATTGCCTACTCGAATACGAACACCAACA  
CTGAAAACGAGAACCGCAATACTGGCGCTGGCGTAGATGTAAATACAAATGCAAATGCAA  
ATGCAAATGCAACTGCAAATGCAACTGCAAATGCAACTGCAAATGCAACTGCAGAGCTGA  
ACCTCCCCACGGTCGATGAGCAAAGACAGTATAAGGTACAACCTGCTATTGCATATCAACA  
GCATATTACTTGCTAGAGTTATTTCAGATGAATAATAGTTTACAAAACAATCTACAGAACA  
ATATAAATAATAGCAATAACAATAACATCATCAGGATACAGCAACTTATATCTCAGTTCC  
TTAAAAGGGTTCATGCCAATCTTCAATGCATATCTCAGATAAACCAAGGAGTGCCCTCAG

72/251

CGAAACCACTGATCCTCACGCCTCCTCAGCTAGCCAACCAGCAGCAACCTCCACAGGATA  
TTCTTTCTAAACTCTATCTTCTCTTGGCAAGAGTGTTGAGATATGGTAG

>YDR073W, 169 aa (SEQ ID NO 92)

MSSEIAYSNTNTNTENENRNTGAGVDVNTNANANANATANATANANATAELNLPVDE  
QRQYKVQLLLHINSILLARVIQMNNSLQNNLQNNINNSNNNNIIRIQQLISQFLKRVHAN  
LQCISQINQGVPSAKPLILTPPQLANQQPPQDILSKLYLLLARVFEIW

>YDR178W, 1046 bp, CDS: 501-1046 (SEQ ID NO 105)

ACGATTAGGCGTCAAGTCCCTTAGACCCCAATGACAACAACACAGCCAACCGTATCATCGA  
GGAATTGTTGAAGTGAATAGATAAAAAAAAAACGCACCAAGTAAGTAAGTAAATAAAGAA  
TAAATAAAC'TATATGAGTAAACACCAAGCGAGGATGTTTCATGTGTCATCCGTGTTCTT  
GATGATCACATAACTGTAAAAGAATAATACGGCACGTAAATGTTATTTTAGAATATATA  
AACACCTTATGTGCCATAAGCATTTAGCCAAATCGCTGCTGTTTTTTTATTCCGGGGCAC  
CTTCGGAAGAACACAGGCGCAATTTAGTTATATAAGGAGAAGCCCTCGAGCGATCAGGGG  
ACCGACTGCGGATCGCTTTAAGGCAAAGATAGAAGGATAAAATATCTGCTTTTGGGAAGATAG  
TCGTATCTAAATTTCCCATTTCTGTTGTTTTCTTGATCTTTCCCTACGCTTTTCGACTTTCTTC  
CTACGCGCTTTTATAATAGCTATGATGTTGCCAAGATCCATGAAATTTATGACTGGAAGGA  
GAATTTTCCATACGTCCACAGTAAGGGCCTTCCAGTCTACCGCTAAGAAGAGCTTAAC'TA  
TCCCATTTTTGCCCCGATTACCCCAGAAACCAGGTGGTGTAGGGGCAC'TCCCAATGATG  
CCTACGTCCCCCCCCCTGAGAATAAATTAGAGGGCTCATACCCTGGTATATGGAAGAAAA  
TCTTTGCCCTTGTCGCTCGTTCCATTGGCTACGACGGCTATGCTGACAACCGGTCCGTAT  
CCACTGCAGCTGATTCTTTCTTTCTGTCATGCTTTTGGGATATTGTTACATGGAATTTA  
ACTCTTGTATCACCGATTATATTTCTGAAAGAGTTTATGGTGT'TTGGCACAAGTACGCCA  
TGTATATGTTGGGCC'TTGGTTCTGCGGTCTCCCTTTTGGGAATCTATAAACTAGAAACCG  
AGAATGATGGTGT'TGTTGGTTTAGTAAAAAGTCTATGGGATTCTTCCGAGAAAGACAACA  
GTCAAAAGATTGAAGCCAAGAAGTAG

>YDR178W, 181 aa (SEQ ID NO 106)

MMLPRSMKFMGTGRRIFHTATVRAFQSTAKKSLTIPFLPVLQKPGGVRGTPNDAYVPPPE  
NKLEGSYHWYMEKIFALSVVPLATTAMLTGPLSTAADSFVSVMLLGICYMEFNSCITDY  
ISERVYGVVHKYAMYMLGLGSAVSLFGIYKLETENDGVVGLVKSLWDSSEKDNSQKIEAK  
K

>YDR202C, 1556 bp, CDS: 501-1556 (SEQ ID NO 107)

GAAT'TCCAACCGGAAAT'TGCAAACAGCAGCAAT'TTCTCGTACCGATGAAGGGGAACATGG  
CCGT'TGTACCGAGGT'TCCATTGGCCGAGTATTAGCCAGGGCCCTAATACGTAAC'TCGGTA  
CGCTCTT'CAGCTTCTTTTCGCATAATCAACGTTCTTGT'TATGTAAC'TCACACGTTCCATG  
GCATCCGCCAACCTTGCTTCC'TTACCAAATATTAATGAGCCTAAGGTGTACATTGCCGCC  
GCAGGTAATATTAGCCACGACGTTGGCATTTCAC'TGGCAAAGTAGCTGTTGATCTCAGT  
AAAGATAACCTCAACATACTCTTTTACTTGTCTTTTTTGTAGCTAATTGCTTTTCTCCC  
CTTCTTTTCCACAAACCGCAACTATTTTTCTCTCAAAAGTTATATGAAGTATATATACTG  
AATGGAGCAATTCGGGGTTGAGTGAATTACAAAAT'TATAGTATCTGATCAAGCACACAGT  
GGAAGTGCTCGAAAAGCAATATGAGTGT'TGATT'TGTTTCCAAATGATAGATTTGGTGCAG  
AAGATAAATACGACAAC'TTAAGGATGCCGTAAAAGAATGCTCCTGGCTCATCGAAGAAA  
TCGTCAAACCGCAAT'TACCCAACATTATTGACAAC'TTTTCTAAATGCCTAGAGATGCTAG  
AGAGTGACCAAATATTCAAATGCCTGTATCTAATGGTATTCCCAACGAAAGTAACAAAC  
AAAACGACTCTCCGACGGTAAAGGGTGTTATCACAAAGACAAGGCCAATACATTGTTGACT  
TTCACATTGTTGTAGATTCCCACAATTTCAAAGGGGTAAACAAGTTATGTTCCGAATGA  
ATACGGGACTGAATTTCTTACTTATTCAATTCAGTAAGATAATGACGCACTTGAAAAATA  
TTTTGGAAATACTGAATCAACTTCAAGTAGCTACAGATGTCAGCGAATTCGTATCCAAAT  
TTGGCGTGGCCATGGAAC'TTTTGAACCATTCTCTAATACTTTTACAAAATCCTCCTAGAG  
ACCTGGTAT'TCCCAGAAGATAACAAC'TTTGCTATGAAGGAAATGTTCCAGGATTGTTACT  
CAGTCTGCGAATCCACAGCTCACATCCTAGGACTGGAAC'TTACGCTTTGTAGGAATGAGC  
TTTGCATAGAACTACGAAATCTAATTAAGGTGACTAAAAAACCTTGGTGCGAGATTGATA  
GTAAACTGGCAGGTCATTTTGGCACCAAATAAGAAATCAAGTGACAAATGAAAGAAACA

73/251

AAACTTTATCTAAGATCCTCTCAGAAAACGGTGTACAAGTCCAGGATTCACATTACTTA  
ACCACATAATTTCTTCTTTTCAAAGTGAAGCTATAACACTTCCAGAAGCTCAGGAATTAT  
TAAGAAGGGGCGTTACTTTTCGATAATAGGGTAGTCATGGAATGTGAAAAGTTAATAGTAT  
CTACAAGTGATCCAACCTTTGATCAGTATAAGCGCCAAATTGAACAGTCTCAAAGCTTCGA  
TGGCGAACCATCAAGCAAATTTGGTAGCTAGCAAACAGTTAAGTACATATAAGTAA

>YDR202C, 351 aa (SEQ ID NO 108)

MSVDLFPNDRFGAEDKYDNFKDAVKECSWLIIEIVKPQLPNIIDNFSKCLEMLESQIFK  
MPVSNIGIPNESNKQNDSPVKGVITRQGYIVDFHIVVRFPPQFQRGKQVMFRMNTGLNFL  
LIQFSKIMTHLKNILEILNQLOVATDVSEFVSKFGVAMELLNLSLILLQNPRLVFPED  
NNFAMKEMFQDCYSVCESTAHILGLELTLCRNELCIELRNLIKVTKKPWCEIDSKTGRSF  
CDQIRNQVTNERNKTL SKILSENGVQVQDSTLLNHIISFQSEAITLPEAQELLRRGVTF  
DNRVMECEKLIVSTSDPTLISISAKLNSLKASMANHQAANLVASKQLSTYK

>YDR256C, 2048 bp, CDS: 501-2048 (SEQ ID NO 115)

GGGAAGAACTAAGAGATGTTATGGCTCGGAGAGTTTTGAAAAGCGAAATAGATTCGCTGC  
AAGTTTGTGAAGAAACCATCGACAAGAATTACAAGGTTATTCTTGATGAAAAGCTGCTAA  
CTAATATTTTAAAGAGAAAGTTGACAGAGGAAGAAAAAGCTCTGTCAAACGTCCTTGCG  
TGAAGAAGTGAGCGGTTGTTCTAACCCTATTTAAAGCCGCAATTAGTAATGCAAAAAGT  
TGGCCGGAATTAGCCGCGCAAGTTGGTGGGGTCCCTTAATCCGAAAAAGGACGGCTTTAA  
CAAATATAAACTCCGAAAATCCCCACAGTGACAGAATTGGAGAAACAACAGTTTTGATA  
TCGCCATACATATAAAGAGATGTAGAAAGCATTCTTCACTGTAATGTCAAATCGTACAT  
TTGAATTTCTTGTAGGTTTATTTAAAAGGTAAGTTAAATAAATATAATAGTACTTACAAA  
TAAATTTGGAACCTTAGAAGATGTCGAAATTGGGACAAGAAAAAATGAAGTAAATTACT  
CTGATGTAAGAGAGGATAGAGTTGTGACAACTCCACTGGTAATCCAATCAATGAACCAT  
TTGTCAACCAACGTATTGGGGAACATGGCCCTTTGCTTTTGCAAGATTATAACTTAATTG  
ATTCTTTGGCTCATTTCAACAGGGAAAATATTCCTCAAAGGAATCCACATGCTCATGGTT  
CTGGTGCCCTTCGGCTATTTTGAAGTAACCGATGACATTACTGATATCTGCGGGTCTGCTA  
TGTTTTAGTAAATTTGGGAAAAGAACGAAATGTCTAACAAGATTTTCGACTGTGGGTGGTG  
ATAAAGGTAGTGCCGACACGGTTCTGATCCAAAGGGGGTTTGCCACCAAATTCACACTG  
AAGAAGGTAATTTAGATTGGGTCTACAATAATACACCGGTATTCTTTATCAGAGACCCTT  
CCAAGTTCCCTCACTTTATCCACACACAGAAGAGAAACCCACAAACCAACCTAAGGGATG  
CTGACATGTTTTGGGATTTCTCACCCTCTGAAAATCAGGTGGCCATTTCATCAAGTAA  
TGATCCTTTTTTCAGACCGTGGTACCCCTGCCAACTACCGTAGTATGCATGGTTATTCTG  
GTCATACCTATAAATGGTCCAATAAAAACGGAGATTGGCATTATGTGCAAGTTTCATATCA  
AAACCGATCAAGGAATAAAGAATTTGACCATAGAAGAGGCTACCAAATTTGCGGGATCCA  
ATCCAGATTACTGCCAGCAGGATTTATTTGAGGCTATTTCAGAATGGAACTATCCTTCCT  
GGACAGTTTATATTCAAACAATGACCGAACGCGATGCCAAAAAATTACCATTTTCAGTCT  
TTGATTTGACTAAAGTATGGCCTCAGGGGCAATTCCTTTACGGCGTGTGGGTAAGATTG  
TTTTGAACGAGAATCCACTGAACTTCTTCGCACAGGTGGAACAAGCTGCCTTCGCCCCCA  
GTACCACGGTTTCCTTACCAAGAAGCAAGCGCTGATCCAGTATTACAGGCCCGTTTGT  
CATATGCGGATGCTCATAGATACAGGCTAGGTCCCTAACTTCCATCAAATACCCGTAACT  
GTCCATATGCATCTAAATTTTCAATCCCGCTATCAGAGATGGACCGATGAATGTTAACG  
GCAACTTCGGCTCAGAACCTACATATTTGGCCAACGATAAATCGTACACGTATATCCAAC  
AGGACAGACCCATTCAACAACACCAAGAGGTATGGAATGGGCCAGCTATCCCTTATCATT  
GGGCAACATCCCCAGGTGATGTAGATTTTCGTGCAAGCAAGAAATCTCTACCGGTTTTGG  
GTAAACAACCTGGACAGCAAAAGAAGTTGGCATATAACATCGGCATTTCATGTAGAAGGCG  
CCTGTCCTCAAATACAGCAGCGGTTTATGATATGTTTGCTCGTGTTGATAAGGGACTAT  
CTGAGGCAATTAAGAAAGTAGCTGAGGCAAAACATGCTTCTGAGCTTTTCGAGTAACTCCA  
AATTTTGA

>YDR256C, 515 aa (SEQ ID NO 116)

MSKLGQEKNEVNYSDVREDRVVTNSTGNPINEPFVTRIGEHPLLLQDYNLIDSLAHFN  
RENIPQRNPHAHGSGAFGYFEVTDITDICGSAMFSKIGKRTKCLTRFSTVGGDKGSADT  
VRDPRGFATKPHYTEEGNLDWVYNNTPVFFIRDPSKFPHFHTQKRNPQTNLRDADMFWDF  
LTPPENQVAIHQVMILFSDRGTPANYRSMHGYSGHTYKWSNKNGDWHYVQVHIKTDQGIK

74/251

NLTIEEATKIAGSNPDYCCQDLFEAIQNGNYPSTVYIQTMTERDAKKLPFSVFDLTKVW  
PQQGFPLRRVGKIVLNENPLNFFAQVEQAAFAPSTTVPYQEASADPVLQARLFSYADHR  
YRLGPNFHQIPVNCPYASKFFNPAIRDGPMNVNGNFGSEPTYLANDKSYTYIQQDRPIQQ  
HQEVWNGPAIPYHWATSPGDVDFVQARNLYRVLGKQPGQQKNLAYNIGIHVEGACPQIQQ  
RVYDMFARVDKGLSEAIKKVAEAKHASELSSNSKF

>YER103W, 2429 bp, CDS: 501-2429 (SEQ ID NO 145)

ACTATTGTCACTTCTCCATTGAGATTCGAAAAACCCCTCGGGTCTTGTTAGAACTAAATT  
ACGTTTCATAGGGGTGGGATTTATATTGTAATTCGCGAGGTTTACACGAAAGATATCTCA  
ACTCTAGCCGCACATCCATTCCGGTATGTACTCTCCACCATTGGGTATTATAGAATGTA  
ATAGGTTTCAAAGCGGATATCTTTTGGCCGGTGAGTTGTTACTTTTTCATTTCGAGCAATG  
AAGTACATTCTAGAAGTTCCTAGAACCTTATGGAAGCACCAAGAAAAAGGAAGTTAAAC  
AAAACACTGATTCAATAAGCAAGGGGGGAAGCTCCTTAGTTTGACGACAGTAACAAAAATG  
TTCGTATAAATTGAACGAACTCAAGCCAATAAAGGACTTTTCAGAGGCCATCTCTTCT  
TTCCTCCACAACCTTTCGAATAAAAAACCCTAATAAAAAAGTAAATAACAAAAACAAGAAAA  
AAATAAACAAAAACAATAATCATGTCAAAAGCTGTTGGTATTGATTTAGGTACAACCTATT  
CATGTGTTGCTCATTTTGCAAACGATAGGGTTGAAATTATCGCTAACGATCAAGGTAATA  
GAACGACGCCCTTCTTATGTGGCTTTTACTGACACAGAAAGGCTAATTGGTGACGCTGCGA  
AGAATCAAGCTGCGATGAACCCACATAATACAGTATTCGATGCTAAGCGTCTGATCGGAC  
GTAAATTCGATGATCCAGAAGTGACGAACGATGCTAAGCATTACCCATTCAAAGTGATTG  
ACAAGGGAGGTAAACCGGTAGTGCAAGTGGAATATAAAGGCGAGACAAAGACATTTACTC  
CAGAAGAAATTTCTCAATGATCTTGACAAAGATGAAGGAGACTGCTGAGAACTTTTTAG  
GAACAGAAGTGAAAGATGCTGTAGTAACGGTTCAGCCTATTTCAACGATTCACAAAGGC  
AAGCAACAAAAGATGCCGGTACAATCGCGGGCTTGAACGTTCTTCGTATCATTAATGAAC  
CTACAGCTGCCGCTATTGCGTATGGGCTGGACAAGAAATCGCAGAAGGAGCACAAACGTCT  
TGATCTTTGATTTAGGTGGTGGTACTTTTGTATGTCCTCTGCTATCCATAGATGAAGGTG  
TCTTTGAGGTTAAGGCTACTGCTGGTGACACTCACTTGGGTGGTGAAGATTTTCGATAGTA  
GGCTGGTTAACTTTCTAGCCGAGGAGTTCAAAGAAAAAATAAAAAAGGATCTAACAACCTA  
ACCAAAGGTCCTTAAGGAGGTTAAGGACCGCCGCTGAAAGGGCCAAGAGAACCTCTGTCTT  
CGTCTGCTCAGACATCTATAGAAATAGATTCAATTATTGAGGGTATCGATTTCTATAGCTT  
CCATTACAAGGGCAAGATTTGAAGAATTATGTGCTGATTTGTTTAGATCTACATTGGAGC  
CAGTGGAAAAAGTTTGGCTGATTCAAAATTAGATAAGTCACAAATTGATGAAATTGTAC  
TTGTTGGTGGTTCAACAAGAATTCCAAAAGTACAAAAACTGGTTTCTGATTTTTCATG  
GTAAAGAACCAAACCGTTCGATTAACCTGATGAGGCCGTCGCTTATGGTGTGCGGTAC  
AGGCTGCCATCTTAACGGGTGACCAGTCGTCGACGCCAAGATTTACTGTTGCTGGATG  
TTGCACCATTATCTCTAGGTATTGAACTGCAGGTGGTATTATGACAAAGTTGATCCCAA  
GAAATTCGACTATCCCAACAAAAAAATCGGAAGTGTTTTCCACCTACGCTGACAACCAAC  
CTGGTGTGTTGATACAAGTTTTTGGAGGTGAAAGGACAAGGACAAAAGACAACAATCTAC  
TGGGTAAATTTGAGTTGAGCGGTATTCCACCCGCTCCAAGAGGCGTACCACAAATTGAAG  
TTACATTTGATATCGATGCAATGGTATTCTGAACGTATCTGCCGTTGAAAAAGGTACTG  
GTAATCTAACAAGATTACAATTACTAACGATAAGGGAAGATTATCGAAGGAAGATATCG  
ATAAAATGGTTGCTGAGGCAGAAAAGTTCAAGGCCAAGATGAACAAGAAGCTCAACGTG  
TTCAAGCTAAGAATCAGCTAGAATCGTACGCGTTTACTTTGAAAAATTC'TGTGAGCGAAA  
ATAACTTCAAGGAGAAGGTGGGTGAAGAGGATGCCAGGAAATTGGAAGCCGCCGCCCAAG  
ATGCTATAAATTGGTTAGATGCTTCGCAAGCGGCTCCACCGAGGAATACAAGGAAAGGC  
AAAAGGAAC TAGAAGGTGTTGCAAACCCCATTTAGTAAATTTTACGGAGCTGCAGGTG  
GTGCCCCAGGAGCAGGCCAGTTCCGGGTGCTGGAGCAGGCCCCACTGGAGCACCAGACA  
ACGGCCCAACGGTTGAAGAGGTTGATTAG

>YER103W, 642 aa (SEQ ID NO 146)

MSKAVGIDLGTTYSCVAHFANDRVEIIANDQGNRTTPSYVAFDTERLIGDAAKNQAAMN  
PHNTVFDKRLIGRKFDDEPVTNDKHYFPKVIDKGGKPVVQVEYKGETKTFTPEEISSM  
ILTKMKETAENFLGTEVKDAVTVTPAYFNDSQRQATKDAGTIAGLNLVRIINEPTAAAI  
YGLDKKSQKEHNVLIFDLGGGTFDVSLLSIDEVFEVKATAGDTHLGGEDFDSRLVNFLA  
EEFKRKNKKDLTTNQRSLRRLRTAAERAKRTLSSAQTSIEIDSLFEGIDFYTSITRARF  
EELCADLFRSTLEPVEKVLADSKLDSQIDEIVLVGGSTRI PKVQKLVSDFNGKEPNRS

75/251

INPDEAVAYGAAVQAAILTGDSSTTQDLLLLDVAPLSLGIETAGGIMTKLI PRNSTIPT  
KKSEVFSTYADNQPGVLIQVFEGERTRTKDNLLGKFELSGIPPAPRGVPQIEVTFDIDA  
NGILNVSAVEKGTGKSNKITITNDKGRLSKEDIDKMVAEAEKFKAEDEQEAQRVQAKNQL  
ESYAFTLKNSVSENNFKEKVGEEDARKLEAAAQDAINWLDASQAASTEYKERQKELEGV  
ANPIMSKFYGAAGGAPGAGPVPGAGAGPTGAPDNGPTVEEVD

>YER150W, 947 bp, CDS: 501-947 (SEQ ID NO 149)

ATACGGGGGAAGAAGAAATATCATATTCAAAGCTAATTCATTGAAATTAGTGCTTGTCTC  
ATCTAGCCTTTAGTGCTTAATCTCTGGAGGAGCACATATGGGGTTAAAGCCATGCCGGGA  
CTGGGGGCCCCCTATCGGGGCTCGAACCCGAATCCCGCGAGTATTTATTTGAAGGTCCGGG  
ACGCAAGTTACCTAATCTGGTTAATTGATATCCCATTTAGGCGATGACGTTCCCTTCCCCT  
CACCCCTCGGCTTGTTAGAAGATCTATTGTTATAGCCTCCTCTGGAAGAATTTATGCCAG  
ATGAAGAAAAAACTTCTCGAAGTTCCCAGATGCCCAAATGAGGGCTTTCCATCCCTGTT  
AGCTGGAAGAGTGTAAGTATATCTATATAAAAAGTCGGCCTACTTTTGCCAGGTTTCGTCT  
TTCACTTGCACTCTCTTGATCTTACTTTCTACTCAAAAAGAATCCAATACACAAAAATAA  
AATCAGTACTATTACTAATAATGTTGTCTAACGCTAAGCTCCTTCTATCATTGGCCATGG  
CCTCTACGGCTCTCGGATTGGTATCTAATTCTAGTTCCCTCTGTAATCGTGGTACCATCAA  
GCGATGCTACTATTGCCGGTAACGATACAGCCACGCCAGCACCAGAGCCATCATCCGCCG  
CTCCAATATTCTACAACCTCGACTGCTACTGCAACACAGTACGAAGTTGTCAGTGAATTCA  
CTACTTACTGCCCAGAACCAACGACTTTCGTAACGAATGGCGCTACATTCACTGTTACTG  
CCCCAATACGTTAACAATTACCAACTGTCCTTGCACTATCGAGAAGCCTACTTCAGAAA  
CATCGGTTTCTTCTACACATGATGTGGAGACAAATTCTAATGCTGCTAACGCAAGAGCAA  
TCCCAGGAGCCCTAGGTTTGGCTGGTGCAGTTATGATGCTTTTATGA

>YER150W, 148 aa (SEQ ID NO 150)

MLSNAKLLLSLAMASTALGLVSNSSSSVIVVPSSDATIAGNDTATPAPEPSSAAPIFYNS  
TATATQYEVVSEFTTYCPEPTTFVTNGATFTVTAPTTLTITNCPCTIEKPTSETSVSSTH  
DVETNSNAANARAIPGALGLAGAVMMLL

>YFR033C, 944 bp, CDS: 501-944 (SEQ ID NO 155)

ATCGAGCCATTTCGGGTCGCTGAGTAAGCGACGGTCATCGGGCGCGCTCGTGACGATGA  
CAAGCGCGAATCACACAAGCATGCAGAGCAAGCACGGCGTAATCGATTAGCGGTCGCGCT  
GCACGAAGTGGCGTCTTTAATCCCCGCGGAGTGGAACAGCAAAATGTGTGCGCCGCGCC  
GTCCAAAGCGACACCGTGAGGCGCGCCTGCCGGTACATCCGTCACCTACAGCAGAACGT  
GAGCACGTGACCGTGACCAATGGGAAGCACGTTCCGGGCATATCGGACTGGGGCGCGCC  
TCCCCTGCGCGGTGCTTGTTATAAGAGGCGCTTTGCTGGAAGTGGCCACACCGGGTTT  
TCGAGATTAGGACCTACTCAGTCTTAAGGGCAGTATTGGTTGGCGCTTATTTGCACATAT  
TGTATACACGCACTCACATTAACAGAAGCACACATATACACTTACACCTACACACACGGA  
TAAAGAAAAAGAAATAGAAAATGGGCATGTTGGAAGTACTGGTGGTACTGGGAACAAC  
TAAAGATAACCGTTGTGCCTGTTGTGGCCGCGCCGAAGATGACGATAACGAGCAGCATG  
AAGAAAAGGCAGCAGAAGGAGAAGAAAAAGAAGAAAATGGGGATGAAGATGAGGATG  
AAGACGAAGACGAAGATGATGATGATGATGACGACGAAGATGAGGAAGAAGAGGAAGAAG  
TCACTGATCAGTTGGAAGATTTGAGAGAACATTTCAAGAACACGGAGGAGGGTAAGGCCC  
TTGTGCACCACTACGAGGAGTGTGCTGAGAGAGTCAAGATACAGCAACAACACCCGGCT  
ACGCGGATCTTGAACACAAGGAGGACTGTGTGGAGGAGTTTTTCCATCTACAGCACTATT  
TGGACACTGCCACGGCACCTAGATTATTTGACAAATTAAAGTAG

>YFR033C, 147 aa (SEQ ID NO 156)

MGMLELVGEYWEQLKITVVPVVAEAEDDDNEQHEEKAAEGEEKEEENGDEDEDEDEDEDD  
DDDDDEDEEEEEVTDQLEDLREHFKNTEEGKALVHHYEECAERVKIQQQPGYADLEHK  
EDCVEEFFHLQHLYLDTATAPRLFDKLG

>YGR086C, 1520 bp, CDS: 501-1520 (SEQ ID NO 175)

GTTGAATATTTACCAATTGGGAAAAAGAACTCGTATTTTCATTCCCCTTTTGGAAAGGGG  
TGGGGAGAGACTGTTGTTACGCCACGTCAATTATTATTTTTTCTTTGGCCCTGCGCTTGT  
CTTATAAAATCCGCAGCCGCTCTATTTTTTTTTTTTTTCGATTTTGGCCACAGGTC



76/251

ATATTGCAAAAACCGAATGGCCGCGCCCCCTCACGCACGGGACGGAAGAAGGGCGGCGT  
CCCCTGTTTTTCTGCTTTGGCTCATCTCTTTGGCTCCGACGGACGAAAGACGGGATTCCC  
CCTCCCGTGTCTTTTATAAATAACAAGTGCTCATTCTGCATCCTTCCTTGTTTCCCGTC  
GTTTGGGTACAATGCGTTGATTATCCCAACCCAAGAAAGAAAATTTGTCTCACATCTGCA  
TCTGCACATTTATTTACCTATACTTTTCCATTGTTAGCAGTATTGCAAAGTGAAGAATAT  
ATCAGCATCAAGTATATAGTATGCACAGAACTTACTCTTTAAGAAATTCAGGGCACCTA  
CCGCCTCTCAATTACAGAACCCACCGCCACCACCATCTACAACCAAAGGTAGATTCTTTG  
GGAAGGGTGGTCTAGCTTACAGCTTTAGGAGAAGTGCTGCTGGAGCTTTTGGCCCAGAAT  
TATCCAGAAAGTTGTCTCAATTGGTTAAGATTGAAAAGAATGTTTGGAGTCCATGGAAT  
TGACAGCCAACGAAAGACGTGACGCTGCTAAGCAATTGTCTATTTGGGGGTTGGAAAACG  
ATGACGATGTTTCCGACATCACTGATAAATTAGGTGTCTTGATCTATGAAGTTAGTGAAT  
TAGACGACCAATTTATCGATCGTTATGACCAATACAGATTGACTCTAAAGTCCATCAGAG  
ATATCGAAGGTTCTGTTCAACCATCTAGAGACCGTAAGGACAAGATCACCGACAAAATCG  
CCTACTTGAAATACAAAGATCCTCAATCACCTAAGATTGAGGTCTTGGAACAAGAATTGG  
TGCGTGCTGAGGCTGAATCTTTGGTCTGCTGAAGCTCAATTATCTAATATCACAAGGTCAA  
AGTTGAGAGCTGCTTTCAACTACCAATTTGACTCCATCATCGAACATTGAGAGAAAATTG  
CTTTAATCGCTGGTTACGGTAAGGCTCTCTTGGAATATTGGACGACTCTCCTGTCACTC  
CAGGTGAAACCAGGCCTGCTTACGATGGGTATGAAGCCTCTAAACAAATCATTATTGATG  
CTGAAAGCGCACTGAATGAATGGACACTAGACTCTGCCAAGTCAAGCCTACTTTAAGTT  
TCAAGCAGGATTACGAAGACTTCGAACCTGAAGAAGGCGAAGAAGAGGAAGAGGAAGACG  
GTCAAGGCAGGTGGTCCGAAGACGAACAAGAAGATGGACAAATTGAAGAACCTGAACAAG  
AAGAAGAAGGTGCTGTTGAAGAACATGAACAAGTCGGACACCAGCAAAGTGAGTCTCTTC  
CCCAACAAACAACAGCTTAA

>YGR086C, 339 aa (SEQ ID NO 176)

MHRTYSLRNSRAPTASQLQNPPPPSTTKGRFFGKGLAYSFRRSAAGAFGPESLRKLSQ  
LVKIEKNVLRSMELTANERRDAKQLSIWGLENDDDVSDITDKLGLVIYEVSELDDQFID  
LYDQYRLTLKSIIRDIEGVSQPSRDRDKDKITDKIAYLKYKDPQSPKIEVLEQELVRAEAS  
LVAEQLSNITRSKLRAAFNYQFDSIIHSEKIALIAGYKALLELLDDSPVTPGETRPA  
YDGYEASKQIIIDAESALNEWTLDSAQVKPTLSFKQDYEDFEPEEEEEEEEDGQGRWSE  
DEQEDGQIEEPEQEEEGAVEEHEQVGHQQSES LPQQT TA

>YGR197C, 2144 bp, CDS: 501-2144 (SEQ ID NO 185)

TCCAGTATGCCACACATTATGCCTTGACACCTAAAGCACATATTTTCGTTATTTTTCAC  
CACAATAGGTGGATCTCGAAAAGGATGGAAAATCAGGAAAAAGAAATGTTGAGAAAAAAA  
TAAACCGATTCCCGTTTAGTTTTCTCCTATTTCCGTGTATATGCGTGGTTATTCGTTTTC  
GAATCCTTTTATGAATGTCCGAGGAGGTGGTACAATCCGAAATAGACTAAAGAAAAGCGA  
AAGCCGTGAGTTTGTGTTGATGATAGATGACTCGCAGCTTTGTCATCAACGGGCCACCCTA  
TTCGAAGAAGGGAATGGAAAACGGACTGGCGTAGTCAATAAGCGTCTTCATATCTTAGCA  
TTGTTGAGAGATACATAGTGTACTCCATATCGTTCCTTTTTTTTTTGTATATATCAAGCCAC  
ATATCCTGTTTCTTTAATCTTTTATACGCCGTAAGAATCGGGTACTGACATAAGTGAAG  
TAGCCGTACAGAGAACAAATATGACTAAATCGGTTGGTGATGAAGAGTCACAGTACATTG  
AGGACCCTAGTTTTGTCAGCAGCAGCTGCATTTACTGGCGGCAGGGACGGGGTTTCGTACA  
GTAATCAGCGATTTGCTGAGGGTTCCGGCCATTCTTCTGACTTAGCAAAGTCATTAGAAG  
ACTATCGGCCTCCTGATGAAAAGCCGTCCTCATTGTCTGTCATCTGTGGGGGAAGGTGGCGCTA  
ATGAGGAAGAGAAGGGCGGTAACGACGGCGGTCCCTTGGAAGAATTCAAACAGGGCTTT  
TTTCTCCAAGACTGCGAAATCATAGGAAAAAGATTCTCTCGAAGTTTGTTTTGAACAAC  
TCTTCATTGCTTGTGTGTGTATCGCTCATATCGATTTACTGGGGTGCCTGTTACGGAA  
CAGATCGTTACTTTTTCAAAGTGAAAAATATTGTTGTATTGCAGGATGCGCCATCTAATA  
CTTCAGTTCAATCTATTTCCGCGATCATACCCTCATTGTTAGCGTCTGTCCCCGGGACAT  
GGCATATATACAACGCAACATCATTTTCATAGGAAATTTGGTACGACGAACTCCACCGAAA  
TTGACAGAAAGATAGTCGATTTAATTTACGATGAGAGATACTGGCTGGCGTTAAACGTTA  
AACCTAATGCTACAGACACTTTGTATAATTCTTTGATTAGCCAAGACGCAAACCTCGGAGT  
TCAATTCATCAATTTTTTTTTGAATCCGTGTTTGAAAGTGGTCGTGACCCATCGAGTGTTA  
AATCGACCATTCTACCACTCATGCAACAATTGGAGGTCCGCCTTCAGAAATATTACGTCA  
AGGAATATCTTCCCTCATTGATGAGCAACATCACTTCTAATGACAGAGATCTTAATATAA

77/251

ACATGGAGAACTGGGCGATTGCAGGACAGTTGTTGTTCACCTACAACGATTATCGTCCCT  
TTGCTGATCGTATTCTAATGGCCCCCTGCAGGTCGGTCTGATTTATTGTATTTGTAA  
CCGTTTTACAACGTCAATTATATGGTAAGTTGCACGGAGAAATGGCCAGAGTTCTGAAGC  
CAAAGCATATTTTAACTACAGGCTTCTAATTTCTGGGCAACTATTTTCTTCTTTCCA  
TTGGATTCTGTACCGTATCTGCAATTTTATAGGATCGATTTACCCCCGCCCTTTGGCAGAG  
GAGGATTTCGTAGTATATTGGATGCTACGTGGTTGGTAATGATGGCTGTTGGTGGTGCCA  
ATGAAAACGTTCTCAGCTTAGTTATAGCTTACTGCCCTCCATACCTGAGTATTTGGTTGA  
TGACGTGGATCATATTAATATTTCTGCTTCATTCTACCCAATGGTTTTGAACAACGAAT  
TTTACAGGTACGGCTACATAATGCCAATCCATAATGCCGTGGATATCTATAAAGTGATTT  
TTTTGAATTTAACCAAAAGAAAAATGGGAAGAAATTACGGTATTCTCGTGGCATGGGTTG  
CCCTCAATACATCCTTGATGCCATTTTGTATGAAGTTTGCAGGTAAAAAATGCAAAAA  
ATGCTATGCAAGCAGCAGAAGCCGCTGTCGACGAGCTACCCAGCGTGCTAGCCGCCCGG  
CAGAGGCCAATACTGATAAAAAATAACAACCCGCCCGGAAATTAA

&gt;YGR197C, 547 aa (SEQ ID NO 186)

MTKSVGDEESQYIEDPSFAAAAAFTGGRDGVSYSNQRFAEGSGHSSDLAKSLEDYRPPDE  
KPSSLSSVGEGBANEEKGGNDGGPLARIQTGLFSPRLRNHRKKILSKFVLNNFFIACVC  
VSLISIWGACYGTDYFFKVKNIIVVLQDAPSNSTSVQISAIIPSLASVPGTWHIYNAT  
SFHRKFGTTNSTEIDRKIVDLIYDERYWLALNVKPNATDTLYNSLISQDANSEFNSSIFF  
ESVFESGRDPSSVKSTILPLMQQLEVLRLQKYVKEYLPSLMSNITSNDRDLNINMENWAI  
AGQLLFTYNDYRPFADRI LMAPLQVGLIYCILLTVLQLSLYKLGEMARVLKPKHILY  
RLISWATYFLLSIGFCTVSAIFRIDFTPAFGRGGFVVYWMSTWLVMMAVGGANENVLSL  
VIAYCPPYLSIWLMTWIILNISASFYPMVLNNEFYRYGYIMPIHNAVDIYKVI FLNLTKR  
KMGRNYGILVAWVALNTSLMPFCMKFAGKKMQKNAMQAAEAAVAAATQRASRP AEANTDK  
NNNPPGN

&gt;YGR250C, 2846 bp, CDS: 501-2846 (SEQ ID NO 191)

TCTTGTGTACGTACGATGTTTCTCCCGCTGATCCGATTACTAGCCGAAGACGTAA AATTG  
GCGCTTGATTCAATTTATGCCCTTCCCGGAATAGTTGACCAAAGGGCAAAAAATTGAG  
TCGGAGATTCCCTATTGGGCGGAATTTAGTAGATCTCTTTCCGTGCATAACGCCCTGCCCG  
TTAGTCGTTATTTTCACGTTAACATTTTCTTGGCCACTGCGCTATATAAATAAATACATAT  
ATATATGTCAAGCACATAAAGAAACTTCCCTTAAATATTGAATAAGTAAATAATAGTTG  
AAAAGTGCCCTTTTGTTCGAAGGATTAGAGTGTTCTTAATTTTAGTTTCGTTCAACGGTCTC  
AAAAAAGTGTTGAACAAGTAAAGCATAGCACATCCCAAATTACAAGGCACCCTGATTA  
AAAATCCAAAAATAAACCATAAGTTTTATTTTACTAAAAACATTATACGTGAAAGACAAA  
CCGCATCAGAAGTTTCGAGGATGAATATTGCAGAAGAACCATCAGATGAAGTAATATCTA  
GTGGCCCCGAGGATACAGATATCTGCAGCCAGCAGACATCAGCGAGCGCAGAAGCTGGAG  
ACCAATCAATAAAAAATTGAAAGGAAAACCTCCACTGGTCTTCAACTGGAACAATTGGCCA  
ACACAAATTTATTAAACCATAAGAATAAAATGGCAGTTACAAGAAGAAGAAGATGATCACT  
GCAACTCTAGAATAACCGATCAAATAATGGACACAATACAGCACTACAAAGGTATCTCCG  
TTAACAACCTCTGATACAGAAACATATGAATTTCTTCCGGATACAAGGAGGTTACAGGTTT  
TCGAACAAAATAAAGACATCTATCTTTACGAGCATGGAAGTCAAGAGTATGAGAAATCTT  
ACAAAGATAACGAAGAGGAAGATGATTGGAGATACGATACCGTTTTTGCAAGCACAAATCA  
AGTACCCCAAGTCATTAGAAAATGCATGTACAGATATCTCGGAATTACTCAAGAGCGAAC  
CTATTGGTCAGCATATTGATAAATGGTCTATCGGTGTGAACAAGCATGCACCTAACCTATC  
CTGGAAATATTTTTGTGCGGGGGAATAGCAAAGAGCCTTTCTATTGGTGAACCTAAGTTTCT  
TATTTTCAAAAATATGGACCAATTTTATCAATGAAATTGATATATGATAAAACGAAAGGCG  
AACCTAACGGATACGGGTTTCATCTCCTACCCCTTGGGTTCTCAAGCTTCACCTTGCATCA  
AGGAACCTAATGGAAGGACGGTAAATGGCTCCACACTATTTATCAACTATCACGTTGAGC  
GAAAGGAGAGAGAAAGAATCCATTGGGACCATGTCAAAGAAAACAACAATGATGATAATT  
TCAGGTGTCTCTTTATAGGCAACTTGCCCTTATCACAATCCTGAAAAAGTAGAGACTTTGA  
TTACACCTAAAGAAGTCATAGAAGTAATCAAGAAGGAGTTATCAAAAAAGTTTCCGGACT  
TTGATATCATTTTCATATTACTTTCCGAAGAGAAGTAATACAAGAAGCAGTAGTTTCAGTAA  
GTTTCAATGAGGAGGGGTCAGTAGAATCAAACAAATCTTCCAATAATACCTAATGGAAATG  
CCCAAGATGAAGATATGTTGAAGGGTTATGGTTTCATCAAGCTTATCAACCATGAACAAG  
CACTAGCAGCCATCGAGACCTTCAATGGGTTTCATGTGGCATGGAAACAGGCTCGTTGTTA

78/251

ATAAGGCGGTTCAACATAAAGTTTACAACAACCACAATAGCCATGACAGGCACCCTTCCA  
TCAGTAACCACAATGATATGGAGGTTTTGGAATTTGCAAATAACCCAATGTATGATTACA  
ATAATTATACATATGATAGATATTACTTCAACAATAATAAAAACGGGAACAGCAACGATA  
CCTCCAATGTACGGTATTTTGATTCTGTAAGATCAACCCCTGTGGCAGAGAAAATGGATC  
TGTTCTATCCTCAAAGGGAATCTTTCAGTGAAGGTCGTGGTCAACGTGTGCCTAGATTCA  
TGGGCAACAAGTTTGACATGTACCAGTACCCATCAACTTCTTACAGCTTACCTATACCAA  
TGAGTAATCAGCAAGAATCAAACCTATATGTCAAGCACATCCCTCTTCTTGGACAGATG  
AAGATTTATATGATTTCTACAAATCTTTCGGTGAAATAATCAGCGTTAAGGTCATTACTG  
TTGGGGGTAGTAAGAACAAGTATCGTCAACAATCGAATGATAGCTCATCAGATAATGATC  
TGCCAGTGGGATCATCAAGAGGTTATGGTTTGTCTTTTGAAGCCCATTAGATGCTG  
CTAAGGCAATTTTGAATACAGACGGGTATCAAGTGAGCAAAGATCAAGTGTTATCTGTTT  
CTTTCGCTCAGAAACGTGGTAATTTATCTTCAAGTGATGATGATGATCAATCCCAAACTG  
ATAACTCATCAAAGTTCCAAAATTTTCAGCCACATAATGATTATCATAAGGCTTATCCAA  
CAAAGTATAATAAGAAATTTATCAATGCCTTGATGACTCAGAACCAATCGCAACAGCAAG  
TCTCGAGGGAAAATTATTTTCATACCACTGCAGTACCCTAATACCAACACAAAGCCCGTGA  
ACAGTTACAACCTTAATAAGTGCAAACCAAAATAACGCTAACTGGATGATGCCAATGTTCC  
CATCATTTGGGTTTATTCCACAGGTGCCGCCAGTGCCCTATATAATACCTCCGCAGAATC  
CTGCAGCAAATCATATTCTTATAATGGCAAACGGTAGTAATGAAGAGGAAGAATTTTCTA  
GTGGTGATTATTCTATGGACTACTAG

&gt;YGR250C, 781 aa (SEQ ID NO 192)

MNIAEEPSDEVISSGPEDTDICSQOTSASAEAGDQSIKIERKTSTGLQLEQLANTNLLTI  
RIKWQLQEEEDDHCNSRITDQIMDTIQHYKGISVNNSDTETYEFLLPDTRRLQVLEQNKDI  
YLYEHGSQEYEKSYKDNEEEDDWRYDTVLQAQFKYPKSLENACTDISELLKSEPIGQHID  
KWSIGVNKHALTYPGNIFVGGIAKSLSIGELSFLFSKYGPILSMKLIYDKTKGEPNGYGF  
ISYPLGSQASLCIKELNGRTVNGSTLFINYHVERKERERIHWDHVKENNNDDNFRCLFIG  
NLPYHNPEKVETLITPKEVIEVIKKELSKKFPDFDIISYFPRKSNTRSSSVSFNEEGS  
VESNKSSNNTNGNAQDEDMLKGYGFIKLINHEQALAAIETFNFGFMWHGNRLVVNKAVQHK  
VYNNHNSHDRHPSISNHNDMEVLEFANNPMYDYNNTYDRYFNNKNGNSNDTSNVRYP  
DSVRSTPVAEKMDLFYPQRESFSEGRGQVRPRFMGNKFDMYQYPSTSYSLPIPMSNQOES  
NLVVKHIPLSWTDEDLYDFYKSFGELISVKVITVGGSKNKYRQQSNDSSDNDLPVGSRR  
GYGFVSFESPLDAAKAILNTDGYQVSKDQVLSVSFAQKRGNLSSDDDDQSQTDNSSKFQ  
NFQPHNDYHKAYPTKYNNKF FINALMTQNQSQQQVSRENYFIPLQYPNTNTKPVNSYNLIS  
ANQNNANWMMPMFPSFGFIPQVPPVPYIIPPQNPAANHPIIMANGSNEEEEFSSGDYSMD  
Y

>YHR001W-A, 797 bp, exon1: 501-506, intron1: 507-569, exon2:  
570-797 (SEQ ID NO 195)

TTCTATTCCGGCTTATAAAAAGCATGGAATCCAAAAGAATTAGGCTTCTCATTCTATTTT  
AATTATACTAGTACGATTTCTCACTCTGTAATTTAATATCAGTGTAATATGCACCTAGTT  
ATGGGTAGTTTTTGCTAACGTTACGAGCCGCGAAACTGTCCTCAATCTTACCCTACCT  
CTAATGACTGAAGAATGCTATGCGATATAACGCTGTGCGACTTTGAATATATACTTATAT  
TTACATAGTTTTCAAGTGCGTATTACTATTGCAAAGTAGTATTTTGTACCGTGATTTTGA  
TCCAATTAAACTAAATATGGTTCAACCCGTTGTTTCCGCATCAAAAAACCATAACATTT  
ATCAAGGGGACGGGATATATCACATAACAGTTTGAATGCATAATTTGTTATAGATATCTT  
CTGGAATAATCTTCACAGCAAAGCGCAAGTCGAATAATATATCGATAAATAACAATCCAT  
AAGACTTAAACTAACCTCAATGGCGGTAAGTATCCTATCATATTATGTGAGCTAGAACC  
GAATTAGTATACTAACATTTATAATACAGTACACTTCTCATCTGTCTTCAAAAACTGGTC  
TACATTTCCGTAGACTTTCTTTAAGAAGTTTAACAGCTTATGCTCCGAATTTAATGTTAT  
GGGGTGGTGCTAGCATGCTTGGGCTATTTGTATTACAGAAGGATGGCCTAAGTTTCAAG  
ATACGCTATACAAAAGATTCCGTTGTTAGGACCTACATTGGAAGATCATACTCCACCAG  
AAGATAAACCTAATTGA

&gt;YHR001W-A, 77 aa (SEQ ID NO 196)

MAYTSHLSSKTGLHFGRLSLRSLTAYAPNMLMLWGGASMLGLFVFTEGWPKFQDTLYKKIP  
LLGPTLEDHTPPEDKPN

79/251

&gt;YJL142C, 893 bp, CDS: 501-893 (SEQ ID NO 225)

TGCTGAATTATTTTTGGGTATACCGATCTTCCCAGGCGCTTCTGAATATAACCAATTAAC  
AAGAATAATAGACACGCTTGGATATCCTCCATCGTGGATGATAGATATGGGTAAAACTC  
TGGAAAATTTATGAAGAAATTGGCACCAGAAGAAAGTTCTTCTTCTACACAAAAGCATCG  
TATGAAAACATTTGAAGAGTTTTGCAGAGAATACAATATAGTGGAAAAGCCCAGTAAACA  
ATATTTTAAGTGGAGAAAGTTACCAGATATTATTAGAACTACAGGTATCCTAAAAGCAT  
ACAGAACTCCCAAGAACTTATCGACCAAGAAATGCAGAATAGGGAGTGTGTTGATCCACTT  
TTTAGGCGGTGTGCTAAATTTGAACCCGTTAGAAAGATGGACACCACAACAAGCTATGCT  
ACACCCCTTCATAACAAAGCAGGAGTTTACAGGTGAGTGGTTTCTCCAGGATCGTCTTT  
ACCGGGTCCTTCAGAAAAACATGACGATGCAAAAGGCCAGCAAAGTGAATATGGAAGTGC  
GAACGACTCTAGTAACAATGCAGGCCACAACATATGTCTATAATCCTAGCTCTGCCACTGG  
TGGTGCTGATAGCGTCGACATTGGTGCTATCAGTAAAAGGAAGGAGAATACATCTGGCGA  
CATCTCCAATAATTTTGTCTGTTACTCATTCTGTTCAAGAAGGGCCACAAGCGCGTTCAA  
TAACTTCACATTGTCTGAAGAATAAATCGTTATTTTGTCTGACTTTTCTTAACATACCCAT  
TTCATTTTATTACGGCTTGGTGCCATAATGATATACTAAATAAATATGAATTTTGCCTTT  
TCTTAATTTTCTTATACGTATAGTCATTACAATTAATAAAGTAACATTATAA

&gt;YJL142C, 130 aa (SEQ ID NO 226)

MTMQKASKVNMEVRTTLVTMQATTMSIILALPLVVLIASTLVLSVKGRRIHLATSPIILL  
LLILFKKGQARSINFTLSKNKSLFCLTFLNYPHFITAWCHNDILNKYEFCLFLIFLIR  
IVITINKVTL

&gt;YJL144W, 815 bp, CDS: 501-815 (SEQ ID NO 227)

AGAAAGAAGTTTCGTGGTATTAACCGACGGCAGCAAGTTGGGTCAATACTTGAAGGATTGC  
CCATATGAAGGGTATGGCGGGAAAGATAAGAAGAACAATCTGACCAAGCAAAATGTCACA  
AATGTCCATCCAACAGAATACGGCCTTTACATTTTACAAAAACAAATCATCGAGGACGTT  
GAGTGATTTGTTGGCATGATCTAATAATAGTCTCTTATATAAACCTATAATAATTTCTT  
ATTTTTGCCTTATATTTCAGGTAAATCACCATCTAACTGTATTATCTCTCACGTATCTTCA  
CTTATATGGCTCAGAAAACACCGTACGAAACGAAGGGGCTGCGAAAATGTTTCTAGAAGG  
TAATGGCAATAATAGGGATACAGATCGATCAGATCCGCCTATATAAAAGACAACGCACCG  
AAGGTGAACAAGATCGCAGATAAAGGTATTTACAAGGGAAAAAAGTCAGCAAAAAACAGA  
GATAAGATAACAAGAAGAAGATGTTAAGGAGGGAACTTCAACAATATACAGGACACACA  
AAAAAAGCAACAGTAGTATACTCAGGAGCCAGCGGGACCAGACTAGAGTGGATTCTTGG  
TAGAGGAGTCTCCCATGGGCGATTTTCGGGATCAATAACCAGCCTACACAGCCTGGCGTGA  
TATACTACTTTGTAGAGCTGACTAATTTAGGCATACAGGAAAACACAAGCAGTAATAATA  
ACAACAACAATAATCATGGTGACGATGAAAACGGCAGTCGATACGGCCACGGCAGCAGTC  
TGGGTGGAGACGTTCACTCTCGCCGTTGTTTCATGA

&gt;YJL144W, 104 aa (SEQ ID NO 228)

MLRRETSTIYRTHKKSNSILRSQRDQTRVDSLVEESPMGDFGINNQPTQPGVIYYFVEL  
TNLGIQENTSSNNNNNNNHGDDENGSRYGHSSLGDDVHSRRCS

&gt;YJL166W, 785 bp, CDS: 501-785 (SEQ ID NO 231)

TGAACAGCTATACCACGAATATGAAGAGTCTATTGCCAAGGATTTGAAGGCCAAAATTTTC  
TCAGGTTCGATGAGTCTCGTGGCTTCAAAGCTGATGTCTTAACTGCGTTCTTGAACAAAGT  
TTACAAGAGAAGCAAAATAGAACTAACGCTAATCGATAAAACATTAGATTTCAAACATAGAT  
AAGGACCATGTATAAGAATATATACTTCCAATATAATATAGTATAAGCTTTAAGATAGT  
ATCTCTCGATCTACCGTTCCACGTGACTAGTCCAAGGATTTTTTTTAAGCCAATGAAAAT  
GAAGAAATGCGTGATCGGAAATTACGGGTAGTACGAGAAGGAACTTGAGCCACCCCCCA  
AATTTTATTTCATATAATAATAGGAAAAGCAACGACCTCATCTCTCGAACATTGTTTACTT  
GAGCAAGTCCGATTAAGAGTAAGTTGTCTGACGTTAAATACAAATAATCAACAAAACACT  
ACACAAAACCTTCTACGATAATGGGTCTCCAAGCGGTAAAACCTTACATGGGATGGTGGG  
GTCACATGGGTGGTCCAAAGCAAAAAGGTATAACCTCATATGCTGTGTCTCCATATGCTC  
AAAAGCCATTACAAGGTATTTTCCATAACGCTGTATTCAATAGTTTTAGAAGATTTAAGT  
CTCAATTTCTATATGTATTAATACCTGCGGGAATTTATTGGTACTGGTGGAAGAACGGTA  
ACGAGTATAATGAATTTCTGTACAGCAAAGCTGGTAGAGAAGAGCTGGAAGAGTTAATG

80/251

TTTAA

&gt;YJL166W, 94 aa (SEQ ID NO 232)

MGPPSGKTYMGWWGHMGGPKQKGITSYAVSPYAQKPLQGIFHNAVNSFRRFKSQFLYVL  
IPAGIYWYWKKNGNEYNEFLYSKAGREELERNV

&gt;YKL117W, 1151 bp, CDS: 501-1151 (SEQ ID NO 247)

TTATAGAACTGTTTTATTGTTTTAAAAGAGCTTGTTATAGTAATCTAAGTGGAAATACACT  
AACAGTAAATAGGGCGTGTGGCGTAGTCGGTAGCGCGCTCCCTTAGCATGGGAGAGGTCT  
CCGGTTCGATTCCGGACTCGTCCAATCTTTTTATACTTATTAATAATTTTTTTCCTGCCG  
TTACTTGCTTTTAAAATAACTGCCTTTTATGAATACAGAGTATAATTTTTGATATACAAA  
GAGGTGACTGTGATAATCAATACTTAATTTGTGGTTATTGGTACACATATACCTACAAA  
AGTTACCAACAACTGTTTCGACTTTTAATGCTACCCGCCTTCCGAGTGTTTTTGAAGGGG  
CGGAGAGGAGCGGCAAGAATTAGCATGGAAAAAAGCATAAAAAGACGAAATGGGTGGCAA  
TGTATTATCTGTTTCGAGAAACCTAGTGGACTCAATTCATTACAACAACAAGTTCCCAAG  
ATCATCGATTCAATAAGTCATGTCCGATAAAGTTATTAACCCTCAAGTTCATGGGCTC  
AAAGGTCTAGTACTACTGATCCAGAAAGAAATTATGTCTTAATAACTGTGTCAATTGCAG  
ACTGTGATGCCCCCTGAGTTAACCATTAAAGCCATCATACATCGAATTAAAGGCTCAATCAA  
AGCCTCATGTTGGCGATGAAAATGTCCATCATTATCAATTACACATTGATCTATACAAGG  
AAATTATACCTGAAAAACAATGCATAAGGTTGCTAATGGCCAGCACTACTTTTTGAAAT  
TGTATAAAAAGGATTTAGAATCTGAATACTGGCCACGTTTGACAAAGGAAAAGGTGAAGT  
ACCCCTTACATCAAACTGATTTTCGATAAATGGGTTGATGAAGATGAACAAGACGAAGTTG  
AAGCTGAAGGTAATGATGCCGCTCAAGGAATGGATTTTCAGCCAAATGATGGGAGGTGCTG  
GAGGTGCTGGAGGTGCTGGAGGCATGGACTTCAGCCAAATGATGGGAGGTGCTGGTGGCG  
CTGGTTCTCCAGATATGGCTCAATTGCAGCAATTATTGGCTCAAAGCGGTGGTAATTTGG  
ACATGGGAGATTTCAAAGAAAACGATGAAGAAGATGAAGAAGAGGAAATAGAGCCGGAAG  
TGAAAGCTTAA

&gt;YKL117W, 216 aa (SEQ ID NO 248)

MSDKVINPQVAWAQRSSTTDPERNYVLITVSIADCDAPELTIKPSYIELKAQSKPHVGD  
NVHHYQLHIDLYKEIIPEKTMHKVANGQHYFLKLYKKDLESEYWPRLTKEKVYPYIKTD  
FDKWVDEDEQDEVEAEGNDAAQGMDFSQMMGGAGGAGGAGGMDFSQMMGGAGGAGSPDMA  
QLQQLLAQSGGNLDMGDFKENDEDEEEIEPEVKA

&gt;YKR075C, 1424 bp, CDS: 501-1424 (SEQ ID NO 257)

TTCAACAGAAATGCCGTAGCCGGAACCCGAAAGCGGGGACAGTGAAGCGTGAGAGGG  
GCCGACAGGGGGAACCTGAATGGGGTATTTTGCTTTTGCTGCATTTTTTCCGCTGGTAC  
CTCTATCTTTAGGCGACCGGAAAAATTCATTTTCTCATCTTTTTTTTTTTTTCGTTCCG  
ACTCGATACTCTTTACAAAGAAACCCCGCGGGGAAATGTTAGATTTGAGCTTTTCCGC  
CAGGAAAAGAAAAAACCTGGGGACATTAATCTTGTTTTTCTTTCTTTCTTTTGTCTCCC  
TTGGATGACTGCAGAAAAAGTACAGTTACCGGGTCTTAGCAAAAAACAAACATATATATAT  
ATATATATGAAAGCGTATGGTCAACACGGTTTTATAGGTTTTACTTTTTGCATTTCAGTTC  
AACTTTGGCCCTTTCTCTTATCGCATTACAGATACTACACACAAGTGTTCATACACACACA  
AATAGATACATATACAGAAAATGACTAGTTTGGACGATACAATAATTCGTACCAGAATA  
TAATGTTACTGGATAACATGACCAACTACAACAAGCCTGCGATTGACTATTTCCATCATG  
AATTTAATGATGCAAGCTTGGAATATCGGCTTCATGGACACTACTATTGAAGATGCGCA  
AACATAAACTACTTCGATTACCAAGTTGCTCTTCAGAGGACGTGCTAGATTACAACATGT  
ACCTCGTTAGGCTACATCATTCCTCTGGAGGCGTTGGTCCATAAATCACTATGGTTTAC  
AGAACTCCAAATCCAATCCACTGTCCATCAACTGGAACAAAGAAACCGATGTAACGGTGT  
TGTACGGTCCAGATTTGACTAACATAGATAGTAATGAAAACGAAATATCGCCGGTCCAGA  
ACCAAATTGACCAGAAACAAACAAAAATCTAAAATCTGCTTTAAAGAAAAATACGGAAT  
GCTGGGTAAACCGAGGAGGTGGATGAGATTAACGCTTCTATAGAGAGCAATGACAACGCTT  
TGGTGAAATTAGAAGACATTTTCATGCCATCGTCTGTTGATTCTCACACGTCTTCCATTT  
TCGACCAGCATTCTACATGCACTAAAATTTCTCCATAGATGAAGATTCTGAAGACCTTA  
TGAACGAAAAGAAGGAACAATTCGCCAGGAAGTTGAAGTTTAAACCAAGCCGTGATGAAGA  
GGGAGATCGACTCAAAGGGGACTATCCGCGAATCCCTCATCAACATAAACGATATCCAAC

81/251

ATTCCCGCCACCATCGCCGTCACCATCGTCGCCATCATCACCATCACCATCAAAATAGTT  
CTCATTCTGATGAAACAATAAAAGAAGCTCATTATGAGTTCAGCAACTATACATTTGGCA  
CTATGGAAGAAGACATTTTTTTATAGGAACCAGGTGTTTTTTTAA

>YKR075C, 307 aa (SEQ ID NO 258)

MTSLDDTIISYQNIMLLDNMTNYNKPAIDYFHFNDASLEISASWTLKKMRKHKLRL  
PSCSSEDVLDYNMYLVRLHHCLWRRWSINHYGLQNSKSNPLSINWNKETDVTVLVYGPDLT  
NIDSNENEISPVQNQIDQKQTKNLKSALKKNTECVWTEEVDEINASIESNDNALVKLEDI  
SCPSSVDSHTSSIFDQHSCTCKISSIDEDSEDLMNEKKEQFPRKLKFNQAVMKREIDSKG  
TIRESLININDIQHSRHHRRHRRHHHHHHHQNSSHSDETIKEAHYEF SNYTFGTMEEDIF  
YRNQVVF

>YLR216C, 1616 bp, CDS: 501-1616 (SEQ ID NO 279)

GAAGAATACAAAGAGGTCCAAGAAGACGAAGACCCGGATGTGTGGGACACGAGAATATCC  
AAGACCGGATGCTACGTAGAGAACCTCGCATTACAGCTGTGCCATGCCGAAACAGGTGAC  
TGGAGGCAGTGCCTCAACGAGATGGCGTTATTTAGGAAGTGTGGGAAAAGAATGGTAAT  
AGAGAGCGCGTAAGCACAGTGGACGTGGATGGGACGACCAGTAAGGATTCGGAAAAGAAG  
AAATGAAAATCTAAATGTCGTGATGTATAACTTGTATATAATAGACAGCTGCAGTGATCG  
AAACACATTGTTTCCCTTTATAGAACATAACTGTTACGCTTTTGAACGGCATTCTATGA  
GCTTCTAGAATATTTTTCCGCCCTAGCTGGAGAAAGTTCAGACAGAAAATTATTTAAATA  
AGTCAATATCAGAGGTGCTGATGCGCTCACATCAGTAACTGGTAAGACAATATT  
CAGGCGATCAAGGAGTAAAATGACTAGACCTAAACTTTTTTTGATATTTCTATTGGAG  
GTAAACCCCAAGGCCGTATAGTTTTTGTGTTGTACAATGACATAGTGCCTAAACCGGCTG  
AAAATTTTTTGAAGTTGTGTGAAGGAAATGCTGGTATGGCAAAGACTAAACCTGATGTAC  
CATTGTGCTACAAAGGTTCCATTTTCCACAGAGTGATCAAAGACTTCATGTGTCAATTTG  
GTGATTTTACCAATTTTAATGGTACTGGCGGTGAGAGCATATACGATGAAAAATTCGAGG  
ATGAAAATTTCACTGTTAAACATGATAAACCATTCTTCTATCCATGGCCAACGCCGGTC  
CAAATACCAATGGATCTCAAGCTTTCATAACCTGTGTTCTACACCTCATTGGACGGGA  
AGCAGCTTGTGTTTGGTGAAGTGATTCAAGGTAAAAGAATTGTTGTTGATTGAAAACC  
ACAATGTGACCAAGAAAACAACAAGCCATTGCGTGATGTAAAGATTGATGACTGTGGCG  
TGTTACCTGACGATTATCAAGTGCCAGAGAATGCCGAAGCTACACCAACAGATGAGTACG  
GCGATAATTATGAAGATGTTTTAAACAAGACGAAAAAGTTGACTTGAAGAATTCGACA  
CCGTCTTGAAAGCTATCGAAACGGTAAAGAACATTGGTACTGAACAGTTCAAGAAACAGA  
ACTATTCCGTGGCTTTAGAAAAATATGTCAAATGTGATAAATTCTTGAAAGAGTATTTCC  
CAGAAGATTTGGAGAAGGAACAAATTGAAAAAATCAATCAATTGAAAGTGTCTATTCCAT  
TGAATATTGCCATCTGTGCTCTTAAATTTAAAGATTACAAGCAAGTATTAGTAGCCTCAT  
CGGAGGTGTTATATGCCGAAGCGGCTGACGAAAAAGCCAAGGCCAAAGCTTTGTACCGTC  
GTGGCCTGGCCTATTACCATGTTAATGACACAGATATGGCTCTCAATGACCTAGAAATGG  
CCACTACTTTCCAGCCAAATGACGCTGCCATTTTGAAGCTATTTCATAATACTAAATTAA  
AAAGAAAGCAACAAAACGAAAAAGCTAAAAAGTCTCTTTTGAAGATGTTCTCTCTGA

>YLR216C, 371 aa (SEQ ID NO 280)

MTRPKTFFDISIGGKPKQGRIVFELYNDIVPKTAENFLKLCEGNAGMAKTKPDVPLSYKGS  
IFHRVIKDFMCQFGDFTNFNGTGGESIYDEKFEDENFTVKHDKPFLLSMANAGPNTNGSQ  
AFITCVPTPHLDGKHVVFGEVIQKRIVRLIENQQCDQENNKPLRDVKIDDCGVLPDDYQ  
VPENAEATPTDEYGDNYEDVLKQDEKVDLKNFDTVLKAIETVKNIGTEQFKKQNSVALE  
KYVKCDKFLKEYFPEDLEKEQIEKINQLKVSIPLNIAICALKLKDYQVLVASSEVLYAE  
AADEKAKAKALYRRGLAYYHVNDTDMALNDLEMATTFQPNDAAILKAIHNTKLKRKQONE  
KAKKSLSKMFS

>YLR346C, 806 bp, CDS: 501-806 (SEQ ID NO 289)

CTTATCTCAGGGTACCCATAATTTCAACCATCCTTAGCTTCCATTAAAAACACAATGAGT  
TGCCTTACTAGCGAAGCGGCTTATCTGTTAATTCTTGCTTGCAAACATCTTAGCTGAAAG  
TGAAAAGGCACAGCGCACCTGCTGAATGCTCAACGTTTGTAAATAATCCGCCTATTTCCGC  
GGAATCAATAGGGCTCCTAGCAGGCCGCCATCAATTTTCAGCGTGCCGCATTAAATATAT  
ATTACCAAGATTTCCATTTCCGCGGCTGATTCTTATCAATATTAAGTAATCAATCTTTTC

82/251

CTCGTGATTCTTTGTGATGCTCATTACAGAGGACTAATTAAGACATGTAGCACAAATATA  
TTCATATAAAAAGTTGGTGCAGTTAATGATTAATTGCATTGTTTTCTTGTCTTTCTGT  
TATACCTGTGCAATTAACATAAAGTGTATATGAATTTAAGGGGCACAAATAACAAAGG  
ATTATTTATCACCTTTAATAATGCAATCGATCAGTAATTGTCCCATCGGGTAGTTTCAA  
AAAACACAATCAATTCAGCTTCCACTATTGCAGAGTGGGTAGCATGTCCATGGAAATATA  
TCAACGTTGTTGGTTCAGGCAGATATGTGAGCAATAAACCTGATAAAATTACCAGATATG  
ATTTACTCAAGGCTGCCCAGGAAGCGGAAATGCAGGAGTTGCTTACAAGAAATGATATGA  
AAGGTAGACATAAACGTAATAAGAAAAGTAAGATAGCATTGGAGACTATAGCGGAAGAAA  
ACTCTTCAACTGAAAGCCTTTTTTAA

&gt;YLR346C, 101 aa (SEQ ID NO 290)

MQSI SNCP IGLVSKNTINSASTIAEWVACPWKYINVVGSGRYVSNKPKITRYDLLKAAQ  
EAE MQEL LTRND MKGRHKRNKKS KIALETIAEENSSTESLF

&gt;YML129C, 713 bp, CDS: 501-713 (SEQ ID NO 297)

TAATCAACTTGGCCAAGCAGAATACGCAATGGTTGTTTCGGCACTGTTAAGGAGCCTGCTT  
ACAAGAGGTACCTACATAACGTTAAAACTGGTTCGAAAAGCATATTAGGGTTCAACTAAT  
GATTGGGGTGTCAACGTAATGTACTTTTTCTCCCAATTTTTCTTTTCATCCGTATATTTT  
ACCGTAAAAATGGACAAGCTAATAGCAAAACGAAAAACACGTTGTCACTTCTATATAACT  
TTGCTTAAGTAAGTATTTTGTCTTTATAATGTTACATACTGTGAAATACACTCTTTAGAA  
AACACTATTTCTCACTCTCGGAAGCAGATTTGGAAGTTCTTCTTACTTCTGAGCTTTG  
CTTCTCCTTCTTGGCATTAAATGTTACCCGGTATACGAAATCGGAGAGGATCAGAATAAA  
TGCATTGAAAGGAGCATAAATCTATACAGCGGTTTGGCAATGGTGAGAGGAAGAGAACAA  
AAAATAGAACGCAGATAGTCATGTCCAAATACGCTTGGTATACCAGAGTTACAGATACAT  
TACATCGTCTAACGGTACTGACGTTGGTTGGTGGTACGTTATACATGTCCGGTGGCTTAG  
CTTACACTTTATACATGAACGGTAAGAAGTACGAACAACAAGTGACCCAACAAAAGGCAC  
TTGAAGAAGACAATCAACAACCTGCAAGTCCTACTGCACCTCCTACCGAGTAA

&gt;YML129C, 70 aa (SEQ ID NO 298)

MSKYAWYTRVTDTLHRLTVLTLVGGTLYMSGGLAYTLYMNGKKYEQQVTQOKALEEDNQ  
LQSPTAPPTE

&gt;YML132W, 1640 bp, CDS: 501-1640 (SEQ ID NO 299)

GTAACCTGGTTCTATGAATCTTCATGTCAGATACGTAGGACAGACTCTTTCCTGTGTAAA  
TATTTGTGACAGCTACGTCATTTTCTACTAGATGTTTACACAGTTTTGTACAGGAAAT  
CTACGCTTAAAAATATGTATTTTCAATCAAGCGGTAACCGCTGTACGAGCAGTGACATTGCT  
GGTCGCACCCATAATGTGAACCAACGTTACGGCACACCGTGATGTACCCGCATTAAAGTT  
TTGTAAATTTCGTTATTACGATTATCGAGTTGGCTAGATAGAAAACCGGAAATGTAATGGA  
TGCCCTTTTTCGAATAGCTGAGTTTCTTTGCCTAAAATAGCCCAATATTGTTGCCCTTTT  
CTATCACGAGGTTACTGAGCCATTGCATGAACGCGCGCGCCTCGGCGGCTTTTTTTTTCT  
GCTGTGCTGTATAAAAGCGAAAAGCCAGAAGTTACTATCTCGAATAAAAAACCCCTCGAA  
CTGCCATCTCACTACCGAAAATGAAAGAGAATGAACTTAAAAATGAGAAGAGTGTAGATG  
TATTATCCTTCAAAACAGCTCGAATCCCAAAAAGATTGTTCTACCTCAAGATCTTTTCAGAA  
GCAGCTTTACCTGGTTTTGTATGAAATTTACAAGTCCTTAGCGTTTCGCATCTGGATGC  
TATTATGGCTACCACTTAGCGTCTGGTGGAACTTTCCAACAATTGTATTTACCCACTTA  
TAGTTTCACTTCTGGTCTTGTCTGGGACCAATATTTGTCTTGTATTTGTGGACTTT  
CTCGTAAGCGTTCCTTATCGAAACAACCTCATTCAGTTTTGCAAAGAGATTACTGAAAACA  
CACCAAGTTCTGATCCTCATGATTGGGAAGTTGTTGCAGCAAATCTAAATTCGTACTTAT  
ATGAAAATAACGTTTGGAATACTAAGTACTTTTTTTTCAATGCCATGGTCTGTCAAGAAG  
CGTTCAAGAACAACCTTCTCGAACCAATTTCTTTTGAAAAAAGATAAAGCTGCCAAGGTTA  
AGTCATTTAAGGATTCCGTCCTTACATTGAAGAAGCATTGGGAGTTTATTTTACAGAAG  
TTGAAAAACAATGGAAATTTGTTTAATACTGAAAAATCATGGAGCCCTGTTGGCCTGGAAG  
ATGCTAAACTTCCCAAGGAAGCTTACCGATTTAAGCTTACTTGGTTTTTAAAGAGGATTT  
CCAATATTTTTATGTTGATACCATTCCCTTAATTTTTTGTGCTGCATATATGTGTCACGGG  
GAATGTGCCTTCTATTACGCACCTTGATCTCGGGTGGATTCTTTTCATGTTGGTACAAG  
GTTTCCAAAATATAAGGGTTTTGATTATGAGCATGGAACACAAGATGCAGTCTTGTCTGA

83/251

CTATTATAAATGAGCAAGAAAGTGGTGCGAATGGATGGGACGAAATTGCAAGGAAAATGA  
ATAGGTACTTGTGAGAAAAAGCCTGGAAGAATGAAGAGTTTTCTTCGACGGGATTG  
ACTGTGAATGGTTTTTAACCACTTCTTCTACCGCGTCTATCTGCGAAGAAATCTATGT  
GGCCTTTACCATTGAATGTGGAACATATGGCCATACATTAAAGAAGCGCAATTATCCCGCA  
GTGAGGTGCTCTTAGTGTAG

>YML132W, 379 aa (SEQ ID NO 300)

MKENELKNEKSVDVLSFKQLESQKIVLPQDLFRSSFTWFCYEIYKSLAFRIWMLLWLPLS  
VWVKLSNNCIYPLIVSLLVFLGPIFVLVICGLSRKRSLSKQLIQFCKEITENTPSSDPH  
DWEVVAANLNSYLYENNWNKYFFFNAMVCQEAFTTLLPEFSLKKDKAAKVKSFKDSV  
PYIEEALGVYFTEVEKQWKLFNTEKSWSPVGLEDAPLKEAYRFKLTWFLKRISNIFMLI  
PFLNFLCCIYVSRGMCLLLRTLGLWILFMLVQGFQNIIRVLIMSMEHKMQFLSTIINEQE  
SGANGWDEIARKMNRYLEKKAWKNEEFFFDGIDCEWFFNHFYRVLSAKKSMMWPLPLNV  
ELWPYIKEAQLSRSEVLLV

>YMR009W, 1040 bp, CDS: 501-1040 (SEQ ID NO 301)

ACCGGTATTTTCATCTCTTCTAGATCAAGACTAACTGCTCGTTCAGTACAAGTATTTTAC  
GATAGTCCATATTACTCTTCAATTAATATTTTTTTTTTATATCTGGCCCGTTTTTGACA  
CAATTTTTTCTCTCTTTTTCTCCCTATAAACTATGCAGAAGTAGCGATAATCACGATC  
TTGTTAATGATTCACATGTGCGCAAGTCGTATTGTCTGTCTAGATAGTGAGATGCCTTCT  
AAATAACAGGAGAGAGGCAAGATAGCATAACGGCGCAATGAAGGTAATTTCTGCCAGTTT  
TCTTTGCATTGACGACTGAAAGGGCCCTTGTAAGAGCCGCTCGACAGGGCGACGCCACAG  
TAGAGTCGCTAACACCGAAATATGCATATTGAAAAACATCAAAGTATAAAAAGAACAAAGA  
GGGTGGCATCTGCAGATCAAAAAACAATAACCACCAAACAAGACACTAAAAAAGGTCTG  
TAAAAAGGTCAAAAGTTAGAATGGTTAAGGTATATATTCATGACAACAAGTTGACTCCG  
ATTATCGCGCACCCCACAATTCTGGAACAGAACTTTCCCTGGATGAATTAGCCAAGTTAG  
GAGTGATTTATAAACTAGTGTGCAAATGAGGAAGAAGTGAATGAAATTGCTAGGCAAAGAG  
AATATAAAAATAGAGATGTGGTCAACATCTGCGAAGGTTCTTTCAAAAGTGAAGCAGAGT  
TTAATGAAAACTAGCAACATTTTACCAAGAGCATTTACATGAAGACGAAGAAATAAGAT  
ACTGTCTCGAGGGTGTGGATACTTTGACGTCAGGGATGCTTCCACACCAGAGAACTGGA  
TTAGCTTGTTTGGTAGAGTCAGGTGATTTACTGATTCTTCCACCAGGCATCTATCATCGTT  
TCACCTTGTTGTTAGTAGCAACCACATCAAGGCCTTGAGACTGTTTAAGGACGAGCCCAAAT  
GGCAAGCTATCAACAGGTCAAATCAGGCTGATTCAATGCCTGTACGCAAGGACTACATTG  
CCCTGATCAATCAGTACTAA

>YMR009W, 179 aa (SEQ ID NO 302)

MVKVYIHDNKVSDYRAPHNSGTELSLDELAKLGVIIKYCANEEVNEIARQREYKNRDV  
VNICEGSFKSEAEFNEKLATFYQEHLEDEEIRYCLEGAGYFDVRDASTPENWIRCLVES  
GDLILPPIYHRFTLTTSNHIKALRLFKDEPKWQAINRSNQADSLPVRKDYIALINQY

>YMR011W, 2126 bp, CDS: 501-2126 (SEQ ID NO 303)

GCAGCTTCACTTTTAAAGTTTCTTTTTCTCCTCACGGCGCAACCGCTAACTTAAGCTAATC  
CTTATGAATCCGGAGAAAAGCGGGTCTTTTAACTCAATAAAATTTTCCGAAATCCTTTT  
TCCTACGCGTTTTCTTCGGGAAGTAGATAGGTGGCTCTTCCACCTGTTTTTCCATCATTT  
TAGTTTTTCGCAAGCCATGCGTGCCTTTTCGTTTTTTCGATGGCGAAGCAGGGCTGGAAA  
AATTAACGGTACGCCGCCTAACGATAGTAATAGGCCACGCAACTGGCGTGGACGACAACA  
ATAAGTCGCCCATTTTTTATGTTTTCAAACCTAGCAACCCCCACCAAACCTGTCTATCGT  
TCCCGGATTACAAAATGATATAAAAAGCGATTACAATTCTACATTCTAACCAAGATTGAG  
ATTTCTCTTTCTCAATTCCTCTTATATTAGATTATAAGAACAACAAATTAAATTACAAA  
AAGACTTATAAAGCAACATAATGTCTGAATTCGCTACTAGCCGCGTTGAAAGTGGCTCTC  
AACAACTTCTATCCACTCTACTCCGATAGTGAGAAATAGAGACGGATGAATCTCCTA  
TTCAAACCAAATCTGAATACACTAACGCTGAACTCCAGCAAAGCCAATCGCCGCATATT  
GGACTGTTATCTGTTTATGTCTAATGATTGCATTTGGTGGGTTTGTCTTTGGTTGGGATA  
CTGGTACCATCTCTGGTTTTGTTAATCAAACCGATTTCAAAGAAGATTTGGTCAAATGA  
AATCTGATGGTACCTATTATCTTTCGGACGTCGGACTGGTTTGATCGTTGGTATCTTCA  
ATATTGGTTGTGCCTTTGGTGGGTTAACCTTAGGACGCTCTGGGTGATATGTATGGACGTA



84/251

GAATTGGTTTGATGTGCGTCGTTCTGGTATACATCGTTGGTATTGTGATTCAAATTGCTT  
CTAGTGACAAATGGTACCAATATTTTCATTGGTAGAATTATCTCTGGTATGGGTGTCGGTG  
GTATTGCTGTCTATCTCCAACCTTTGATTTCGGAACAGCACCAAAACACATTAGAGGTA  
CCTGTGTTTCTTTCTATCAGTTAATGATCACTCTAGGTATTTTCTTAGGTTACTGTACCA  
ACTATGGTACTAAAGACTACTCCAATTCAGTTCAATGGAGAGTGCCTTTGGGTTTGAAC  
TTGCCTTCGCTATTTTCATGATCGCTGGTATGCTAATGGTTCCAGAATCTCCAAGATTCT  
TAGTCGAAAAAGGCAGATACGAAGACGCTAAACGTTCTTTGGCAAAATCTAACAAAGTCA  
CCATTGAAGATCCAAGTATTGTTGCTGAAATGGATACAATTATGGCCAACGTTGAAACTG  
AAAGATTAGCCGGTAACGCTTCTTGGGGTGAGTTATTCTCCAACAAAGGTGCTATTTTAC  
CTCGTGTGATTATGGGTATTATGATTCAATCCTTACAACAATTAAGTGGTAACAATTACT  
TCTTCTATTATGGTACTACTATTTTCAACGCCGTCGGTATGAAAGATTCTTTCCAACTT  
CCATCGTTTTAGGTATAGTCAACTTCGCATCCACTTTCGTGGCCTTATACACTGTTGATA  
AATTTGGTCGTGTAAGTGTCTATTGGGTGGTTCTGCTTCCATGGCCATTTGTTTTGTTA  
TCTTCTCTACTGTGCGTGTCAAGCTTATATCCAATGGTAAAGATCAACCATCTTCCA  
AGGCTGCCGGTAACGTCATGATTGTCTTTACCTGTTTATTCAATTTCTTCTTCGCTATTA  
GTTGGGCCCCAATTGCCTACGTTATTGTTGCCGAATCCTATCCTTTGCGTGTCAAAAATC  
GTGCTATGGCTATTGCTGTTGGTGCCAACCTGGATTGTTGGGGTTTCTTGATTGGTTTCTTCA  
CTCCCTTCATTACAAGTGCAATTGGATTTTCATACGGGTATGTCTTCATGGGCTGTTTGG  
TATTTTCAATCTTCTACGTGTTTTTCTTTGTCTGTGAAACCAAGGGCTTAACATTAGAGG  
AAGTTAATGAAATGTATGTTGAAGGTGTCAAACCATGGAAATCTGGTAGCTGGATCTCAA  
AAGAAAAAAGAGTTTCCGAGGAATAA

>YMR011W, 541 aa (SEQ ID NO 304)

MSEFATSRVESGSQQTSIHSTPIVQKLETDESPIQTKSEYTNAELPAKPIAAYWTVICLC  
LMIAFGGFVFGWDTGTISGFVNQTDKRRFGQMKSDGYTLLSDVRTGLIVGIFNIGCAFG  
GLTLGRLGDMYGRRIGLMVCVVLVYIVGIVIQIASSDKWYQYFIGRIISGMVGGIAVLSP  
TLISETAPKHIRGTCVSFYQLMITLGIPLGYCTNYGTDYSNSVQWRVPLGLNFAFAIFM  
IAGMLMPESPRLVEKGRYEDAKRSLAKSNKVTIEDPSIVAEMDTIMANVETERLAGNA  
SWGELFSNKGAILPRVIMGIMIQLQLTGNNYFFYYGTTIFNAVGMKDSFQTSIVLGIV  
NFTCLFIFFFAISWAPIAYVIVAESYPLRVKNRAMAIAVGANWIWGLIGFFTFFITSA  
IGFSYGYVFMGCLVFSFFYVFFVFCETKGLTLEEVNEMYVEGVKPKWKSWSKEKRVSE  
E

>YMR099C, 1394 bp, CDS: 501-1394 (SEQ ID NO 307)

AACAGTTCACCTCGATCTACATATATTTCAATGCGAGAATGATTAATTCTTGCCATTGAC  
AAACAACCCTTTTACTGCCAGCGCCTTTTATAACCATGTAGTTTTATATGCCTAATTATA  
ATAAAGCATGACATATAATGCCAACCCCATATTTATATAGTTAACTTGAAACCGAGATTC  
ATCTATTGCACCAGGAAAAGTGCCTTCTTCTTAAACATAAGTTACGTCCCGACCATTCA  
TCTAAACGGCATCAATCATTGCAGCAGAAGAAATAGTGTGTAGATGTCCTCGTTTCGCTAG  
ACGCAGTCAATGATAACAAGGTCTTTCTTCAAGCTGTCTTTCCATAAAAAGGTATCGCAA  
ATGGGGTCACCAATGCGCCTTTTATTTTTACGCCGAAAGAAAACCTTAGTAGGTCCCTAG  
AAATGAATAAAGAGGTGATTCTGAGGTTCAATTATAAGCCTTTGGTAAAACCTGAACCAAG  
AAAGATTAAAACACAAAGCCATGCCTATCAAAGAACTGATAAAGAAGTTGTTTTGACTC  
ATCCAGCTGATGAGACCACGAGCTTCATATTCTAAAGTACGGTGCTACAGTTTATTCTT  
GGAAATTGAAATCTGAAGAACAGTTGTGGTTGTCTACTGCTGCTAAATTGGATGGTAGCA  
AACCTGTGAGAGGTGGTATACCTTTGGTCTTTCCTGTATTTCGGGAAAAATAGCACCGATG  
AACATTTGAGTAAATTACCTCAACATGGTCTTGCAAGAAATCTACTTGGGAGTTTTTGG  
GTCAAACCTAAGGAAAACCCACCGACCGTACAATTTGGCTTGAAACCAGAAATTGCTAACCC  
CAGAATTGACCAAAATTGTGGCCAATGGATTATCTTTTGATTTTGAATTTAGGCT  
CCGATTATTTGAAAACCTGCCATAGAAGTAGAAAACACATCTAGTTCCAAGGAATTAAAGT  
TCAACTGGTTGTTCCATACATACTTCCGTATCGAAGATATTGAAGGAACAATGGTCTCTA  
ATTTAGCTGGCATGAACTTTATGACCAACTGTTGAAGGAATCCTACGTGACAAGCACC  
CAGTCGTTACCTTCAATCAAGAAACCGATGTAATTTATCAGAATGTCAGCGCCGAACGGG  
CCATTCAAATAGTTGACAAGGGCGTTCAAATTCACACTCTAAAAAGATACAACCTGCCCCG  
ACACTGTTGTTTGAATCCATGGATTGAGAAGTCTCAAGGGATGGCCGATTTTGAACCAA

85/251

AAACTGGTTACCAACAAATGATATGTATTGAACCTGGTCATGTTTCATGATTTTATTTTCCT  
TGGCTCCTGGTAAAAAATGGAATGCTTATCAATTACTTTGCAAAGAAGAATTGAAATATC  
AAGCTATTCAATAA

>YMR099C, 297 aa (SEQ ID NO 308)

MPIKETDKEVVLTHPADETTSVHILKYGATVYSWKLKSEEQLWLSTAALKDGSKPVRGGI  
PLVFPVFGKNSTDEHLSKLPQHGLARNSTWEFLGQTKENPPTVQFGLKPEIANPELTKLW  
PMDYLLILTVELGSDYLKTAIEVENTSSSKELKFNWLFHTYFRIEDIEGTMVSNLAGMKL  
YDQLLKESYVDKHPVVTFNQETDVIYQNVSAERAIIQIVDKGVQIHTLKRYNLPDTPVVWNF  
WIEKSQGMADFEPKTYQQMICIEPGHVHDFISLAPGKKWNAYQLLCKEELKYQAIQ

>YMR110C, 2099 bp, CDS: 501-2099 (SEQ ID NO 311)

AAGAGAGAGAAGCTAGATTATCATTACAGCAGCCACATAGTATACCAAATTCCAGTACAG  
GCACACCAGAACATGATCAAGACACTTAGAGGAAATGGAACAACGAATTTCCAGCCAAAA  
ATTCCGAGTAGTTTCATGATGAAAGATTTTACATGCATTTTATATATAAATATATACCGT  
CCTATATGGATTTTCATGCCAACAGGGTATATAATAGACAATTACCGGTGTACTGATATAT  
CAACTATCGACTCCAAGCCTTTTATCTATCAGTCAATTTTACATCAAGATCCCACTTTTA  
GATAGGTTTCGAAAATTCAATCTAATATTAGTGATTTAATTAGATGGTGGATTGCTTACCC  
TTTTTTTTTGTCGTTTTAGGAGGAGATTCTTCGGATTTTAGGGATAAACGGATACTCCATA  
TATAAAAAACAAAACCTTCAGGCATATTGATTATCTAAAAGGAATATTCTAAAACCATAGC  
CATAGTAATTTTATCACCACATGTCAAACGACGGCTCAAAAATATTGAATTATACCCCAG  
TGTCTAAAATAGATGAAATAGTTGAAATCTCAAGAAATTTCTTCTTTGAGAAACAATTGA  
AATTGTCCACGAAAATAACCCAAGGAAAAAGATCTAGAATTTCAGGCAGTTGCAGTTGA  
AAAAACTCTATTATGCCGTCAAAGATCATGAGGAAGAACTGATCGATGCTATGTACAAGG  
ACTTTCATCGGAACAAAATTGAATCGGTTCTGAATGAAACGACCAAACCTTATGAACGATA  
TACTTCACCTAATTGAGATTTTACCAAATTTGATCAAACCTCGGAGAGTATCTGATTCTT  
CTCCTCCATTTATGTTTGGTAAAACAATCGTGGAGAAAATATCAAGGGGCAGTGTCTTGA  
TTATTGCTCCTTTCAATTTTCCCCTACTTTTAGCATTTGCCCATTTGGCAGCAGCTCTTG  
CTGCAGGTAACACCATTGTTCTGAAGCCAAGTGAACCTAACACCACACACTGCTGTAGTTA  
TGGAAAATTTGTTAACCACAGCTGGTTTCCCTGATGGATTGATTCAAGTAGTTTCAGGGAG  
CTATAGATGAAACTACAAGACTACTAGATTGTGGAATAATTGACCTAATATTCTACACAG  
GTTCTCCCCGTGTCGGATCAATAGTTGCTGAGAAAGCAGCAAAAAGTCTAACACCTTGTG  
TACTTGAACCTGGTGGTAAATCACCTACCTTTATTACAGAAAATTTCAAAGCAAGTAACA  
TAAAAATTGCTTTGAAAAGGATTTTTTTTTGGTGCTTTTCGGAAATTTCTGGCCAGATTTGTG  
TTTCACCAGATTATTTGTTAGTACATAAATCTATCTATCCAAAAGTCATTAAAGAGTGTG  
AATCAGTACTAAATGAATTTTATCCAAGCTTTGATGAACAAACAGATTTCACTCGTATGA  
TTCATGAGCCTGCTTACAAAAGGCCGTTGCAAGTATAAACTCAACTAACGGCTCCAAGA  
TTGTGCCTTCAAAAATTTCTATCAATTCAGATACTGAGGATCTATGCCTTGTACCACCAA  
CCATAGTTTATAACATTGGTTGGGATGATCCTTTGATGAAACAGGAAAACCTTTGCTCCTG  
TATTGCCCATCATTGAGTACGAGGATCTTGATGAGACCATTAAACAAGATAATAGAAGAAC  
ATGACACTCCATTGGTGAATACATATTCTCTGATAGCCAAACTGAAATAAATCGTATCT  
TGACGCGCTTAAGATCTGGTGACTGTGTTGTGCGGTGATACAGTGATTCATGTAGGAATTA  
CCGACGCTCCATTTGGAGGGATCGGTACTTCAGGTTATGGTAACCTATGGTGGATATTATG  
GATTCATACCTTTAGTCATGAAAGAACAATTTTTAAACAACCATATTGGAATGATTTTA  
CCCTTTTTATGAGATACCCTCCAAATAGCGCACAAAAGGAAAAGCTCGTCCGTTTTGCGA  
TGGAAAGAAAACCTTGGTTTGACAGAAATGGCAATAACAAGTGGGGGTACGCCAATATT  
TTTCATTATCTGCCGCCGTTATTTTAATTAGTACCATTTACGCTCATTGTTCTTCTCTGA

>YMR110C, 532 aa (SEQ ID NO 312)

MSNDGSKILNYTPVSKIDEIVEISRNFFFKQLKLSHENNPRKKDLEFRQLQLKKLYYAV  
KDHEELIDAMYKDFHRNKIESVLNETTKLMNDILHLIEILPKLIKPRRVS DSPPFMF  
KTIVEKISRGSVLIIAPFNFPLLLAFAPLAAALAAGNTIVLKPSELTPHTAVVMENLLTT

86/251

AGFPDGLIQVVQGAIDETTRLLDCGKFDLIFYTGS PRVGSIVA EKAASLT P CVLELG GK  
SPTFITENFKASNIKIALKRIFFGAFNGSQICVSPDYLLVHKSIYPKVIKESV LNEF  
YPSFDEQTDFTMRIHEPAYKKAVASINSTNGSKIVPSKISINSDTEDLCLVPPTIVYNIG  
WDDPLMKQENFAPVLP I IEYEDLDETINK I IEHDTPLVQYIFSDSQTEINRILTRLRSG  
DCVVGDTV I HVGITDAPFGGIGTSGYGNYG GYG FNTFSHER TIFKQPYW NDFTLFMRYP  
PNSAQKEKLVR FAMERK PWFDRNGNNKWGLRQYFSLSA AVILIST IYAHCSS

>YMR173W-A, 1685 bp, CDS: 501-1685 (SEQ ID NO 691)

AAAAAACCACTCCGAAGGTTCTGAGGATGACAAATCGCCCCCTTAGCTGTGGCCATACAAGC  
TTGGCACCCGACGAAAAAGGGAAAAAGGAAAAAGAATGTCGTACAAGAACTCTTACAACCAC  
GTTGAGATTTTCATTTAACAACGCCCCCTTTCCATTATATAAGAAGGCATTAATTTTTAT  
GTAATAAAAAAGAATTTCTCGAAAATGTCTTACAATTAATTTTTCTTTTGTAGAGTAG  
GGCTTTAATAGACTGATATATACGGTATTATAAGTGAACGAAAAAACAGCAATGGGTTT  
ATTTGATAAAGTGAAGCAATTTGCTAACAGCAATAATAACAACAATGATTCTGGCAATAA  
CAATCAAGGCGATTATGTTACCAAAGCTGAGAATATGATCGGCGAAGATAGAGTCAATCA  
ATTCAAAAGCAAAATCGGAGAGGACAGATTTGATAAGATGGAGTCCAAGGTTTCGTCACAA  
ATTTTCTAATACCTCTATAAATGACAACGACTCCAACAACAACGACTCATATGGTCTTAA  
TAACAACGATTTCATATGGTCTTAACAACAATGATTTCATATGGCTCTAACAACAATGATTC  
ATATGGCTCCAACAACAATGATTTCATATGGCTCTAACAACGATGATTCTACGGTCTTTC  
CAACAAGAAGAAGAGCTCTTATGGTCTTAACAATGACGATTTCGTACGGCTCCAGCAACAA  
CAATGACTCTTACGGTTCACAACAATGACTCTTACGGTTCACAACAATGACTCTTA  
CGGTTCCAACAATGACGACTCTTACGGTTCGTCAAACAAGAATAAGAGCTCTTACGGTTC  
CAACAATGACGATTCTTATGGCTCTAACAATGATGATTTCATATGGTCTTCCAACAAGAA  
GAAGAGTTCTTATGGTTCAGCAACAACGATTCGTATGGTCTTAACAACGATGATTCATA  
TGGTCTTAACAACAATGATTTCATATGGCTCTAACAACGATGATTCTACGGTCTTCCA  
CAAGAAGAAGAGCTCTTATGGTCTTAACAATGACGATTTCGTACGGCTCCAGCAACAACAA  
TGACTCTTACGGTTCACAACAATGACGACTCTTACGGTTCGTCAAACAAGAATAAGAGCTC  
TTACGGTCTTCTTAGCAACGATGATTCTTACGGATCTTCCAATAACGACGACTCTTACGG  
TTCTTCCAACAAGAAGAAGAGTTCTTATGGTTCACAACAATGACGATTCTTATGGCTCTAA  
CAATGATGATTTCATATGGTCTTCCAACAAGAAGAAGAGTTCTTATGGTTCAGCAACAA  
CGATTTCGTATGGTCTTAACAACGATGATTCTACGGTCTTCTTAACAAAAGAAGAGTTC  
TTATGGTTCACAACAACGATGATTTCATACGGCTCCAGCAACAACAATGACTCTTACGGTTC  
CAACAATGACGACTCTTACGGTTCCTCTAATAGAAACAAGAACTCCTATGGGTCTTCCA  
CTACGGTTCATCCAACAATGATGACTCTTATGGTTCATCTAATAGAGGCGGTTCGTAATCA  
ATACGGTGGTGACGACGATTACTAAGTTTTTGGATGTCTTCGATAAAAAAATATATTAT  
TGTGTTTAGACTTAAGTATGAAAATTTTATGTATGAGCTGTGGCTATGTATCCGCTGGCA  
AATAG

>YMR173W-A, 394 aa (SEQ ID NO 692)

MTTTPTTTTTHMVLITTIHMLVLTMIHMLTMIHMAPTTMIHMLTMIPTVLPTRRRAL  
MVLMTIRTAPATTMTLTVPTMTLTVPTMTLTVPTMTLTVRQTRIRALTVPMTILM  
ALTMIMHMLVPTRRRVLMVPATTIRMVLTMIHMLVLTMIHMLTMIPTVLPTRRRALM  
VLTMTIRTAPATTMTLTVPTMTLTVRQTRIRALTVLLATMILTDLPITTTTLVLPTRRR  
VLMVPTMTILMALTMIMHMLVPTRRRVLMVPATTIRMVLTMIPTVLLTKRRVLMVPTTM  
IHTAPATTMTLTVPTMTLTVPLIETRTPMGLPTTVHPTMTMLMVHLIEAVVINTVVTTI  
TKFLDVFDKKNILLCLDLSMKILCMSCGYVSAGK

>YNL031C, 911 bp, CDS: 501-911 (SEQ ID NO 325)

CAACAGCCCGAGCGAGTGAACAACATATTAAATTAAACGCCTTCTGTCAAGTTGTTTT  
GTTCTGGTCTGGTCTGCATTTTCGCGCCCGAAAAAGCTTGAGACGCGAAGCTCCCAGAACG  
TCCTGCCATACAAATGCGAACTCTCGGTCTAGTACCACTTTCCCGGTGCCAAACGACCA  
CAGTTGTCCGTTCCGAGCACTTCGCATTAAGCGCGTGAACTATTGGCAGGCCCTAAGGG  
GCTCCTACGGATGGGAGTTGGTCATTTAGCGTTCATTATCGCCCAATGTGACGCACAATC  
ACGGCTATGGCTCGGTGTCAAACATAGTTTGCCTGATAACAGCGTGTGTGCTCTCTCG  
CGTTGCTTCTTGTGACCGCAGTTGTATATAAATAATCTTTTCTTGTCTTTTATATAGG  
ACCACTGTTTTGTGACTTCCACTTTGGCCCTTCCAACGTCTTCCCCTTTTACTAAAGG

87/251

ATCCAAGCAAACACTCCACAATGGCCAGAACTAAACAAACAGCTAGAAAATCCACTGGTG  
GTAAAGCCCCAAGAAAACAATTAGCCTCCAAGGCTGCCAGAAAATCCGCCCCATCTACCG  
GTGGTGTTAAGAAGCCTCACAGATATAAGCCAGGTACTGTTGCCTTGAGAGAAATTAGAA  
GATTCCAAAAATCTACTGAACTGTTGATCAGAAAGTTACCTTTCCAAAGATTGGTCAGAG  
AAATCGCTCAAGATTTCAAGACCGACTTGAGATTTCAATCTTCTGCTATCGGTGCTTTGC  
AAGAATCCGTCGAAGCATACTTAGTCTCTTTGTTTGAAGACACTAATCTGGCTGCTATTC  
ACGCTAAGCGTGTTACTATCCAAAAGAAGGATATCAAATTGGCCAGAAGACTAAGAGGTG  
AAAGATCATGA

>YNL031C, 136 aa (SEQ ID NO 326)

MARTKQTARKSTGGKAPRKQLASKAARKSAPSTGGVKKPHRYKPGTVALREIRRFQKSTE  
LLIRKLPFQRLVREIAQDFKTDLRFQSSAIGALQESVEAYLVSLFEDTNLAAIHAKRVTI  
QKKDIKLARRLRGERS

>YNL134C, 1631 bp, CDS: 501-1631 (SEQ ID NO 331)

AAACTCGGAAACTCTTTTTCTATTCATCTTCCCTTCTCGTACGTGCCCCACGGAAGCAATA  
AAAAGAACCGAAATAACCAACACCCGTAACGTCAAAGCATTATGCTTAGAATGGAAACC  
ATTTCTGTGAATGAAATGGCAAATTGATCACATTGATTGCTCGTTCCACTACCTGTGTCC  
GCAATTTTTTAATGGTCATCACAGCCCTGCTGACTAAAGTTCCTCGGATCCGCTTACGG  
TTGTGCGCGGTTCCGCCCCCTGCGTACTCTTAGTACCTAGCATATGGGCTCCCTCCGTTG  
GATTGGCATCGATTAGTAAGGACAGATGTTAAGGATTTAAGACCGTTTTTAAGGTATTTTC  
GGCAATGCTTCGATTTAAAGGAGAGAGTTTTTTTTTTGCCGTTTTCTTCTCTCACTTC  
TTGATTAGTACTGTAATTCTAGTTGAAAAAAAATCGTTAACTATACACAGCAAAAAGCAA  
TATCATACTGCATATCAAGCATGTCCGCCTCGATTCCAGAAACCATGAAAGCCGTTGTCA  
TTGAAAATGGCAAGGCTGTAGTCAAACAGGACATTCCAATTCCCTGAATTAGAAGAAGGAT  
TTGTTCTAATTAAGACTGTCGCCGTTGCCGTAACCCCTACCGATTGGAAACATATTGATT  
TCAAGATTGGTCCTCAAGGTGCCCTCTTAGGCTGTGATGCAGCCGGCCAAATCGTAAAGT  
TGGGCCCCAATGTTGATGCTGCACGCTTTGCCATTGGTGATTACATTTATGGGGTTATTC  
ACGGTGCTTCAGTGAGGTTCCCTCAAACCGGTGCCTTTGCTGAGTACTCTGCCATTTTCAT  
CCGAGACTGCTTATAAACCAGCCAGAGAGTTTAGATTGTGCGGTAAAGACAAGCTACCAG  
AAGGCCCCGTAAATCTTTAGAAGGGGCAGTATCCCTCCCAGTCTCATTGACCACGGCTG  
GTATGATCCTTACACATAGTTTTGGCTTGGACATGACATGGAAGCCCTCCAAAGCGCAAA  
GAGATCAACCCATCTTATTTTGGGGTGGTGCCACTGCTGTTGGCCAGATGCTTATTCAAT  
TGGCAAAAAAACTAAACGGTTTCAGCAAGATCATCGTCGTTGCTTCTCGTAAACATGAAA  
AATTGTTGAAAGAGTACGGTGCAGATGAACTTTTTGACTACCACGATGCTGACGTTATCG  
AACAGATAAAAAAGAAGTACAACAACATTCTTACTTGGTGGACTGTGTCTCCAACACAG  
AACTATTCAACAGGTGTACAAATGTGCCGCTGATGACTTAGACGCTACGGTCGTTCAAT  
TGACCGTTTTTAACCGAAAAAGATATCAAGGAGGAAGACAGGAGGCAAAACGTCAGTATTG  
AAGGAACCCCTTCTATATTTGATAGGAGGTAACGACGTCCCATTTGGCACGTTTACTTTGC  
CAGCAGACCCTGAATACAAGGAAGCCGCATATAAATTTATTAAGTTCATCAATCCAAAAA  
TCAATGATGGTGAAATCCACCACATCCCAGTGAAAGTTTACAAGAACGGGTTAGATGATA  
TCCCACAGTTACTTGATGATATTAAGCACGGGAGGAATTCTGGCGAAAAGTTGGTTGCCG  
TCTTGAAATAA

>YNL134C, 376 aa (SEQ ID NO 332)

MSASIPETMKAVVIENGKAVVKQDIPIPELEEGFVLIKTAVAGNPTDWKHIDFKIGPQG  
ALLGCDAAAGQIVKLGPVDAARFAIGDYIYGVHIGASVRFPSNGAFAEYSAISSETAYKP  
AREFRLCGKDKLPEGPVKSLEGAVSLPVSLTTAGMILTHSFGLDMTWKPSKAQRDQPILF  
WGGATAVGQMLIQLAKKLNGFSKIIVVASRKHEKLLKEYGADELFDYHDADVIEQIKKKY  
NNIPYLVDCVSNTEIQQVYKCAADDLDATVVQLTVLTEKDIKEEDRRQNVSIEGTLLYL  
IGGNDVPFGTFTLPADPEYKEAAIKFIKFINPKINDGEIHHPVKVYKNGLDDIPQLLDD  
IKHGRNSGEKLVAVLK

>YNR002C, 1349 bp, CDS: 501-1349 (SEQ ID NO 339)

ATGGACAATTTGAAGTTCTTGACTACCCCTATCTCACACTAGTACGTAATTCAATGTATC  
ATTCGTATTGTAAGTAGATAGAGACGCAATACAGGAAAGCTGACCTTCCTTCCAATCACC

88/251

ACGGCTGAAATGCTTTGTTGACCAATTACGGACGCTTAAGAGCGGACGCGGCTGGAACGG  
CTCCATCCTAAATCGGCGGAGGGAGAAGTCCGATACCAGCCGACATGGCAATAATAGTGA  
CAGTAGATGCTACCAGCCCCGCAATAATTTACAGTAGATCATCAACAGTCTCCTCATTTT  
CTGGAAATGATCAGCAACTTCGACGGATTTAACTCTCAAGCAGTTACGCAC'TCCGAGAAC  
AGCCGTGATCATCTTTGAACAAGCAAAATATATAAAGCAGGAGAACTGTCC'TACCTAGAG  
CTAGAATAGCCATAACTAACTATGTAACATTCTACAGATCAATCAAAAACAATCTTCAAT  
CACAGAAAAAATAAAAAGGCATGTCTGACAGAGAACAAAGCAGCGGCAACACCGCTTTTG  
AGAACCCTAAGGCACTCGATTCTTCCGAGGGTGAGTTCATCTCTGAAAAACAACGATCAGA  
GCCGCCACTCGCAAGAGTCCATATGCAAAATATATACTGCGGGCAAAAACAACGAGTATA  
TTTACATCGGCCGTCAAAAATTTTTAAGGGATGATTTGTTCGAGGCATTCCGGTGGTACTC  
TGAATCCCGGTTTAGCCCCCGCGCCAGTCCATAAATTCGCAAATCCTGCTCCACTAGGAC  
TTTCCGGTTTTGCCCCTCACTACGTTTGTCTTATCCATGTTCAATGCAAGAGCCCAAGGCA  
TCACTATCCCTAATGTTGTTGTTGGGTGTGCCATGTTTTACGGTGGCCTCGTTCAACTCA  
TTGTGTTGTTGGGAAATCGCTTTAGAGAACACTTTCCGGTGGTACAGCCCTGTGTTCTCT  
TCGGCGGTTTTTTGGTTAAGCTTCGGTGTCTATATACATCCCTTGGTTTGGAAATCTGATG  
CCTATAAGGACAAGGAATCCGACCTTGGAAATGCGCTAGGGTTTTACCTCCTAGGATGGG  
CACTCTTCACCTTCGGTCTTTCCGTCTGCACCATGAAATCAACTATAATGTTTTTTGCCT  
TATTCTTCTCTTAGCAGTGACCTTCTTACTTCTATCCATTGCAAACTTCACAGGCGAAG  
TTGGCGTCACTAGAGCTGGTGGGGTCTTGGTGTGATAGTAGCCTTCATTGCCTGGTACA  
ACGCTTACGCAGGTATTGCCACAAGACAAAACCTCGTACATTATGGTCCATCCATTTCGCAT  
TACCTAGCAATGATAAGGTGTTCTTCTAA

&gt;YNR002C, 282 aa (SEQ ID NO 340)

MSDREQSSGNTAFENPKALDSSEGEFISENNDQSRHSQESICKIYTAGKNNEYIYIGRQK  
FLRDDLFEAFGGTLNPLAPAPVHKFANPAPLGLSGFALTTFVLSMFNARAQGITIPNVV  
VGCAMFYGGVLVQLIAGIWEIALENTFGGTALCSFGGFWLSFGAIYIPWFGILDAYKDKES  
DLGNALGFYLLGWALFTFGLSVCTMKSTIMFFALFFLLAVTFLLLSIANFTGEVGVTRAG  
GVLGVIVAFIAWYNAYAGIATRQNSYIMVHPFALPSNDKVFF

&gt;YOL139C, 1142 bp, CDS: 501-1142 (SEQ ID NO 347)

ACAAGTTTGGATACTGGTATTGTGACTCTTGTAAGAAGAAGAATACATCTTGTGTTCTAT  
GTGAAAGACCATTAAAGAAACTGACCATGGTCATCCTCCCCTGTGGACACGAAGGTCACT  
TCCAGTGCATACAAGAATGGTTTTCTCGATGAGAATGAACAAGAATGTCCCGGCGGTTGCC  
CCGGTGTTCATTTCATCTAGGTTCTCCACATAATGTATAGTTTAAACATATCATCACCATT  
GTTTAGTTAAATCGTTTAGAGTAATATTACCCGTCAAAAAGGTCGGGTAAAATTTTATTA  
CCCTCTCCGAAAAGAAAATTTTTTTCGTCTGTCATAGAGTTTAAATGCAATACCTGATAAA  
GAGAGTTTTACATTGCAAGAGGTAGTGTAAATCTGGATTTATATTGTACATATGTGTTT  
GTGTTAGTGCTTGAGTACTTCTTAGGAGTTTTACGAAAATAAAAGCATTTTTGTCTGAA  
AACTAGTGAAAGGAAGAAAATGTCCGTTGAAGAAGTTAGCAAGAAGTTTGAAGAAAACG  
TTTCAGTCGATGATACCACAGCTACTCAAAGACTGTTTTAAGTGACAGTGCTCACTTCG  
ATGTCAAGCACCCATTGAACACCAAATGGACTTTATGGTACACAAAGCCAGCCGTCGATA  
AATCTGAGTCGTGGTCTGATCTATTACGTCCCGTCACTTCATTCCAAACTGTTGAAGAAT  
TTTGGGCTATCATTCAAAATATTTCCTGAGCCACACGAAGTACCATTGAAATCAGATTACC  
ACGTCTTCCGTAATGACGTTAGACCTGAATGGGAAGATGAAGCCAATGCTAAAGGTGGTA  
AATGGTCTTTCCAACCTAGAGGAAAAGGTGCTGATATTGATGAATTATGGCTAAGAACTT  
TACTAGCAGTTATTGGTGAAACAATTGATGAAGACGACTCCCAAATTAACGGTGTGCTTT  
TAAGCATTAGAAAAGGTGGTAACAAGTTTGCCTTATGGACTAAATCTGAAGACAAAGAAC  
CACTATTGAGAATTGGTGGTAAATTCAAGCAAGTTTTAAATTAACCGATGACGGGCATT  
TGGAATTCTTTCCACATTCCAGTGCCAATGGTAGACACCCTCAACCATCAATCACCTTGT  
AA

&gt;YOL139C, 213 aa (SEQ ID NO 348)

MSVEEVSKKFEENVSVDDTTATPKTVLSDSAHFDVKHPLNTKWTLWYTKPAVDKSESWS  
LLRPVTSFQTVEEFWAIIQNIPEPHELPLKSDYHVFVRNDVRPEWEDEANAKGGKWSFQ  
LKGKADIDELWLRTLLAVIGETIDEDDSQINGVVL SIRKGGNKFALWTKSEDKEPLLRI  
GKFKQVLKLTDDGHLEFFPHSSANGRHPQPSITL

89/251

&gt;YOR120W, 1439 bp, CDS: 501-1439 (SEQ ID NO 353)

TGTCTTACATATTGCAATGGATATGCTTGGGTGATCATACTTCCTGGCTTTAGATATTTG  
AAACTTAACTCTTGTCAACAACTTCCTATGGAGTGATAAGAATTGTAAGTTATAACAC  
CGGCGAACAATCGGGGCAGACTATTCCGGGGAAGAACAAGGAAGGGCGGTCTTTTCTCCC  
TCATTGTCATAGCAAGGTCATTTTCGCCTTCTCAGAAAGGGGTAGAATCAATCTAGCACGC  
AGATTGCAAACACGGCTTAATAATATGCCTATCAGGCATTCACCCGTGTGACGAATCGCA  
CACCGCTGCTCTCCTTAATTCCCTAGAGTAGAAACCGAGCTTTCAGGAAAAGACTACGGC  
AGTAAAGAATTGCTTTACTGGGCGTATAAAACCGGGAGAATCAAGACATTCTAATGACTT  
GATTTCAGGATGAGAGCTTAATAGGTGCATCTTAGCAAGCTAAAATTTGGACAGCTCTCAT  
TACTAAATTAAGATAGAAAAATGCCTGCTACTTTACATGATTCTACGAAAATCCTTTCTC  
TAAATACTGGAGCCCAAATCCCTCAAATAGGTTTAGGTACGTGGCAGTCGAAAGAGAACG  
ATGCTTATAAGGCTGTTTTAACCGCTTTGAAAGATGGCTACCGACACATTGATACTGCTG  
CTATTTACCGTAATGAAGACCAAGTCGGTCAAGCCATCAAGGATTCAGGTGTTCTCGGG  
AAGAAATCTTTGTTACTACAAAGTTATGGTGTACACAACACCACGAACCTGAAGTAGCGC  
TGGATTAATCACTAAAGAGGTTAGGATTGGACTACGTAGACTTATATTTGATGCATTTGGC  
CTGCCAGATTAGATCCAGCCTACATCAAAAATGAAGACATCTTGAGTGTGCCAACAAAGA  
AGGATGGTTCTCGTGCAGTGGATATCACCAATTGGAATTTTCATCAAAACCTGGGAATTAA  
TGCAGGAACCTACCAAGACTGGTAAAATAAGGCCGTTGGAGTCTCCAACCTTTTCTATAA  
ATAACCTGAAAGATCTATTAGCATCTCAAGGTAATAAGCTTACGCCAGCTGCTAACCAAG  
TCGAAATACATCCATTACTACCTCAAGACGAATTGATTAATTTTTGTAAAAGTAAAGGCA  
TTGTGGTTGAAGCTTATTCTCCGTTAGGTAGTACCGATGCTCCACTATTGAAGGAACCGG  
TTATCCTTGAAATTGCGAAGAAAAATAACGTTCAACCCGGACACGTTGTTATTAGCTGGC  
ACGTCCAAAGAGGTTATGTTGTCTTGCCAAAATCTGTGAATCCCGATCGAATCAAAACGA  
ACAGGAAAATATTTACTTTGTCTACTGAGGACTTTGAAGCTATCAATAACATATCGAAGG  
AAAAGGGCGAAAAAAGGGTTGTACATCCAAATTGGTCTCCTTTTCAAGTATTCAAGTAA

&gt;YOR120W, 312 aa (SEQ ID NO 354)

MPATLHDSTKILSLNTGAQIPQIGLGTWQSKENDAYKAVLTALKDGYRHIDTAAIYRNE  
QVQQAIKDSGVPREEIFVTTKLWCTQHHEPEVALDQSLKRLGLDYVDLYLMHWPARLDP  
YIKNEDILSVPTKKDGSRAVDITNWNFIKTWELMQELPKTGKTKAVGVSNFSINNLDLL  
ASQGNKLTPAANQVEIHPLLPQDELINFCKSKGIVVEAYSPLGSTDAPLLKEPVILEIAK  
KNNVQPGHVVISWHVQRGYVVLPKSVNPDRIKTNRKIFTLSTEDFEAINNISKEGKEKRV  
VHPNWSPFVFK

>YOR122C, 1090 bp, exon1 : 501-513, intron1: 514-722, exon2:  
723-1090 (SEQ ID NO 357)

AGGAAGAGGAGGCTGCGTTTGACGACGAAGAGGATGATAATGAGGAAGAAGAAGAAG  
AGGACGCGGATGAAGAGAACGCCTCTCGTCTAAGAAATTTAAAAAGAGAAGGAGCAGCAA  
TGTACAGAGAAGAGGAAGAAGAAGAAAAAGATAGGAGCGAGACAAAAGAAGAAGGGTTG  
CGGTTCATCGAGGACGACGAAGACGAGGATTAGAGGAGACGTTACTTTGTTTATATATATT  
AGTATGTACAATCGCAAAGAAATGGAGTGATGACATGTTGTAGTATTTAGTATGAGGTTA  
CTGTGTGGGAGGTTTTACCATGATTTTTTGGCGAGAACACGCCATGAAATGTCTTTGTACG  
AAACTCATTACCCGCATTAATATTTTTTTCTTTTTTAAAGCTCAGTTGACCCTTTCTCAT  
TCCCTTCTTAAACAACCTGTGTGATCCTTGAGAAAAGATAAATTACATACACAACATAAA  
CCCAACTACGATCGCAAATTATGTCTTGGAAGGTATGTGAACGAGACAATTATCAATTG  
ATTAAGAAAGAAATGAGTCGGAGGTTAGCTTGTGTGACAATGTTTGGCAATGCCCGATTT  
TTGTTGATGCGCGTAATTTCAAGATTAACCACTCAGAGTAAATTACTAACTGGAATATC  
AAAAACATATGAAATTTCAACATGAATTTCTTTCCGTTTTTTTCTCCTACTTTTAAAC  
AGCATACACTGATAACTTAATAGGAACCGGTAAAGTCGACAAAGCTGTCATCTACTCGAG  
AGCAGGTGACGCTGTTTGGGCTACTTCTGGTGGCCTATCTTTGCAACCAAACGAAATTGG  
TGAAATTGTTCAAGGCTTCGACAATCCAGCTGGTTTGCAAAGCAATGGTTTGCATATTCA  
AGGCCAAAAGTTCATGTTGTTGAGAGCTGACGATAGAAGTATCTACGGTAGACATGATGC  
TGAGGGTGTGTTTGTGTAAGAACTAAGCAAACCGTTATTATTGCTCATTATCCACCAAC  
CGTACAAGCCGGTGAGGCCACCAAGATTGTGCGAGCAATTGGCTGACTACTTGATTGGTGT  
TCAATACTAA

90/251

&gt;YOR122C, 126 aa (SEQ ID NO 358)

MSWQAYTDNLIGTGKVDKAVIYSRAGDAVWATSGGLSLQPNEIGEIVQGFDPAGLQSNGLHIQGGQKFMLLRADDRSIYGRHDAEGVVCVVRTKQTVIIAHYPPTVQAGEATKIVEQLADYLIGVQY

&gt;YOR261C, 1517 bp, CDS: 501-1517 (SEQ ID NO 361)

GTAAGGTAAGGCATCATTAGCAGGATCCATATTCACCTACCTGGGAATGTCTTCCGATGGCATTGAAGAACTGTGAGCAGCCGTTGCAATAGGTTGACTTCCCTGAACCTGGTGGACCAATAACAATCTGAGCGAAGGGCATTATTGTACTCTCTAGTAGAAAATCAAACTATTGACACAACAACAATCAAATGAAAACAAACCATTCTATTACGGTAAGTAGTGAAGACTCACAAATGCAATCTTTCAATGAGCATCACTTACTTTAAGTAGCAATATTCCTAATCACTTATTACGAAATTTGATTTTACTAAAGTTCGGGGATACCTCAGTGGCAAATCGTTACTCAAGTTGCACGTAACTGAGAATCTACAATGAAATAATTGTGAAGCCAACAGCTAAGCAATCTATAGTGTAAACGTGGCTTTCTGTACAACCTGCTACTGATTGAGGGCATTTCGAATTTAAAAAGAAAGAAAGAAAGGAAAATCAAATTACAATGTCTCTACAACACGAGAAAAGTTACCATTGCACCACCTAGTTTTGCTATCTGCTTTGGATCATTATGAGCGTACGCAGACAAAAGAAAACAAAAGATGCGTTGGTGTCTATCTTAGGTGATGCTAACAGTTCCACTATCAGAGTCACTAATTCCTTTGCCTTACCGTTTGAAGAAGATGAGAAAACTCTGACGTGTGGTTTTTAGACCATAATTATATTGAAAACATGAATGAAATGTGTAAAAAGATTAAATGCCAAGGAAAACTCATTTGGATGGTATCATAGTGGTCTCTAAATTAAGGGCTTCTGACCTCAAGATTAATGAGCTGTTTAAAAAATATATCTCAGAATAATCCGCTATTATTAATTGTTGATGTCAAACAACAAGGTGTTGGTTTACCAACAGATGCATATGTGCGGATTGAGCAAGTTAAGGATGATGGTACGTCTACAGAAAAGACGTTCTTCATTTGCCTTGTACTATTGAGGCCGAAGAAGCTGAAGAAATTGGTGTAGAACACTTATTGAGAGACGTACGTGATCAAGCAGCAGGTGGCTTATCTATCCGGTTGACCAACCAATTAAATCTTTGAAAGGATTACAAAGCAAACCTAAAAGACGTTGTGCGAGTACTTAGACAAAAGTCATTAATAAGGAATTACCGATAAACACACTATATTGGGCAAGCTACAAGATGTTTTCACACCTTTTACCAAATCTGGGAACACCTGATGATGACGAAATAGATGTGGAGAATCATGACAGAATTAATATTTCAAATAACTTACAAAAGGCTTTAACTGTGAAAACCTAATGATGAATTAAATGGTTATATATATAAGCAATTTGGTTAGGTCAATTATCGCGTTTGTATGATTGATTGAAAACAAAATTCAAAATAAAAAAATTCAAGAACAAGAGTAAAGGACAAACAATCAAAAGTCTCTGATGACAGTGAGAGTGAGAGTGGTGACAAAAGCAACTGCGCCATTGATCCAACGAAAGAACAAGAAAAATTAA

&gt;YOR261C, 338 aa (SEQ ID NO 362)

MSLQHEKVTTIAPLVLLSALDHYERTQTKENKRCVGVILGDANSSTIRVTNSFALPFEEDEKNSDVWFLDHNYYIENMNEMCKKINAKEKLIGWYHSGPKLRASDLKINELFKKYTQNNPLLIVDVKKQQGVGLPTDAYVAIEQVKDDGTSTEXTFLHLPCTIEAEEAEEIGVEHLLRDVRDQAAGGLSIRLTNQLKSLKGLQSKLKDVVEYLDKVINKEPINTILGLQDVFNLLPNLGTPTDDDEIDVENHDRINISNNLQKALTVKTNDELMVIYISNLVRSIIAFDDLIENKIQNKKIQEQRVKDKQSKVSDDSESESGDKEATAPLIQRKNKK

&gt;YPL271W, 689 bp, CDS: 501-689 (SEQ ID NO 391)

CAGCAGCGACAAGTCAGAGTGCTTACAAAAAAGAGTTGATCCGGCTAAAGAAAGTCGATTTACGTATTTATCCAGGTTCAAACGGATTGCCAAAAATAGTCGATAACCTCGGAGTAAGCAAAGCAACAATATATTTGTTCTTCGAAAAGGTAACTTCTTAATCTTATAGAACATTGTACTAGTTCTCTCGAAGAAAAAACTAAGAAAGCTATAGCTGTATCTTACCAAGCCATGAACCTTGAGGAATTGGTAATCCTTATTAGGAAATACGCTAACTAGGTAATAGCAGATGATTTACTAGCTTACTATCTCACACTAAGTCTGGCAACGCGCTATTTTTTAATACTTTTATACGAACCAATGAAATTTGATCCTCCCTTTTTTCGTCTAGTTAAATGAAGAGATACAAGTAGGCCTTTCTATTGAGTACTTAGCAAGATATGTATTCTAAGAAACATCAACAGTTTCAGCCACAACCGATTCAAAAATGTCTGCCTGGAGGAAAGCTGGTATATCATATGCTGCATATTTGAATGTGGCCGCTCAGGCTATCCGTTCTTCATTGAAAACCTGAATTACAAACCGCTAGTGTCTTAAACAGATCGCAAACAGATGCTTTTTATACCCAATATAAAAATGGCACTGCAGCTTCTGAACCCACTCCAATAACAAAATAG

91/251

&gt;YPL271W, 62 aa (SEQ ID NO 392)

MSAWRKAGISYAAYLNVAQAIRSSLKTELQTASVLNRSQTDIFYTQYKNGTAASEPTPI  
TK

&gt;YPR035W, 1613 bp, CDS: 501-1613 (SEQ ID NO 395)

TAGTGCCATTTGTGGTCATTATTATTCCTCCCAAATATGCGAAAATAGTACACTATTTTTGG  
CAGGAGAGTAGGCTGATATGCCGCATTGATGTCTGTGTAGCGAAACACAAACAAAAAA  
GAAAAAGTAGGATGAAAAAAGAAAAGTAATATGAAAAAGAGTGAAAAATTAATTCATT  
TGTTAGTGTAAAGCGTCAGGTGTAAGTAGTAGGCTTGATAATGAATTAAAGATGACTCCG  
ACGCATATTGTTTGCCATGTTTTTATTTTAGTTTGTAGATTTCCTTTTTTTGTAAATATATA  
AGGGAGTGATTCTATATATCGAATTCTCAGGCTTGGTTGGTTCGTAGGTTGTTCTGTCTT  
TGTTTTCGTTAGGTAAGAACATCACACAAAGATAACTATAGAATCACATACATATTGTG  
AGAAATTAACCTTCATTTTATTTATAGAAGAAGTTCAACCGAAAACAAAAATTAAACATAAT  
ATAATATAATATAATCAAAAATGGCTGAAGCAAGCATCGAAAAGACTCAAATTTTACAAA  
AATATCTAGAACTGGACCAAAGAGGTAGAATAATTGCCGAATACGTTTGGATCGATGGTA  
CTGGTAACCTTACGTTCCAAAGGTAGAACTTTGAAGAAGAGAATCACATCCATTGACCAAT  
TGCCAGAATGGAACCTTCGACGGTTCTTCTACCAACCAAGCGCCAGGCCACGACTCTGACA  
TCTATTTGAAACCCGTTGCTTACTACCCAGATCCCTTCAGGAGAGGTGACAACATTTGTTG  
TCTTGGCCGCATGTTACAACAATGACGGTACTCCAAACAAGTTCAACCACAGACACGAAG  
CTGCCAAGCTATTTGCTGCTCATAAGGATGAAGAAATCTGGTTTGGTCTAGAACAAGAAT  
ACACTCTATTTGACATGTATGACGATGTTTACGGATGGCCAAAGGGTGGGTACCCAGCTC  
CACAAGGTCCTTACTACTGTGGTGTTGGTGCCGGTAAGGTTTATGCCAGAGACATGATCG  
AAGCTCACTACAGAGCTTGTTTGTATGCCGGATTAGAAATTTCTGGTATTAACGCTGAAG  
TCATGCCATCTCAATGGGAATTCCAAGTCGGTCCATGTACCGGTATTGACATGGGTGACC  
AATTATGGATGGCCAGATACTTTTTGACAGAGTGGCAGAAGAGTTTGGTATCAAGATCT  
CATTCATCCAAAGCCATTGAAGGGTGACTGGAACGGTGCCGGTTGTACAGCTAACGTTT  
CCACCAAGGAAATGAGACAACCAGGTGGTACGAAATACATCGAACAAGCCATCGAGAAGT  
TATCCAAGAGACACGCTGAACACATTAAGTTGTACGGTAGCGATAACGACATGAGATTAA  
CTGGTAGACATGAAACCGCTTCCATGACTGCCTTTTCTTCTGGTGTCGCCAACAGAGGTA  
GCTCAATTAGAAATCCCAAGATCCGTCGCCAAGGAAGGTTACGGTTACTTTGAAGACCGTA  
GACCAGCTTCCAACATCGACCCATACTTGGTTACAGGTATCATGTGTGAAACTGTTTGCG  
GTGCTATTGACAATGCTGACATGACGAAGGAATTTGAAAGAGAATCTTCATAA

&gt;YPR035W, 370 aa (SEQ ID NO 396)

MAEASIEKTQILQKYLELDQGRGRIIAEYVWIDGTGNLRSKGRITLKKRITSIDQLPEWNFD  
GSSTNQAPGHDSDIYLPVAYYPDPFRRGDNIVVLAACYNNDGTPNKFNRHEAAKLF  
HKDEEIIWFGLEQEYTLFDYDDVYGPWPKGGYPAPQGPYYCGVGAGKVYARDMIEAHYRAC  
LYAGLEISGINAEVMPQSWEFQVGPCTGIDMGDQLWMARYFLHRVAEEFGIKISFHPKPL  
KGDWNGAGCHANVSTKEMRQPGGTYIEQAIIEKLSKRHAHEIKLYGSDNDMRLTGRHETA  
SMTAFSSGVANRGSSIRIPRSVAKEGYGYFEDRRPASNIDPYLVTGIMCETVCGAIDNAD  
MTKEFERESS

YBR133C, 2984 bp, CDS: 501-2984 (SEQ ID NO 53)

AACCTACGACAGAGTTGTAATGAATGCTACTGATGTCTGCTCTACTGCCA  
TCCGCTGTCCTTTTCATGCATAAAAGCTCCATTCTTTATTTATCTCATACC  
ACGAGAAAAAAAATCACCTGACATATTTTTATAACCCGCCTTTTAGACC  
CTAAAACAGATCTCAGGGCTCGAGTACTGTTTTATCTGAAAATTCTTCGA  
GCCCTCGTTTTGCACTGAGCTAAACCAAAAAGAAAAATAACAATCACAAA  
TGGAACCCGAAACAGCACGCTGCGCAGTGTTTTTATATTTTTTTGAAACA  
AATGGCTTTATACAATGTGTATGTGTGATAGAAAAATGGTATATTTTGA  
GTGACTTGTGATCCTATTTCCAAGCCCTATAGGAGCTATTTCAAATTGCG  
TGTGTGAAAGCGTGTGTGTGTGTGTGTGTGGAATTGTGCGGACGTTCC  
TCTTCTTTTATACATATAATTTTTATATATACAAAGGGTTCAGTTTGCAT  
ATGCATAGCAACGTATTTGTTGGTGTCAAACCAGGCTTTAATCATAAACA  
GCACAGCAAAAAGTCACGTTTCTAGAAAATGTCTCTAGTCATTCCACCAG



92/251

AACTGCCTAGTAACTATGATTACGTTTTGCTTCCTATAACAACGCCAAGA  
TATAAGGAAATAGTTGGGCAAGTTTTCAAAGATTTCCAAAGACAATCCAT  
ACAGAACTGGAAACCGCTTCAAATTCCTGAACCGCAGTTGCAGGATATCT  
GTATACCCCGTTCAACGTCAAGAAGCTAGACAATGACGATACGCCGTCT  
TACATAGGGCTGTTATCCTCTTGGCTGGAGCTGGAGAGTCGCGATCCAAA  
TGTAAGAGATCTTGGCTTAAAGGTCCTTCTAAACGAATGTAAGTACGCGA  
GGTTTGTGGAATCAATAAGCTAATATTGGCGCCTCCACGGGACCTGTCC  
AACCTGCAATTGTATGGACAGATGATTTACAGGCTCCTGCAAAATCGCAT  
CGTCTTTGCTGCGCCTGCGTTAACCATATCCATTTCTCTGCCACTTTACG  
AAGACAGCGATCCATTGGCCACTTGGGAACTGTGGAATACCGTGCGGAAA  
CAATGCGAATATCATCCCTCTTTGACTATCTCTTTGGCTTTGCCAAGAAC  
CAGGACTCCTTCGTATGTGCTGAATAGATGGTTAGCCGAACCCGTCTCGT  
GTCTTTTGGTATCTTCATCCATCTTTGCCAGTAATCAGTACGATTATCCC  
GTTTTACACAAGTTTAACCAGAATTTGATTTTAAAGTTCCAAAAGGTTAA  
TGGAGATTACAAAATTTTGGGTAATGAATTATGCGTGATATTGCATGGGA  
TGGAGAAATATGCCAATAATGTTAAGGGCGGAGAATCTGCCTATTTGGAA  
TATATAAACTACTTATTGAAAAAGGGCGACAAAGTATTAAATTCCAATAG  
TAATCACC AATTTTGTCTCCAAGAGGACTCTCGGATAATGCCGCCTCTGA  
AACCTCATT CAGATAATTTATTAAATTCCACATATTTGACTTTTGAAAA  
GATTTGGTGAAGTACGATCTTTACGAATCTGCCATATTAGAGGCGCTTCA  
AGATCTTGCTCCTCGAGCGAGTGCCAAGAGACCGTTGGTGATCCTAGTAG  
CCGGTGCGGGAAGAGGACCTTTAGTGGATCGAACTTTTAAGATAATATCA  
ATGTTGTTTATGGATAGTAAGGTTTCTATAATTGCCATTGAAAAAATCC  
ACAGGCATATCTGTACTTGCAAAAAAGAAATTTGACTGTTGGGATAATA  
GAGTGAAATTAATCAAGGAGGATATGACCAAATGGCAAATCAACGAGCCG  
TCGGAAAAGCGTATT CAGATAGATCTGTGCATAAGTGAAGTGTGGGTTT  
GTTCCGGTTGCAATGAATTATCACCAGAATGTCTCTGGTCTATTGAAAAAT  
ATCATTCCCACAATGACACAATTTTCATACCGAGGTCATACTCTTCATAC  
ATGACACCCATTTTCTGTCACCATTTCTACCAAAAACTCTCACAAACAAA  
TCGCTCTTTTGGAGGCGCCCTGGATAGTCCATAGAGTGCCATACTGTATAT  
TATCCTCAAGGGTAAATGAAGTGTGGCGGTTTCGAGCATCCCATGGCCCAA  
AAAGATACTGTCCAAGACGAAGATGATTTTACAGTTGAATTTTCTCAAAG  
TTCATTAAATGAGTTCAAGATAAAGCACC GCGCGAAATCCATGGCTTTA  
TCGGATTCTTCTCGGCAAACTTATATAACAATATATTCTTGTCAACTTTG  
CCCAATGACAGCACAGTCCGTTTAAAATTTAGCGAAGAAACGTTGATGAA  
TACCAGACGAGAAGAAAATCTAATCAAGAAATGTGACCATAACCAAATA  
TGACCTCGTGGTCTCCAATTATCTTTCCTTTGAAGCAACCAATATCCTTT  
ATAGATGACTCCGAACCTTCTGTGCTGATGTCTCGGATACACTCCGATAC  
AGAACAAAAAGTTTTGGTATGAATGGTCTTTGGAGAGTTTCATATACCTTA  
TGTTGTCAAATTACACTTCGGCGGTAAGTGTGCAAGCATGACTATTCCG  
AGGTCTATAGTTACAGATGACACTAAAACCTTTAGCCCATAAATCGACATTA  
TTCAGCGACTACCAATCAAAGCTAGATAATCAAATTGATCTTGACCAAG  
ACATTGAAAACGAAGAAGAACAGGGATTCTATCCAATCTAGAAACTGGT  
TGGCAAAGCGTACAAGATATTACGGGACTCAGCGAAACCGCCAAACCGGA  
CCATTTAGATTCTATCAATAAGCCTATGTTTGATCTCAAATCTACTAAAG  
CGTTTGAACCCTCTAACGAATTGCCAAGGCACGAAGACCTCGAGGAAGAT  
GTTCCAGAAGTTTATGTGAGTCAAGACTAGTGTTCACGCTACATAA  
TGCTGTGGCAGAGCCTTTTCCCTGCCTCTGTGA

YBR133C, 827 aa (SEQ ID NO 54)

MHSNVFVGKPGFNHKKSRFLENVSSHPELPSNYDYVLLPITTPR  
YKEIVGQVFKDFQRQSIQNWKPLQIPEQLQDICI PPFNVKKLDNDTPS  
YIGLLSSWLELES RDPNVRDLGLKVLLNECKYARFVGINKLILAPPRDLS  
NLQLYGMIMYRLQNRI VF AAPALTISISLPLYEDSDPLATWELWNTVRK  
QCEYHPSLTISLALPRTPTSYVLNRWLAEPVSCLLVSSSIFASNQYDYP  
VLHKFNQNLILKFQKVNGDSQILGNELCVILHGMEKYANNVKGGESAYLE

93/251

YINYLLKKGDKVLNSNSNHQFLQEDSRIMPPLKPHSDNLLNSTYLTFEK  
DLVKYDLYESAILEALQDLAPRASAKRPLVILVAGAGRGPLVDRTFKIIS  
MLFMDSKVSIIEKPNQAYLYLQKRNFDCWDNRVKLIKEDMTKWQINEP  
SEKRIQIDLCISELLGSFGCNELSPECLEWSIEKYHSHNDTIFIPRSYSSY  
IAPISSPLFYQKLSQTNRSLEAPWIVHRVPYCILSSRVNEVWRFEPMAQ  
KDTVQDEDDFTVEFSQSSLNEFKIKHRGEIHGFIGFFSANLYNNIFLSTL  
PNDSTVRLKFSEETLMNTRREENLIKCDHTPNMTSWSPPIIFPLKQPISE  
IDDSLSVLMSRIHSDTEQKVWYEWSELSFIYMLSNYTSAVTAASMTIP  
RSIVTDDTKTLAHRHYSATTNQLDNQIDLDQDIENEEQGFSLNLETG  
WQSVQDIHGLSETAKPDHLDKSTKALEPSNELPRHEDLEED  
VPEVHVRVKTSTLHNVCGRFSLPL

YBL085W, 3443 bp, CDS: 501-3443 (SEQ ID NO 31)

AAAGGGAAGTATGGCATGCCTAGAAATCTTTCTGGAAAACCTGAAGCAT  
ATCATATAATTGTATGAACCTGTCCTTCAAAGATGTTACCAAATATTCA  
AGAGTATGTGAGCTTTCTATTCTATTGACGCGTAAGAAAGGCTATCACGT  
GTGGGGGGGAGAGCTCAGCCACATTGCACTACTTTGAAACCGCGTAGTC  
GGAAACGACATTCCCCGTACCAAAACAAACGAAAGGACGTGAAAGGTAA  
ATGAATAACATGGCACTAAAAATTTGGCAGAAAACGAAAAAAAAGGAA  
AAAGAACTGAAACTATACGCTTCCCTTAGGATACTTTCTGATTTACAT  
CCGAAGAATTGGGTGCGTCAATTAAAGGCAATTCTTCGCTCTATCAAGCA  
GTTTTACTGCGTCTGTCTAAAGAAACAATTGTTTTACTGAATTTCAACAA  
AGTTCTAACTCGAGGTGACCGGAGGCCACTGTAATAATAAAAAATAGAAG  
ATGAGTCTCGAAGGAAATACCTTAGGCAAAGGGGCCAAATCTTTTCCTCT  
GTATATTGCGGTAAATCAGTACTCTAAACGAATGGAGGACGAGCTCAATA  
TGAAACCAGGTGATAAAATTAAAGTCATTACTGATGATGGGGAGTACAAT  
GACGGCTGGTATTATGGGCGCAATTTGAGAACCAAAGAGGAAGGTTTATA  
CCCAGCGGTATTTACCAAAAGAATAGCAATAGAAAAACCAGAGAACCTGC  
ACAAATCACCAACCCAAGAGAGTGGAAATTCTGGTGTTAAATATGGAAT  
TTAAATGATTCTGCGAGTAACATAGGTAAAGTCTCCTCGCATCAACAGGA  
GAACAGATATACATCATTGAAAAGTACAATGAGCGATATAGACAAAGCCT  
TGGAAGAGCTAAGAAGTGGTTCAGTTGAACAAGAGGTATCAAATCGCCC  
ACACGCGTGCCCGAAGTTAGCACTCCACAGTTGCAAGATGAACAGACTTT  
GATTCAGAAAAAACAGAAATGAGGAAAACACGACACATGACTCGTTAT  
TTTCTAGCACAGCGGATTTAACTTAAGTTCTGAATCTTTGAAGAATATA  
AGTAAGTCAAATATATCAACAAAATCCCTAGAACCGAGTTCGGAATCAGT  
TCGTCAATTAGATTTGAAAATGGCTAAAAGTTGGAGCCCAGAAGAGGTTA  
CTGATTACTTTAGCTTGGTTGGATTTGATCAATCCACTTGCAATAAATTC  
AAAGAGCATCAAGTCTCCGGAAAAATACTACTGGAATTAGAACTGGAACA  
CCTAAAAGAATTGGAATAAATTTCTTTTGGTATAAGATTTTCAGATATTCA  
AAGAAATAAGGAACATCAAGTCTGCAATTGATTTCGTCTGCAATAAACTG  
GACGCCGACTACTCTACCTTTGCTTTTGAACCAAGCTGCCCACTAAT  
GCCTGCAGCCACTGTAAATAGAGACGAAATCCAACAACAAATTTCTCTCA  
AGTGTAAACAAGTTGTCAAGTGAAAGCTCTGATAGAAAATCATCTTCGGTC  
ACCACAGAATTGCAAAGACCAAGCTCGGTTGTTGTTAATCCAATTTTAA  
ACTTCACGACCCAGCTGAGCAGATCCTAGATATGACAGAAGTTCCTAATT  
TGTTTGCTGATAAAGATATTTTCAATCACCGGGAAGGGCTCCAAAACCA  
CCATCATATCCAAGTCCAGTTCAACCTCCACAATCGCCCTCTTTTAATAA  
CAGGTACACAAATAATAACGCAAGGTTTCTCTCAAACAACATATCCAC  
CTAAAAACAAGAACCAACCGTTTATTCAAATGGGCTAATTCCAAATTCT  
TCGACATCTTCCGATAATTCAACGGGCAAGTTCAAATTCCTGCCATGAA  
TGGTCATGACTCGAACTCTAGGAAAACAACACTGACATCTGCTACTATAC  
CTTCTATTAAACACGGTTAACACAGATGAATCTCTACCCGCAATTTCAAAT  
ATATCTTCAAATGCTACATCTCATCATCCGAACAGAAATTCGGTTGTTTA  
CAATAACCATAAGAGGACGGAATCCGGAAGCTCATTTGTTGATTTGTTCA  
ACAGGATTTCAATGCTATCGCCAGTCAAGTCAAGTTTCGACGAAGAAGAA

94/251

ACGAAACAACCTTCAAAAGCTAGCAGAGCAGTTTTTGGACTCAGCACGCAG  
AAAGTCGTCTTACGGACATTCAAGAGATGCCTCACTTTCTGAAATGAAAA  
AGCATAGGAGAACTCTTCTATATTATCTTTTTTTTCTTCAAAAAGTCAG  
TCTAATCCAACGTCACCAACCAACAACTTTCACTATCGATCCCGCAA  
GATGACTTCCCATTTCTCGTTCTCAGTCGAATTCCTATTTCGCATGCAAGAT  
CACAACTTTACTCCCATAGTAGAAAACACTCGTTAGTTACCAGCCCCCTTG  
AAAACCTCTTTAAGCCCTATAAATTCCAAATCCAATATTGCTTTAGCGCA  
TAGCGAAACTCCTACTAGTAGTAATAATAAGGAGGCAGTATCACAACCAA  
GTGAAGGGAAGCACAAGCACAAGCACAAGCACAAGCACAAGCACAACAC  
AAGAACAGTAGCTCCAAAGATGGCTCTTCCGAAGAAAAAAGCAAAAAGAA  
ATTATTTAGTAGCACCAAAGAATCATTTGTAGGAAGCAAGGAATTCAAAA  
GATCTCCCAGTGAACCTACCCAAAAATCTACCAAATCGATACTTCCCAGG  
TCGAATGCTAAAAAGCAACAAACATCTGCTTTTACCGAAGGTATACGCTC  
TATCACAGCAAAGGAATCTATGCAAACCTGCGGACTGTTTCAGGCTGGATGA  
GCAAAAAAGGTACCGGTGCTATGGGGACTTGGAACAACGGTTTTTCACA  
CTTCATGGAACAAGGCTTTCTTATTTTACGAATACCAATGATGAGAAGGA  
GCGTGGCCTGATAGATATAACGGCACATAGGGTCTTACCTGCCAGTGATG  
ATGATAGGCTCATTTTCCTTATACGCTGCGAGCTTAGGAAAAGGAAAATAC  
TGTTTTCAAATTGGTCCCTCCGCAACCGGGGTCCAAAAAGGGGCTAACCTT  
TACAGAACCTCGCGTTCACTATTTTGCAGTTGAGAATAAATCTGAAATGA  
AGGCATGGCTGTGAGCCATAATAAAGGCCACTATTGATATTGATACAAGC  
GTCCCTGTCAATTAGTTCATATGCCACACCAACGATACCTCTAAGCAAGGC  
ACAGACGCTATTGGAAGAAGCTAGGTTACAAACCCAGTTAAGAGATGCTG  
AAGAGGAAGAGGGAAGAGATCAATTTGGATGGGATGACACCCAAAATAAA  
AGAAATTCTAATTATCCAATCGAACAAGATCAATTTGAGACCAGCGATTA  
CCTGGAAAGTTTCAGCATTTGAATACCCTGGTGGCAGACTTTGA

YBL085W, 980 aa (SEQ ID NO 32)

MSLEGNTLGKGAKSFPLYIAVNQYSKRMEDELNMKPGDKIKVITDDGEYN  
DGWYYGRNLRKTKEGLYPVFTKRIAIEKPENLHKSPTQESGNSGVKYGN  
LNDSASNIGKVSSHQENRYTSLKSTMSDIDKALEELRSGSVEQEVSKSP  
TRVPEVSTPQLQDEQTLIQEKTRNEENTTHDSLFSSTADLNLSSSLKNI  
SKSNISTKSLEPSSSVRQLDLKMAKSWSPVEVTDYFSLVGFQDQSTCNKF  
KEHQVSGKILLELELEHLKELEINSFGIRFQIFKEIRNIKSAIDSSSNKL  
DAHYSTFAFENQAAQLMPAATVNRDEIQQQISSKCNKLSSESSDRKSSSV  
TTELQRPSSVVVNPFLHDPAEQILDMTEVPNLFADKDFESPGRAPKP  
PSYPSPVQPPQSPSFMNRYTMNARFPPQTTYPPKNKNPTVYSNGLIPNS  
STSSDNSTGKFKFPAMNGHDSNSRKTTLTSATIPSINTVNTDESLPAISN  
ISSNATSHHPNRNSVVYNNHKRTESGSSFVDLFNRISMLSPVKSSFDEEE  
TKQPSKASRAVFDASARRKSSYGHSDASLSEMKKHRRNSSILSFFSSKSQ  
SNPTSPKQTFITIDPAKMTSHSRQSNSYSHARSQSYSHSRKHS�VTSPL  
KTSLSPIINSKSNIALAHSETPTSSNNKEAVSQPSEGGKHKHKHKHKSKHKH  
KNSSSKDGSSEKSKKKLFSSTKESFVGSKEFKRSPSELTQKSTKSILPR  
SNAKKQQTSAFTEGIRSITAKESMQTADCSGWMSKKGTGAMGTWKQRFPT  
LHGTRLSTYFTNTNDEKERGLIDITAHRLVLPASDDRLISLYAASLGKGY  
CFKLVPQPGSKKGLTFTEPRVHYFAVENKSEMKAWSAIIKATIDIDTS  
VPVISSYATPTIPLSKAQTLLLEEARLQTLRDAEEEEGRDQFGWDDTQNK  
RNSNYPIDQDQFETSDYLESSAFEYPPGRL

YDR545W, 5891 bp, CDS: 501-5891 (SEQ ID NO 137)

TTCTATTATATTGGTCTTTTCGAGAGCGGAAGAAGTTGTAGGCTAAGCGC  
AGGCTAAGCGTAGGTCCATATTTAAAGTATCCAAGAGAATATCCACGAAG  
CGGCTGAGCAACGAACAGAATCCTGGTTCTCCTCGACTAAGCAGATAGTT  
AAGATACTGTGCACCATGGAAAATTGAAAACGAAAGTACGTACCGACTACT  
TTATTTTTGCAGGCCGGAATCAAGCGATGAATGAGACATCCTTCTGTTT  
TCTATGTTGGGACAGACAGTCGCTTATCTTAGTGAGATTTCTTATTAAT

95/251

GAATTTTCTTTGCTGCTGCTGGAGATTTGCACCTGCATAGCGCAGATTCT  
GCTTCTTCTCAATAGAGTAGCTTAATTATTACATTCTTAGATGATGATAA  
GACGGAACTGGACAATCTTTTGTATATTGATGGATTTCTTGTCAAAA  
AGCATAACAATCAACATACTATTGTTAATTTCGAACTTACAAAAATAAA  
ATGAAAGTTTCCGATAGGCGTAAGTTTGAAAAAGCAAACCTTGACGAGTT  
TGAGTCGGCTCTAAATAACAAAAACGACTTGGTACATTGTCCCTCAATAA  
CTTTATTTGAATCGATCCCCACGGAAGTGCGGTCATTCTACGAAGACGAA  
AAGTCTGGCCTAATCAAAGTGGTAAAATTCAGAACTGGTGCAATGGATAG  
GAAAAGGTCTTTTGAAAAAATTGTCATTTCCGTCATGGTCGGGAAAAATG  
TACAAAAGTTCTTGACATTTGTTGAAGACGAACCAGATTTCCAGGGCGGA  
CCAATCCCTTCAAAGTATCTTATTCCCAAGAAAATCAACTTGATGGTCTA  
CACGTTGTTTCAAAGTGCATACTTTGAAATTCAATAGAAAGGATTACGATA  
CCCTTTCTCTTTTTTACCTCAACAGAGGATACTATAATGAGTTGAGTTTC  
CGTGTCTGGAACGTTGTCACGAAATAGCGAGTGCCAGGCCGAACGACAG  
CTCTACGATGCGTACTTTCACTGACTTTGTTTCTGGCGCACCTATTGTAA  
GGAGTCTTCAGAAAAGCACCATAAGGAAATATGGGTACAATTTGGCACCC  
TACATGTTCTTGTACTACACGTAGATGAGCTATCGATTTTTTCTGCATA  
CCAAGCAAGTTTACCTGGCGAAAAGAAAGTCGACACAGAGCGGCTGAAGC  
GTGATCTATGCCCACGTAAACCCATTGAGATAAAGTACTTTTCACAGATA  
TGTAACGATATGATGAACAAAAAGACCGATTGGGTGATATTTTGCATAT  
TATCTTGCGAGCATGTGCGCTCAATTTCGGGGCGGGTCCCCGTGGTGGCG  
CTGGTGACGAAGAGGATCGATCTATTACGAATGAAGAACCATTATTCCC  
TCTGTGGACGAGCATGGCTTGAAAGTATGTAAGTTGCGTAGTCCCTAACAC  
TCCACGAAGACTCAGAAAAACACTAGATGCCGTGAAAGCTTTATTGGTGT  
CGTCTTGTGCTTGTACTGCAAGGGATTTAGATATATTGATGACACCAAC  
GGCGTTGCAATGTGGAATGGATCAAAATTCTGTACCACGAAGTAGCGCA  
GGAAACCAAGCTGAAGGACTCTTATAGAATAACTTTGGTACCTTCTTCTG  
ATGGTATATCAGTATGTGGAACCTTTTAAATCGCGAGTATGTCCGCGGC  
TTTTACTTTGTCATGCAAGGCTCAGTTCGATAACCTTTGGGGAGAGTTGAA  
CAACTGCTTTTATATGCCTACAGTGGTTGATATTGCCAGCCTCATTTTGC  
GTAATCGAGAAGTTTGTTCAGAGAGCCAAAGCGAGGAATTGACGAGTAT  
CTGGAAAACGATTCTTTTCTTCAAATGATACCTGTTAAATATCGTGAAAT  
TGTGCTGCCCAAGTTGAGAAGAGATACTAACAAAATGACCGCGGCTCTTA  
AAAATAAAGTCACTGTTGCAATTGACGAGCTTACGGTGCCACTTATGTGG  
ATGGTCCATTTTGCCGTAGGATACCTTACCGTTATCCAGAGCTTCAGCT  
ACTCGCTTTTGCCGGTCTCAGCGCAACGTATACGTCGATGATACAACAA  
GACGCATCCAACGTACACTGATTACAACAAGAACGGTTTCATCGGAGCCT  
CGACTTAAGACGCTTGACGGACTCACTTCAGATTACGTGTTTTATTTTGT  
CACTGTGCTAAGGCAAATGCAAATATGTGCGCTTGGTAACAGTTATGACG  
CTTTTAAATCATGATCCTTGGATGGATGTGGTGGGATTGAGGATCCAGAT  
CAAGTAACAAATCGAGACATTTGAGGATAGTTTTGTATTCTTACATGTT  
TCTGAATACCGCGAAGGGCTGTCTGGTTGAATACGCAACTTTTCGGCAGT  
ACATGAGGGAACCTCCGAAGAATGCACCTCAGAAGCTGAATTTTCGGGAG  
ATGCGTCAGGGGTTGATTGCCCTAGGACGGCACTGCGTAGGTAGCAGATT  
TGAAACAGATTTGTACGAGTCGGCGACGAGTGAACATGAGCAATCATT  
CCGTTCAAACAGGGCGAAATATTTACGGTGTGGATTCTTTTTCTGTTAACT  
AGTGTGAGTGGGACGACCGCCACTTTATTGAGGAACGAGCTTCCGAGCG  
CTGGATTCAATGGTTAGGCCTTGAAAGCGACTACCATTGTTTCTTCTA  
GTACTCGGAATGCGGAAGACGTAGTGGCAGGTGAGGCGGCGAGTTGAGAT  
CATGATCAAAAAATTTCAAGAGTAACGCGAAAAAGCCCCGAGAGCCCAA  
GAGTACAAACGATATCCTCGTCGAGGCCAGAACTCTTTGGCAGCTCCT  
TTGAATTCAGGGACTTGCATCAGTTGCGCTTATGTGATGAAATATACATG  
GCAGACACACCCTCTGTGGCAGTACAGGCCCCACCGGGCTATGGTAAGAC  
GGAGTTATTTTCATCTCCCCTTGATAGCACTGGCGTCTAAGGGCGACGTGA  
AATATGTGTCGTTTTCTGTTTGTACCGTACACAGTGTGCTTGCTAATTGC  
ATGATCAGGTTGAGCCGATGCGGTTGCTTGAATGTGGCCCCCTGTAAGAAA

96/251

CTTTATTGAAGAAGGTTGCGATGGCGTTACTGATTTATACGTGGGGATCT  
ACGATGATCTTGCTAGCACTAATTTACAGACAGGATAGCTGCGTGGGAG  
AATATTGTTGAGTGACCTTTAGGACCAACAACGTAAAATTGGGTTACCT  
CATTGTAGATGAGTTTCACAACCTTTGAAACGGAGGTCTACCGGCAGTCGC  
AATTTGGGGGCATAACTAACCTTGATTTTGACGCTTTTGAGAAAGCAATC  
TTTTTTGAGCGGCACAGCACCTGAGGCTGTAGCTGATGCTGCGTTGCAGCG  
TATTGGGCTTACGGGACTGGCCAAGAAGTCGATGGACATCAACGAGCTCA  
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TAGCCCTCTTTGAAATTGAACCAGAGTCGAAGGCCATTGTAGTTGCAAGC  
ACAACCAACGAAGTGGAAGAATTGGCCTGCTCTTGAGAAAAGTATTTTAG  
GGTGGTATGGATACACGGGAAGCTGGGTGCTGCAGAAAAGGTGCTCTCGCA  
CAAAGGAGTTTGTCACTGACGGTAGCATGCGAGTTCTCATCGGAACGAAA  
TTAGTGACTGAAGGAATTGACATTAAGCAATTGATGATGGTGATCATGCT  
TGATAATAGACTTAATATTATTGAGCTCATTCAAGGCGTAGGGAGACTAA  
GAGATGGGGGCTCTGTTATCTATTATCTAGAAAAAACAGTTGGGCGGCA  
AGGAATCGTAAGGGTGAATTACCACCGATTAAAGGAAGGCTGTATAACCGA  
ACAGGTACGCGAGTTCTATGGACTTGAATCAAAGAAAGGAAAAAAGGGCC  
AGCATGTTGGATGCTGTGGCTCCAGGACAGACCTGTCTGCTGACACAGTG  
GAACTGATAGAAAGAATGGACAGATTGGCTGAAAAACAGGCGACAGCTTC  
CATGTGCGATCATTGCGTTACCGTCTAGCTTCCAGGAGAGCAATAGCAGTG  
ACAGGTGCAGAAAGTATTGCAGCAGTGATGAGGACAGCGACACGTGCATT  
CATGGTAGTGCTAATGCCAGTACCAATGCGACTACCAACTCCAGCACTAA  
TGCTACTACCACTGCCAGCACCAACGTGAGGACTAGTGCTACTACCACTG  
CCAGCATCAACGTGAGGACTAGTGCGATTACCACTGAAAGTACCAACTCC  
AGCACTAATGCTACTACCACTGCCAGCACCAACGTGAGGACTAGTGCTAC  
TACCACTGCCAGCATCAACGTGAGGACTAGTGCGACTACCACTGAAAGTA  
CCAACTCCAACACTAGTGCTACTACCACCGAAAGTACCGACTCCAACACT  
AGTGCTACTACCACCGAAAGTACCGACTCCAACACTAGTGCTACTACCAC  
TGCTAGCACCAACTCCAGCACTAATGCCACTACCACTGCTAGCACCAACT  
CCAGCACTAATGCCACTACCACTGAAAGTACCAACGCTAGTGCCAAGGAG  
GACGCCAATAAAGATGGCAATGCTGAGGATAATAGATTCCATCCAGTCAC  
CGACATTAACAAAGAGTCGTATAAGCGGAAAGGGAGTCAAATGGTTTTGC  
TAGAGAGAAAGAACTGAAAGCACAAATTTCCCAATACTTCCGAGAATATG  
AATGTCTTACAGTTTCTTGGATTTCGGTCTGACGAAATTAAACATCTTTT  
CCTCTATGGTATTGACGTATACTTCTGCCAGAGGGAGTATTCACACAAT  
ACGGATTATGCAAGGGCTGTCAAAGATGTTTCGAGCTCTGTGTCTGTTGG  
GCTGGCCAGAAAGTATCGTATCGGAGGATGGCTTGGGAAGCACTAGCTGT  
GGAGAGAATGCTGCGAAATGACGAGGAATACAAAGAATACTTGGAAGACA  
TCGAGCCATATCATGGGGACCTGTAGGATATTTGAAATATTTTAGCGTA  
AAAAGGGGAGAGATCTACTCTCAGATACAGAGAAATTATGCTTGGTACCT  
GGCCATTACTAGAAGAAGAGAAACAATTAGTGTATTGGATTGACAAAGAG  
GCAAGCAAGGGAGCCAAGTTTTCCGCATGTCTGGAAGGCAGATCAAAGAG  
TTGTATTATAAAGTATGGAGCAACTTGCGTGAATCGAAGACAGAGGTGCT  
GCAGTACTTTTTGAACTGGGACGAGAAAAAGTGCCGGGAAGAATGGGAGG  
CAAAAGACGATACGGTCTTTGTGGAAGCGCTCGAGAAAGTTGGAGTTTTT  
CAGCGTTTTGCGTTCCATGACGAGCGCTGGACTGCAGGGTCCGCAGTACGT  
CAAGCTGCAGTTTAGCAGGCATCATCGACAGTTGAGGAGCAGATATGAAT  
TAAGTCTAGGAATGCACCTTGCGAGATCAGCTTGCGCTGGGAGTTACCCCA  
TCTAAAGTGCCGCATTGGACGGCATTCTGTGCGATGCTGATAGGGCTGTT  
CTACAATAAAACATTTCCGCAGAACTGGAATATCTTTTGGAGCAGATTT  
CGGAGGTGTGGTTGTTACCACATTGGCTTGATTTGGCAAACGTTGAAGTT  
CTCGCTGCAGATAACACGAGGGTACCGCTGTACATGCTGATGGTAGCGGT  
TCACAAAGAGCTGGATAGCGATGATGTTCCAGACGGTAGATTTGATATAA  
TATTACTATGTAGAGATTTCGAGCAGAGAAGTTGGAGAGTGA

97/251

YDR545W, 1796 aa (SEQ ID NO 138)  
MKVSDRRKFEEKANFDEFESALNNKNDLVHCPSITLFESIPTEVRSFYEDE  
KSGLIKVVKFRTGAMDRKRSFEKIVISVMVGKNVQKFLTFVEDEPDFQGG  
PIPSKYLI PKKINLMVYTLFQVHTLKFNRKDYDTLSLFYLNRGYYNELSF  
RVLERCHEIASARPNDSSMTMRTFTDFVSGAPIVRSLQKSTIRKYGYNLAP  
YMFLLLHVDELSIFSAYQASLPGEKKVDTERLKRDLCPRKPIEIKYFSQI  
CNDMMNKKDR LGDILHIILRACALNFGAGPRGGAGDEEDRSITNEEPIIP  
SVDEHGLKVCKLRSPNTPRRLRKTLDVAKALLVSSCACTARDLDIFDDTN  
GVAMWKWIKILYHEVAQETTLKDSYRITLVPSSDGI SVCGKLFNREYVRG  
FYFACKAQFDNLWGELNNCFYMP TVVDIASLILRNREVLFREPKRGIDEY  
LEND SFLQMI PVKYREIVLPKLRRDTNKM TAALKNKVTV AIDELTVPLMW  
MVHFVAVGYPYRPELQLLAFAGPQRNVYVDDTTRRIQLYTDYNKGSSEP  
RLKTL DGLTSDYVFYFVTVLRQM QICALGNSYDAFNHDPWMDVVG FEDPD  
QVTNRDISRIVLYSYMFLNTAKGCLVEYATFRQYMREL PKNAPQKLN FRE  
MRQGLIALGRHCVGSRFETDLYESATSELMANHSVQTGRNIYGVDSFSLT  
SVSGTTATLLQERASERW IQWLGLES DYHCSFSSTRNAEDVVAGEAASSD  
HDQKISRVT RKRPREPKSTNDILVAGQK LFGSSFEFRDLHQLRLCHEIYM  
ADTPSAVAVQAPPGYGKTELFHLPLIALASKGDVKYVSFLFVPYTVLLANC  
MIRLSRCGCLNVAPVRNFIEEGCDGVTDLYVGIYDDLASTNFTDRIA AWE  
NIVECTFR TNNVKLGYLIVDEFHNFETEVRQS QFGGITNLDFDAFEKAI  
FLSGTAPEAVADAALQRIGLTGLAKKSMDINELKRSEDL SRGLSSYPTRM  
FNLIKEKSEVPLGHVHKIWKVESQPEEALKLLLALFEIEPESKAIVVAS  
TTNEVEELACSWRKYFRVWVIHGKLGAAEKVSRTKEFVTDGSMRVLIGTK  
LVTEGIDIKQLMMVIMLDNRLNIIELIQGVGR LRDGGLCYLLSRKNSWAA  
RNRKGELPPIKEGCITEQVREFYGLSEKKGKKGQHVGCCGSRDLSADTV  
ELIERMDRLAEKQATASMSIIALPSSFQESNSSDRCKYCSSDESDT CI  
HGSANASTNATNSSTNATTTASTNVRTSATTTASINVRTSAITTESTNS  
STNATTTASTNVRTSATTTASINVRTSATTTTESTNSNTSATTTTESTDSNT  
SATTTTESTDSNTSATTTASTNSSTNATTTASTNSSTNATTTTESTNASAKE  
DANKDGN AEDNRFHPVTDINKESYKRKGSQMVLLERKKLKAQFPNTSENM  
NVLQFLGFRSDEIKHFLY GIDVYFCPEGVFTQYGLCKGCKMFELCVCW  
AGQKVSYRRMAWEAL AVERMLRNDEEYKEYLEDIEPYHGD PVGYLKYFSV  
KRGEIYSQIQ RNYAWYLAI TRRRETISVLDSTRGKQGSQVFRMSGRIKE  
LYYKVWSNLRESKTEVLQYFLNWDEKKCREWEAKDDTVFVEALEKGVF  
QRLRSMTSAGLQGPQYVKLQFSRHRQLRSRYELSLGMHLRDQLALGVTP  
SKVPHWTAFLSMLIGLFYNKTFRQKLEYLLEQISEVWLLPHWLDLANVEV  
LAADNTRVPLYMLMVAVHKELDSDDVPDGRFDIILLCRDSSREVGE

YCR005C, 1883 bp, CDS: 501-1883 (SEQ ID NO 71)  
AGAGTTGTTGCCACAACATAAGCCGCTTTGGAGTGTGAACAAATCCGTC  
CTTGGGTCATTCAATCAATGGCTTGGCGGTATCTCAAAAGAGCGCAAAC T  
AATAGCGCGCACATTCGACGCATTTATCCGGTGGTCATCGACTAGGGGCG  
AAGAGGTCACGACCTATTTTTTCTTGCAGAAAAAAGTGTGACCTTTTCC  
GTAGCTAGACGCTATCAGGGCGTCAGCAATGGGAGGCACAGCGGAAAAA  
CAATAACAATGGTAAGCGCAATTACCTTTTGAGCGTTACATTTCGTATGAA  
ATTGGTGACGTTAATCTAAAGATAGTCATGCTCTCAAAAGGGCCCATTAT  
TCTCGACGTTGAGCGTATATAAGACTATTAAAACCTGGTTCTTTAGATAT  
GGTGTTCGTTCCCTCATTATTAAGTTTCAGGGAACAATATCAACACATATC  
ATAACAGGTTCTCAAACTTTTTGTTTTAATAATACTAGTAACAAGAAAA  
ATGACAGTTCCTTATCTAAATTCAAACAGAAATGTTGCATCATATTTACA  
ATCAAAATTCAGCCAAGAAAAGACTCTAAAAGAGAGATTTAGCGAAATCT  
ACCCCATCCATGCTCAAGATGTAAGGCAATTCGTTAAAGAGCATGGCAAA  
ACTAAAATTAGCGATGTTCTATTAGAACAGGTATATGGTGGTATGAGAGG  
TATTCCAGGGAGCGTATGGGAAGGTTCCGTTTTGGACCCAGAAGACGGTA  
TTCGTTTCAGAGGTCGTACGATCGCCGACATTCAAAAGGACCTGCCCAAG  
GCAAAAGGAAGCTCACAACTACCAGAAGCTCTCTTTTGGTTATTGCT

98/251

AACTGGCGAGGTTCCAACCTCAAGCGCAAGTTGAAAACCTTATCAGCTGATC  
TAATGTCAAGATCGGAACTACCTAGTCATGTCGTTCAACTTTTGGATAAT  
TTACCAAAGGACTTACACCCAATGGCTCAATTCTCTATTGCTGTAACGTC  
CTTGGAAAGCGAGTCAAAGTTTGTCTAAGGCTTATGCTCAAGGAATTTCCA  
AGCAAGATTATTGGAGTTATACTTTTGAAGATTCACTAGACTTGTGGGT  
AAATTGCCAGTTATTGCAGCTAAAATTTATCGTAATGTATTCAAAGATGG  
CAAAATGGGTGAAGTGGACCCAAATGCCGATTATGCTAAAAATCTGGTCA  
ACTTGATTGGTTCTAAGGATGAAGATTTTCGTGGACTTGATGAGACTTTAT  
TTAACCATTCATTCCGATCACGAAGGTGGTAATGTATCTGCACATACATC  
CCATCTTGTGGGCTCAGCACTATCATCACCTTATCTGTCCCTTGCATCAG  
GTTTGAACGGGTGGCTGGCCCACTTCATGGGCGTGCTAATCAAGAAGTA  
CTAGAATGGTTATTTGCACTTAAAGAAGAGGTAAATGATGACTACTCTAA  
AGATACGATCGAAAAATATTTATGGGATACTCTAAACTCAGGAAGAGTCA  
TTCCCGGTTATGGTCATGCTGTGCTAAGGAAACTGATCCTCGTTATATG  
GCTCAGCGTAAGTTTGCCATGGACCATTTTCCAGATTATGAATTATTCAA  
GTTAGTTTTCATCAATATACGAGGTAGCACCTGGCGTATTGACTGAACATG  
GTAAACTAAAAATCCATGGCCAAATGTAGATGCTCACTCTGGTGTCTTA  
TTACAATATTATGGACTAAAAGAATCTTCTTTCTATACCGTTTATTGG  
CGTTTCAAGGGCATTGGTATTCTTGCTCAATTGATCACTGATAGGGCCA  
TCGGTGCTTCCATTGAAAGGCCAAAGTCCTATTCTACTGAGAAATACAAG  
GAATTGGTCAAAAACATTGAAAGCAAACATATAG

YCR005C, 460 aa (SEQ ID NO 72)

MTVPYLSNRNVASYLQSNSSQEKTLKERFSEIYPIHAQDVRQFVKEHGK  
TKISDVLLLEQVYGGMRGIPGSVWEGSVLDPEDGIRFRGRTIADIQKDLPK  
AKGSSQPLPEALFWLLLTGEVPTQAQVENLSADLMSRSELPSHVQLLDN  
LPKDLHPMAQFSIAVTALESESKFAKAYAQGISKQDYWSYTFEDSLDLG  
KLPVIAAKIYRNVFKDGKMGVEVDPNADYAKNLVNLIGSKDEDFVDLMRLY  
LTIHSDHEGGNVSAHTSHLVGSALSSPYLSLASGLNGLAGPLHGRANQEV  
LEWLFALKEEVNDYSKDTIEKYLWDTLNSGRVIPGYGHAVLRKTDPRYM  
AQRKFAMDHFDPDYELFKLVSSIYEVAPGVLTEHGKTKNPWPVNDAHSGVL  
LQYYGLKESSFYTVLFGVSRAFGILAQLITDRAIGASIERPKSYSTEKYK  
ELVKNIESKL

YOL126C, 1772 bp, CDS: 501-1772 (SEQ ID NO 345)

ATCCCCCTCACTTTTCCGTTTGTATCTCCTACTTTCTTACTTCCTTTTT  
TTCTTCTTTATTTGCTTGGTTTACCATTGAAGTCCATTTTTACTACAGAC  
AATAGCTAGTCATTGCTATCTTCCGTTTGTCACTTTTTTTCAAATTTCT  
CATCTATATAGCGAAGTACGGAAAAGATGTCACTTGCCGGCATCTCGGCC  
TTCCCCGGCCAAATGGACTCATCATCTACGATACGGCCCCCTTTAATCCGC  
AATTACTTTGCCCCATTGCGCCGTAGCCGTTCTAAAGCCGCCGTGCCTTGC  
CCCCAATACTCCCCTAATGATCCGGGAAGTTCCGGTTTTTTTCTTTGTT  
TAGTGGCATTTTGTGTTGCCCAAGGTTGGGAAGGTCCGATTTGACTTTAA  
GGAACACGGAAGGTATCTAAGGTTTCTAAAAACAATATACACGCGCGTG  
CGTAGATATATAAAGATAAAGATTTATCGATATGAGATAAAGATTGCTGC  
ATGATTCTCTCTTGATTCTTTTCCCTGTATATATTTTCTCCCCTTCTG  
TATAAATCGTACAGTCAGAAGTAGTCCAGAATATAGTGCTGCAGACTATT  
ACAAAAGTTCAATACAATATCATAAAAGTTATAGTAACATGCCCTCACTCA  
GTTACACCATCCATAGAACAAGATTTCGTTAAAAATTGCCATTTTAGGTGC  
TGCCGGTGGTATCGGGCAGTCGTTATCGCTGCTTTTGAAAGCTCAGTTGC  
AATACCAGTTAAAGGAGAGCAACCGGAGCGTTACCCACATTCATCTGGCT  
CTTTACGATGTCAACCAAGAAGCCATCAACGGTGTACCGCCGACTTGTCT  
TCATATAGACACCCCCATTTCCGTGTCGAGCCACTCTCCTGCAGGTGGCA  
TTGAGAACTGTTTGCATAACGCTTCTATTGTTGTCATTCTGCAGGTGTT  
CCAAGAAAACCTGGCATGACTCGTGATGACTTATTTAACGTGAATGCTGG  
TATCATTAGCCAGCTCGGTGATTCTATTGCAGAATGTTGTGATCTTTCCA

99/251

AGGTC TTCGTTCTTGTCAATTTCCAACCCTGTAAATCTTTAGTCCCAGTG  
ATGGTTTCTAACATTCTTAAGAACCATCCTCAGTCTAGAAATTCGGGCAT  
TGAAAGAAGGATCATGGGTGTCACCAAGCTCGACATTGTCAGAGCGTCCA  
CTTTTCTACGTGAGATAAACATTGAGTCAGGGCTAACTCCTCGTGTTAAC  
TCCATGCCTGACGTCCCTGTAATTGGCGGGCATTCCTGGCGAGACTATTAT  
TCCGTTGTTTTACAGTCAAAC'TTCC'TATCGAGATTAATGAGGATCAAT  
TGAAATATTTAATACATAGAGTCCAATACGGTGGTGATGAAGTGGTCAAG  
GCCAAGAACGGTAAAGGTAGTGTACCT'TATCGATGGCCCATGCCGGTTA  
TAAGTGTGTTGTCCAATTTGTTTCTTTGTTATTTGGGTAACATTGAGCAGA  
TCCATGGAACCTACTATGTGCCAT'TAAAAGATGCGAACAACT'TCCCCATT  
GCTCCTGGGGCAGATCAAT'TATTGCCCTCTGGTGGACGGTGCAGACTACTT  
TGCCATACCATTAACTATTACTACAAAGGGTGTTCCTATGTGGATTATG  
ACATCGTTAATAGGATGAACGACATGGAACGCAACCAAATGTTGCCAATT  
TGCGTCTCCAGTTAAAGAAAAATATCGATAAGGGCTTGGAATTCGTTGC  
ATCGAGATCTGCATCATCTTAA

YOL126C, 423 aa (SEQ ID NO 346)

MILLILFLPCIFYFLPCINRTVRSSPEYSAADYYKSSIQYHKSYSNMPHS  
VTPSIEQDSLKIALGAAGGIGQSLSLLLKAQLQYQLKESNRSVTHIHLA  
LYDVNQEAINGVTADLSHIDTPI SVSSHSPAGGIENCLHNASIVVIPAGV  
PRKPGMTRDDL FNVNAGIISQLGDSIAECCDLSKVFLVISNPVNSLVPV  
MVSNILKNHPQSRNSGIERRIMGVTKLDIVRASTFLREINIESGLTPRVN  
SMPDVPVIGGHSGETIIPLFSSQSNFLSRLNEDQLKYLIHRVQYGGDEVVK  
AKNGKGSATLSMAHAGYKCVVQFVSLLLGNIEQIHGTYYVPLKDANNFPI  
APGADQLPLVDGADYFAIPLTITTKGVSYVDYDIVNRMNDMERNQMLPI  
CVSQLKKNIDKGLEFVASRSASS

YBR019C, 2600 bp, CDS: 501-2600 (SEQ ID NO 39)

ATCGCTTCGCTGATTAATTACCCAGAAATAAGGCTAAAAAATAATCGC  
ATTATCATCCTATGGTTGTTAATTTGATTTCGTTAATTTGAAGGTTTGTGG  
GGCCAGGTTACTGCCAATTTTTCCTCTTCATAACCATAAAAGCTAGTATT  
GTAGAATCTTTATTGTTCCGGAGCAGTGC GGCGCGAGGCACATCTGCGTTT  
CAGGAACCGGACCCGTGAAGACGAGGACGCACGGAGGAGAGTCTTCCGTC  
GGAGGGCTGTGCCCCGCTCGGCGGCTTCTAATCCGTACTTCAATATAGCA  
ATGAGCAGTTAAGCGTATTACTGAAAGTTCCAAAGAGAAGGTTTTTTTAG  
GCTAAGATAATGGGGCTCTTTACATTTCCACAACATATAAGTAAGATTAG  
ATATGGATATGTATATGGTGGTAATGCCATGTAATATGATTATTAACTT  
CTTTGCGTCCATCCAAAAAAAAGTAAGAATTTTTGAAAAATTC AATATAA  
ATGACAGCTCAGTTACAAAAGTGAAGTACTTCTAAAAATGTTTTGTTTAC  
AGGTGGTGTCTGGATACATTGGTTCACACACTGTGGTAGAGCTAATTGAGA  
ATGGATATGACTGTGTTGTGCTGATAACCTGTGCAATTC AACTTATGAT  
TCTGTAGCCAGGTTAGAGGTCTTGACCAAGCATCACATTCCCTTCTATGA  
GGTTGATTTGTGTGACCGAAAAGGTCTGGAAAAGGTTTTCAAAGAATATA  
AAATTGATTTCGGTAATTCACTTTGCTGGTTTAAAGGCTGTAGGTGAATCT  
ACACAAATCCCGCTGAGATACTATCACAATAACATTTTGGGAACTGTCGT  
TTTATTAGAGTTAATGCAACAAATACAACGTTTCCAAATTTGTTTTTTCAT  
CTTCTGCTACTGTCTATGGTGATGCTACGAGATTCCCAAATATGATTCCCT  
ATCCCAGAAGAATGTCCCTTAGGGCCTACTAATCCGTATGGTCATACGAA  
ATACGCCATTGAGAATATCTTGAATGATCTTTACAATAGCGACAAAAAA  
GTTGGAAGTTTGCTATCTTGCGTTATTTTAACCAATTGGCGCACATCCC  
TCTGGATTAATCGGAGAAGATCCGCTAGGTATACCAAACAATTTGTTGCC  
ATATATGGCTCAAGTAGCTGTGGTAGGCGCGAGAAGCTTTACATCTTCG  
GAGACGATTATGATTCCAGAGATGGTACCCCGATCAGGGATTATATCCAC  
GTAGTTGATCTAGCAAAAGGTCATATTGCAGCCCTGCAATACCTAGAGGC  
CTACAATGAAAATGAAGGTTTGTGTCTGTGAGTGGAAC TTGGGTTCCGGTA  
AAGGTTCTACAGTTTTTTGAAGTTTATCATGCATTCGCAAGCTTCTGGT



100/251

ATTGATCTTCCATACAAAGTTACGGGCAGAAGAGCAGGTGATGTTTTGAA  
CTTGACGGCTAAACCAGATAGGGCCAAACGCGAACTGAAATGGCAGACCG  
AGTTGCAGGTTGAAGACTCCTGCAAGGATTTATGGAAATGGACTACTGAG  
AATCCTTTTGGTTACCAGTTAAGGGGTGTCGAGGCCAGATTTTCCGCTGA  
AGATATGCGTTATGACGCAAGATTTGTGACTATTGGTGCCGGCACCAGAT  
TTCAAGCCACGTTTGCCAATTTGGGCGCCAGCATTGTTGACCTGAAAGTG  
AACGGACAATCAGTTGTTCTTGGCTATGAAAATGAGGAAGGGTATTTGAA  
TCCTGATAGTGCTTATATAGGCGCCACGATCGGCAGGTATGCTAATCGTA  
TTTTCGAAGGGTAAGTTTAGTTTATGCAACAAAGACTATCAGTTAACCGTT  
AATAACGGCGTTAATGCGAATCATAGTAGTATCGGTTCTTTCCACAGAAA  
AAGATTTTGGGACCCATCATTCAAAATCCTTCAAAGGATGTTTTTACCG  
CCGAGTACATGCTGATAGATAATGAGAAGGACACCGAATTTCCAGGTGAT  
CTATTGGTAACCATAACGTATACTGTGAACGTTGCCCCAAAAAAGTTTGA  
AATGGTATATAAAGGTAAATTGACTGCTGGTGAAGCGACGCCAATAAATT  
TAACAAATCATAGTTATTTCAATCTGAACAAGCCATATGGAGACACTATT  
GAGGGTACGGAGATTATGGTGCGTTCAAAAAAATCTGTTGATGTCGACAA  
AAACATGATTCTACGGGTAATATCGTCGATAGAGAAATTGCTACCTTTA  
ACTCTACAAAGCCAACGGTCTTAGGCCCCAAAAATCCCCAGTTTGATTGT  
TGTTTTGTGGTGGATGAAAATGCTAAGCCAAGTCAAATCAATACTCTAAA  
CAATGAATTGACGCTTATTGTCAAGGCTTTTCATCCCGATTCCAATATTA  
CATTAGAAGTTTTAAGTACAGAGCCAACCTTATCAATTTTATACCGGTGAT  
TTCTTGCTGCTGGTTACGAAGCAAGACAAGGTTTTGCAATTGAGCCTGG  
TAGATACATTGATGCTATCAATCAAGAGAAGTGGAAAGATTGTGTAACCT  
TGAAAAACGGTGAACTTACGGGTCCAAGATTGTCTACAGATTTTCTCTGA

YBR019C, 699 aa (SEQ ID NO 40)

MTAQLQSESTSKIIVLTGGAGYIGSHTVVELIENGYDCVVADNLSNSTYD  
SVARLEVLTKHHIPFYEVDLCDRKGLEKVFKEYKIDSVIHFAGLKAVGES  
TQIPLRYYHNNILGTVVLLLELMQQYNVSKFVSSSATVYGDATRFPMIP  
IPEECPLGPTNPYGHYKYAIENILNDLYNSDKKSWKFAILRYFNPIGAHP  
SGLIGEDPLGIPNNLLPYMAQVAVGRREKLYIFGDDYDSRDGTPIRDYIH  
VVDLAKDHLIAALQYLEAYNENEGLCREWNLGSGKGSTVFEVYHAFCKASG  
IDLPHYKVTGRRAGDVLNLTAKPDRAKRELKWQTELQVEDSCKDLWKWTTTE  
NPFQYQLRGVEARFSAEDMRYDARFVTIGAGTRFQATFANLGASIVDLKV  
NGQSVVLGYENEELNPD SAYIGATIGRYANRISKGFSLCNKDYQLTV  
NNGVNNANHSSIGSFHRKRFLGP I IQNPSKDVFTA EYMLIDNEKDTEFPD  
LLVTIQYTVNVAQKSL E MVYKGLTAGEATPINLTNHSYFNLNKPYGDTI  
EGTEIMVRSKKSVDVDKNMIPTGNIVDREIATFNSTKPTVLGPKNPQFDC  
CFVVDENAKPSQINTLNNELTLIVKAFHPDSNITLEVELSTEPTYQFYTG  
FLSAGYEARQGFAIEPGRYIDAINQENWKDCVTLKNGETYGSKIVYRFS

YDR345C, 2204 bp, CDS: 501-2204 (SEQ ID NO 123)

TCTTAGCTATATTCTTCCAGCTTCGCCTGCTGCCCCGGTCATCGTTCCTGT  
CACGTAGTTTTTCCGGATTTCGTCCGGCTCATATAATACCGCAATAAACAC  
GGAATATCTCGTTCCGCGGATTTCGGTTAAACTCTCGGTCGCGGATTATCA  
CAGAGAAAGCTTCGTGGAGAATTTTCCAGATTTTCCGCTTTCCCGGATG  
TTGGTATTTCGGAGGTCATTATACTGACCGCCATTATAATGACTGTACA  
ACGACCTTTCGGAGAAAGAACTCAATAACGATGTGGGACATTGGGG  
GCCCACTCAAAAAATCTGGGGACTATATCCCAAGAGAATTTCTCCAGAAG  
AGAAGAAAAGTCAAAGTTTTTTTTTCGCTTGGGGGTTGCATATAAATACAG  
GCGCTGTTTTATCTTACGATGAATATTCCATAATTTTACTTAATAGCTT  
TTCATAAATAATAGAATCACAAACAAAATTTACATCTGAGTTAAACAATC  
ATGAATTCAACTCCAGATTTAATATCTCCACAAAAGTCAAGTGAGAATTC  
GAATGCTGACCTGCCTTCGAATAGCTCTCAGGTAATGAACATGCCTGAAG  
AAAAAGGTGTTCAAGATGATTTCCAAGCTGAGGCCGACCAAGTACTTACC  
AACCCAAATACAGGTAAAGGTGCATATGTCACTGTGTCTATCTGTTGTGT

101/251

TATGGTTGCCTTCGGTGGTTTCGTTTTTCGGTTGGGATACGGTACCATTT  
CTGGTTTTCGTCGCCCAAACCTGATTTCTTGAGAAGATTTCGGTATGAAGCAT  
AAAGATGGTAGTTATTATTTGTCTAAGGTTAGAACTGGTTTAAATTGTCTC  
CATTTTTCAACATTGGTTGTGCCATTGGTGGTATTATTTTGGCTAAATTGG  
GTGATATGTACGGTCGTAAAATGGGTTTGATTGTCGTTGTTGTTATCTAC  
ATCATCGGTATTATTATTCAAATTGCATCCATCAACAAATGGTACCAATA  
TTTCATCGGTAGAATTATTTCCGGTTTGGGTGTTGGTGGTATTGCCGTTT  
TATCTCCTATGTTGATTTCTGAAGTCGCTCCTAAGGAAATGAGAGGTACT  
TTAGTCTCCTGTTACCAACTGATGATTACCTTGGGTATTTTCTTGGGTTA  
CTGTACCAACTTCGGTACTAAGAACTACTCCAACCTCTGTGCAATGGAGAG  
TTCCATTAGGTTTGTGTTTTGCCTGGGCTTTGTTTATGATCGGTGGTATG  
ACTTTCGTTCCAGAATCCCCACGTTATTTGGTTGAAGCTGGTCAAATTGA  
CGAAGCAAGAGCATCTCTTCCAAAGTTAACAAGGTTGCCCCAGACCATC  
CATTCATTCAACAAGAGTTGGAAGTTATTGAAGCTAGTGTGAAGAAGCT  
AGAGCTGCTGGTTTCAGCATCATGGGGTGAGTTGTTCACTGGTAAGCCGGC  
CATGTTTAAGCGTACTATGATGGGTATCATGATCCAATCTCTACAACAAT  
TGACTGGTGATAACTATTTCTTCTACTATGGTACTACCGTTTTTAACGCT  
GTTGGTATGAGTGATTTCTTTCGAAACTTCTATTGTTTTCGGTGTCTGTC  
CTTCTTCTCTACTTGTGTTCTTTGTACACTGTCGATCGTTTTGGACGTC  
GTAAGTGTGTTTATATGGTGCCATTGGTATGGTCTGCTGTTATGTAGTT  
TACGCTTCTGTTGGTGTCAACAGACTATGGCCAAATGGTGAAGGTAATGG  
TTCATCCAAGGGTGCTGGTAAGTGTATGATTGCTTTGCCTGTTTCTATA  
TTTTCTGTTTTGCTACCACTTGGGCTCCAATTGCTTATGTTGTTATTTCT  
GAAACTTTCCCATGAGAGTCAAGTCTAAGGCTATGCTTATTGCTACAGC  
TGCTAATTGGTTGTGGGGTTTCTTGATTGGTTTCTTCACCTCCATTTATTA  
CTGGTGCTATTAACCTTCTACTACGGTTACGTTTTTCATGGGCTGTATGGTT  
TTCGCCCTACTTCTACGTTTTCTTCTTTGTGCCAGAACTAAGGGTTTGAC  
TTTGGAAGAAGTCAATGATATGTACGCTGAAGGTGTTCTACCATGGAAGT  
CTGCTTCATGGGTTCCAACATCTCAAAGAGGTGCTAACTACGATGCTGAT  
GCATTGATGCATGATGACCAGCCATTCTACAAGAAAATGTTTCGGCAAGAA  
ATAA

YDR345C, 567 aa (SEQ ID NO 124)

MNSTPDLI SPQKSSSENSNADLPSNSSQVMNPPEEKGVQDDFQAEADQVLT  
NPNTGKGAYVTVSICCMVAFGGFVFGWDTGTISGFVAQTDFLRRFGMKH  
KDGSYYLSKVRTGLIVSIFNIGCAIGGIILAKLGDYGRKMGLIVVVVIY  
IIGIIIIQIASINKWYQYFIGRIISGLGVGGI AVLSPMLISEVAPKEMRGT  
LVSCYQLMITLGI FLGYCTNFGTKNYSNSVQWRVPLGLCF AWALFMIGGM  
TFVPESPRYLVEAGQIDEARASLSKVNKVAPDHPFIQQELEVIEASVEEA  
RAAGSASWGELFTGKPAMFKRTMMGIMIQLSLQQLTGDNYFFYYGTTVFNA  
VGMSDSFETSIVFGVVNFSTCCSLYTVDRFGRNCLLYGAIGMVCCYV  
YASVGVT RLWPNGEGNGSSKGAGNCMIVFACFYIFCFATWAPIAYVVIS  
ETFPLRVKSKAMSIATAANWLWGFLIGFFT PFITGAINFYGYVFMGCMV  
FAYFYVFFFVPETKGLTLEEVNDMYAEGVLPWKSASWVPTSQRGANYDAD  
ALMHDDQPFYKMF GK K

YKR097W, 2150 bp, CDS: 501-2150 (SEQ ID NO 263)

ATAGGAAAAAACCGAGCTTCCTTTTCATCCGGCGCGGCTGTGTTCTACATA  
TCACTGAAGCTCCGGGTATTTTAAGTTATACAAGGGAAAGATGCCGGCTA  
GACTAGCAAGTTTTAGGCTGCTTAACATTATGGATAGGCGGATAAAGGGC  
CCAAACAGGATTGTAAAGCTTAGACGCTTCTGGTTGGACAATGGTACGTT  
TGTGTATTAAAGTAAGGCTTGGCTGGGGATAGCAACATTGGGCAGAGTATA  
GAAGACCACAAAAAAAAGGTATATAAGGGCAGAGAAGTCTTTGTAATGTG  
TGTAACCTTCTCTCCATGTGTAATCAGTATTTCTACTTACTTCTTAAATA  
TACAGAAGTAAGACAGATAACCAACAGCCTTTCCAGATATACATATATA  
TCTTTATTTTCAGCTTAAACAATAATTATATTTGTTTAACTCAAAAATAAA

102/251

AAAAAAAAACCAAACTCACGCAACTAATTATTCCATAATAAAATAACAAC  
ATGTCCCCCTTCTAAATGAATGCTACAGTAGGATCTACTTCCGAAGTTGA  
ACAAAAATCAGACAAGAAATTGGCTCTTAGTGACGAAGTCACCACCATCA  
GACGCAATGCTCCAGCTGCCGTTTTGTATGAAGATGGTCTAAAAGAAAAAT  
AAAACGTGCATTTTCATCAAGCGGTGCATTGATCGCTTATTCGGGTGTTAA  
AACCAGGAAGATCTCCAAAGGACAAACGTATTGTTGAAGAACCTACCTCGA  
AAGACGAAATTTGGTGGGGTCCGGTCAATAAACCATGTTCTGAAAGAACA  
TGGTCTATCAACCGTGAAAGAGCTGCAGATTACTTGAGAACAAGAGACCA  
CATTTATATTGTTCGATGCATTTGTCAGGATGGGATCCAAAAATACAGAATCA  
AAGTCCGCGTTGTTTGTGCCAGGGCTTACCACGCTTTATTCATGACAAAT  
ATGCTTATTAGACCTACAGAAGAAGAAATTAGCCCATTTTGGAGAACCTGA  
TTTACTGTCTGGAAACGCTGGTCAGTTCCAGCCAAATTTACACACCCAGG  
ATATGTCCTTCAAAGAGTACTATAGAAATTAACCTTCAAAGCAATGGAAATG  
ATCATTTTATAGGTACCGAATACGCCGGTGAAATGAAAAAAGGTATTTTCAC  
AGTTATGTTTTTACTTGATGCCTGTGCACCATAACGTTTTAACTTTGCACT  
CTTCCGCCAACCCAGGGTATTCAAACGGTGACGTTACTTTATTCCTTTGGC  
CTAAGTGGTACCGGGAAAACCACTTTATCCGCAGACCCACATAGATTGTT  
GATCGGCGATGATGAACATTGTTGGTCCGACCATGGTGTCTTCAATATCG  
AAGGTGGTTGTTACGCCAAGTGATTAAATTTATCTGCCGAAAAGGAGCCT  
GAAATTTTCGACGCTATCAAGTTTGGTTCTGTATTAGAAAACGTTATCTA  
TGACGAGAAGTCGCATGTAGTCGACTATGACGACTCTTCTATTACTGAAA  
ATACTAGATGTGCCTACCCAATTGACTACATTCCAAGTGCCAAGATTCCA  
TGTTTTGGCGGACTCTCATCCAAAGAACATTATCCTGCTAACTTGTGATGC  
TTCCGGGTGTTTTTACCACCAGTATCTAAATTGACTCCTGAACAAGTCATGT  
ACCATTTTCATCTCTGGTTACACTTCTAAATGGCTGGTACTGAGCAAGGT  
GTCCTGAACCTGAACCAACATTTTCATCTTGTTCGGACAACCCCTTCCCT  
AGCCTTGACCCCTATTAGATACGCAACCATGTTAGCTACAAAGATGTCTC  
AACATAAAGCTAATGCGTACTTAATCAACACCGGCTGGACTGGTTCTTCC  
TACGTATCTGGTGGTAAACGTTGCCCATTTGAAGTACACAAGGGCCATTCT  
GGATTCTATTTCATGATGGTTCGTTAGCCAAATGAAACGTACGAAACTTTAC  
CGATTTTCAATCTTCAAGTACCTACCAAGGTTAACGGTGTTCAGCTGAG  
CTTTTGAATCCTGCTAAAACTGGTCTCAAGGTGAATCCAAATACAGAGG  
TGCAGTTACCAACTTGGCCAACTTGTTTGTTCAAAATTTCAAGATTTATC  
AAGACAGAGCCACACCAGATGTATTAGCCGCTGGTCCCTCAATTCGAGTAA

YKR097W, 549 aa (SEQ ID NO 264)

MSPSKMNATVSGSTSEVEQKIRQELALSDEVTTIRRNAPAAVLYEDGLKEN  
KTVISSSGALIAYSVKTGRSPKDKRIVEEPTSKDEIWWGPVKNKPCERT  
WSINRERAADYLRTRDHIYIVDAFAGWDPKYRIKVRVVCARAYHALFMTN  
MLIRPTEEEELAHFGEPDFTVWNAGQFPANLHTQDMSSKSTIEINFKAMEM  
IILGTEYAGEMKKGIFTVMFYLMPVHHNVLTLHSSANQGIQNGDVTLLFFG  
LSGTGKTTLSADPHRLIGDDEHCWSDHGVFNIEGGCYAKCINLSAEKEP  
EIFDAIKFGSVLENNVIYDEKSHVVDYDDSSITENTRCAYPIDYIPSAKIP  
CLADSHPKNIILLTCDASGVLPPVSKLTPEQVMYHFISGYTSKMAGTEQG  
VTEPEPTFSSCFGPFLALHPIRYATMLATKMSQHKANAYLINTGWTGSS  
YVSGGKRCPLKYTRAILDSIHDGSLANETYETLPIFNLQVPTKVNGVPAE  
LLNPAKNWSQGESKYRGAVTNLANLNFVQNFKIYQDRATPDVLAAGPQFE

YMR173W, 1793 bp, CDS: 501-1793 (SEQ ID NO 313)

AAACAAGTGTAACATAAATACATTCTGTAAATCTACAAAAATCGTTAGTG  
CTGTTTTCTTTTTGAGATTGAAAAGTACGAATCATAACATCTCTTATTC  
TGAGAAGGGTGCAATATGACGTAAATCAATGCGTACAAAGCGGTTTCCGGT  
GCTGGCCTGGCCCAACACAGTTTTTGGCGTGGTTGATTTTAAAAACCTTCG  
GGAAGGTGAAAAAACCACTCCGAAGGTTGAGGATGACAAATCGCCCCCTT  
AGCTGTGGCCATACAAGCTTGGCACCGACGAAAAAGGGAAAAAGGAAAAAG  
AATGTCGTACAAGAACTCTTACAACCACGTTGAGATTTTCATTTAACAACG

103/251

CCCCCCTTTCCATTATATAAGAAGGCATTAATTTTTATGTAATAAAAAA  
GAATTTCTCGAAAATGTCTTACAATTAATTTTTCTTTGTAGAGTAGGG  
CTTTAATAGACTGATATATACGGTATTATAAGTGAACGAAAAAACAGCA  
ATGGGTTTATTTGTATAAAGTGAAGCAATTTGCTAACAGCAATAATAACAA  
CAATGATTCTGGCAATAACAATCAAGGCGATTATGTTACCAAAGCTGAGA  
ATATGATCGGCGAAGATAGAGTCAATCAATTCAAAAGCAAAATCGGAGAG  
GACAGATTTGATAAGATGGAGTCCAAGGTTTCGTCAACAATTTTCTAATAC  
CTCTATAAATGACAACGACTCCAACAACAACGACTCATATGGTTCTAATA  
ACAACGATTCATATGGTTCTAACAACAATGATTCATATGGCTCTAACAAC  
AATGATTCATATGGCTCCAACAACAATGATTCATATGGCTCTAACAACGA  
TGATTCCTACGGTTCTTCCAACAAGAAGAAGAGCTCTTATGGTTCTAACA  
ATGACGATTCTGACGGCTCCAGCAACAACAATGACTCTTACGGTTCCAAC  
AACAATGACTCTTACGGTTCCAACAACAATGACTCTTACGGTTCCAACA  
TGACGACTCTTACGGTTTCGTCAACAAGAATAAGAGCTCTTACGGTTCCA  
ACAATGACGATTCTTATGGCTCTAACAATGATGATTCATATGGTTCTTCC  
AACAAGAAGAAGAGTTCTTATGGTTCCAGCAACAACGATTCGTATGGTTCT  
TAACAACGATGATTCATATGGTTCTAACAACAATGATTCATATGGCTCTA  
ACAACGATGATTCCTACGGTTCTTCCAACAAGAAGAAGAGCTCTTATGGT  
TCTAACAATGACGATTCGTACGGCTCCAGCAACAACAATGACTCTTACGG  
TTCCAACAATGACGACTCTTACGGTTTCGTCAACAAGAATAAGAGCTCTT  
ACGGTTCTTCTAGCAACGATGATTCCTTACGGATCTTCCAATAACGACGAC  
TCTTACGGTTCTTCCAACAAGAAGAAGAGTTCTTATGGTTCCAACAATGA  
CGATTCTTATGGCTCTAACAATGATGATTCATATGGTTCTTCCAACAAGA  
AGAAGAGTTCTTATGGTTCCAGCAACAACGATTCGTATGGTTCTAACAAC  
GATGATTCCTACGGTTCTTCTAACAAAAAGAAGAGTTCTTATGGTTCCAA  
CAACGATGATTCATACGGCTCCAGCAACAACAATGACTCTTACGGTTCCA  
ACAATGACGACTCTTACGGTTCTTCTAATAGAAACAAGAACTCTATGGG  
TCTTCCAACCTACGGTTCTATCCAACAATGATGACTCTTATGGTTCTATCTAA  
TAGAGGCGGTCTGAATCAATACGGTGGTGACGACGATTACTAA

YMR173W, 430 aa (SEQ ID NO 314)

MGLFDKVKQFANSNNNNNDSGNNNQGDYVTKAENMIGEDRVNQFKSKIGE  
DRFDKMESKVRQQFSNTSINDNDSNNNDSYGSNNNDSYGSNNNDSYGSNN  
NDSYGSNNNDSYGSNNDDSYGSSNKKKSSYGSNNDDSYGSSNNNDSYGSN  
NNDSYGSNNNDSYGSNNDDSYGSSNKNKSSYGSNNDDSYGSNNDDSYGSS  
NKKKSSYGSNNNDSYGSNNDDSYGSNNNDSYGSNNDDSYGSSNKKKSSYG  
SNNDDSYGSNNNDSYGSNNDDSYGSSNKNKSSYGSNNDDSYGSNNDD  
SYGSSNKKKSSYGSNNDDSYGSNNDDSYGSSNKKKSSYGSNNNDSYGSNN  
DDSYGSNNKKKSSYGSNNDDSYGSNNNDSYGSNNDDSYGSNNRKNKNSYG  
SSNYGSNNDDSYGSNNRGRNQYGGDDDY

YIL057C, 995 bp, CDS: 501-995 (SEQ ID NO 217)

CCCAACAGATTTCAAGTCTGTGCCTTAACCACTCGGCCATAGTGCCTAA  
AACAATGTAGGTTATTTAAGCAAGTATTGTAGATACTTTTCGTAATAAAC  
TACAATGCACCCACGACTCGCGGTGTAATGATGGCATGAAATCATTGAAC  
GAAGTTTTGCGGCTATACGGCTGAAGGACGAGACTAAAGGGACAGGAATT  
ATTAATGCGGGGTATAATTTGAATAGTATTAACGGGCACTGCCGTTTAGC  
CATCAAATGCTATTGTTGGGGTATTCTCTCTACTTTTTGTTCTTGGCTTG  
AACCTTTTCGGCGGTTGGCAATCGTCCGTATATAAGCATCGGCTGTCCCA  
ATCCTCTATTGCCCTTTTCCCTTGCACCTCCTTCTCAATTCTTCGTATCT  
TTCGCGTAAAGGTAGATCTTGATTCACCTATCTGTGAAACACGATTAAG  
TGCAAACGAAACAACGTACAGTATATAACAAAGTATTTTAAATAATAAGA  
ATGACGAAAAAGGATAAGAAAGCAAAGGGTCCTAAGATGTCCACCATCAC  
TACAAAAAGTGGTGAGTCCTTAAAGGTTTTTGAGGATTTGCATGATTTTG  
AAACATATTTAAAGGGTGAGACGGAAGATCAAGAGTTTCGACCATGTCCAT  
TGCCAACTGAAGTACTATCCACCTTTGTCTGTCATGATGCGCATGATGA

104/251

TCCGGAAAAGATCAAAGAGACTGCCAATTCGCACTCTAAGAAGTTTGTTTC  
GCCATTTACACCAGCATGTTGAGAAGCACCTGCTAAAGGACATCAAAACC  
GCTATCAACAAGCCAGAATTGAAATTCCACGATAAGAAAAAGCAGGAATC  
CTTTGACCGGATTGTTTGAATTATGGCGAAGAAACGGAGTTGAACGCCA  
AGAAATTCAAGGTGTCTGTCTGAAGTTGTATGTAAACACGATGGCGCAATG  
GTAGATGTTGATTACAAGACAGAACCCTTGACGCCACTCATCTAA

YIL057C, 164 aa (SEQ ID NO 218)

MTKKDKKAKGPKMSTITTKSGESLKFVFDLHDFETYLKGETEDQEFDHVH  
CQLKYYPFVLHDAHDDPEKIKETANSHSKKFVRHLHQHVEKHLKDIKT  
AINKPELKFHDKKKQESFDRIVWNYGEETELNAKKFKVSVEVVKHDGAM  
VDVDYKTEPLQPLI

YDR544C, 929 bp, CDS: 501-929 (SEQ ID NO 135)

TAAAGTAGTCGGTACGTACTTTCGTTTTCAATTTCCATGGTGCACAGTAT  
CTTAACATATCTGCTTAGTCGAGGAGAACCAGGATTCTGTTTCGTTGCTCAG  
CCGCTTCGTGGATATTCTCTTGGATACTTTAAATATGGACCTACGCTTAG  
CCTGCGCTTAGCCTACAACCTTCTTCCGCTCTCGAAAAGACCAATATAATA  
GAAAGTTATAAATTACATTTCCCTTATTAGGTATACGACCTCGCGCTTCGA  
AGTAGAGGAGCCCTTTTGGCGTACCTACATATGGCGCGTCAGACAGACA  
AACTTCCCCCAAAAATGTATTACCCCGCCGAATAAGAAAACAGACCCATT  
CACCCACGACGTATCAAGTTACTTCCCTTGGTGCAATGTCCCACTATAAAA  
AAATTCCTTGACGCTAGATCGTTGGACTAAAATCTGCGTCACAATCGCCT  
AAACAGGAAATATTGCCTATTTTCGTACAAGGTTACTTCCTAGATGCTAT  
ATGTCCCTACGGCCTTGTCTAACACCATCCAGCATGCAATACAGTGACAT  
ATATATACACACCACACCACACCCACACACACCACACCACACCCACCACA  
CCCACACCACACCACACCACACCACACCACACCACACCACACCACACA  
CCAGAGAGAAGCCTAAGCCTAAGACTAAGACAAGCCAAGCCTGACCAACC  
TGTCTCTCAAATTACCCTCCATTACCCTACCTCCCCACTCGTTACCCTGA  
CTCATTTCAACTATACCACCCCAACCACCATCCATCTCCCTGTGTACTACC  
ACCAACCGACCGTCCACCATAACCGTTACCCTCCAATTACCCATATCCAA  
CTCCACTACCACTTACCCTACCATCTCCCATCTACTACTCACCATACTAT  
TGTTCTACCCACCACTATTGAAACGCTAA

YDR544C, 142 aa (SEQ ID NO 136)

MSLRPCLTPSSMQYSDIYIHTTTPHPHTPHHHTHTTPTPTPHPHTHTPT  
PERSLSRLRLQAKPDQPVQSQITLHYPTSPLVTLTHSTIPPQPPSISLCTT  
TNRPSTITVTLQLPISNSTTTYPTISHLLLLTILLFYPPLLKR

YKR040C, 1004 bp, CDS: 501-1004 (SEQ ID NO 255)

GGGCTTTTCCAGTGCCGCGGCTCGAGATCCAGGCACCAGGAAGTAGGCA  
CGCTGTGTATTCTAACACATTGAAGGGCCTAGGCCGCTGACGTGGGGTC  
TAGTTCCACTTTTTTCATTACCTTTTTCTCGGTCTTTTTCTTGCTCCACAGG  
CCGTTAATGGCCTGAAACAGTTTGTGACTTTGGACTTATGATAACGATG  
TTTGTCCGGGTGCCACCGGATTCTATCGCGGCGAATCAAGTCTAGTCTGT  
TTGCATCCATCAAGGCACTGCTCATTGTGTAAAATTGTTCTACGCTTTTG  
TCATCAATCATATCTAAACTCACAGCCGCTAGGGTAGGTGTGCCTGGCAG  
TGGTAAGGTAGCCGGCTCGTCTTTGGTCATGCGCCAATACTGTGCAACGG  
CCCGCGCGTAGCGTTCTTCCGCTTCAACCTTAGAGCTGATACCTTTTGCC  
TGGTCAAAGGCGAAAACGTCTACCTCGCTTTCACTGCTGCTTTTCGCTTTC  
ATGACTTCGTTTCAAGCGGTCTCTTTCGCTCTCGGTTGTAACACACTTGT  
AGCCTGCTATGCTTTCACCGTACTCGAAAAGCGTAGCCTCATGACTAGTT  
GTACCAACGCCCTTTCTTTTCTTTTTTCTCTTGACACTTCGGCGTATT  
CATCGCCACTGGTACAAGCCGATGGTGCTTTTTTGCTCATTTTCGTTTT  
GACGTTGCGATGGTTTCGCGGACCAATCGCATGGGTGGTGGTGGATGTTG  
TCTTTGCTAGTTGCAACGTAGTCTTCTCTCTCTCGCTTTCTGACGAA

105/251

AATTGGCCTTACGTATCTTTTTTCGGCGTCGTTGTCGTCATCGCTGTTCA  
TATAATCGTCGTCACCTCATATCGGCGCTTTTACTGCATGCTGCTTTTTGA  
AGAGAGTTTCATTGAAAAGTAGTGAAGAAAAAAAAAAAAAAAAAAAAAAAAA  
AAAAAGGAAAAAAGCTTACATACGGAAGAGAAAAAAAAAAAAAAAAAGAAATT  
TTAA

YKR040C, 167 aa (SEQ ID NO 256)

MTSFQAVSFALGCNTLVACYAFTVLEKRLMTSCTNALSFLFFLLTLRRI  
HRHWYKPYGAFLLIFVLTLRWFRGPIAWVVVDVVFASCNVFFSPALSDE  
NWPYVSFFGVVVVIAVHIIVVTHIGAFTACLLKRVSLKSSEEKKKKKKK  
KKEKSLHTEREKKKKKF

YNL338W, 659 bp, CDS: 501-659 (SEQ ID NO 337)

TAAAGTAGTCGGTACGTACGTTTCGTTTTCAATTTCCATGGTGCACAGTAT  
CTTAACATATCTGCTTAGTCGAGGAGAACCAGGATTCTGTTCGTTGCTCAG  
CCGCTTCGTGGATATTCTCTTGGATACTTTAAATATGGACCTACGCTTAG  
CCTGCGCTTAGCCTACAAC'TTCTTCCGCTCTCGAAAAGACCAATATAATA  
GAAAGTTATAAATTACATTTCCCTATTAGGTATACGACCTCGCGCTTCGA  
AGTAGAGGAGCCCTTTTGGCGTACCTACATATGGCGCGTCAGACAGACA  
AAC'TTCCCCCAAAAATGTATTACCCCGCCGAATAAGAAAACAGACCCATT  
CACCCACGACGTATCAAGTTACTTCC'TTGGTGCAATGTCCCACTATAAAA  
AAATTCCTTGACGCTAGATCGTTGGACTAAAATCTGCGTCACAATCGCCT  
AAACAGGAAATATTGCCATTTTTCGTACAAGGTTACTTCC'TAGATGCTAT  
ATGTCCTTACGGCCTTGTCTAACACCATCCAGCATGCAATACAGTGACAT  
ATATATACCCACACCCACACCCACACACCACACCCACACACCCACACCCAC  
ACCCACACCCACACACCCACACCCACACCCATCACAACCCTAACCTACC  
CTATTCTAA

YNL338W, 52 aa (SEQ ID NO 338)

MSLRPCLTPSSMQYSDIYIPTPTPHHTHTPTPHPHPTHHTHTHNPNT  
LF

YJR115W, 1010 bp, CDS: 501-1010 (SEQ ID NO 235)

GCCAGTATCCCTTTCTGAAATAAGCTAAACCCCTTGCAACCACCAGGGTG  
CCGCCGTCCCTAACTTTCCAGCCTGGCAGCGCGTCGAGTCGCCGAATGTTG  
CGGGCGCTGCCCCGCCCCGAACACCGCGCCCCGCCCTGCCTCAGCTTAACC  
GAAACCACACGGGTCTGCCATCTTCCATATACCCCTGGCTCTTCTTTCACA  
ATGCCCGCTCACAACGCCAACTGCAAAAGAAGCCCGCCCTTAGTCGGTTT  
TCCCCACTTTGATATAACCCCCCCCCCCCCCCCCCGCATCAACTGGTAA  
TTTAACCCAAACACCACGGGGTCATAATTTAAAAGCGAAAAACCTTAAAG  
CGTTCTCGAAGAAATCTTCC'TGTAGATGATGTCGTAGCAAAC'TTATCTTT  
TAGAGTGTTTGTGCTTACTGCATTGTCAGATCAAAATTTACGTAGCCGCC  
CTTTTCAACCCCTGTTCGAAGAGTAGCATAACAGCAGCGTAGTGAACGTGC  
ATGTTCAAAAATACAGTACAATATTAATATACAATAGTAAGGTGATGAA  
CACACACACACACACACACACACACACACACACATATATATATATA  
CAGGAGATCAAGTTAGTGTGAGGGGACGACTACTGAGTTTGAAGTTCTTT  
AAAGTGTTAAAGTTATTTTCCCTCTCCACCTCGTTGGCAACCTCTCA  
CCCACCGCTTAGCAGCATGTC'TCCGTACATGACCATACCTCAGCAATACT  
TATACATAAGCAAGATACGTTCCAAAGCTGTCTCAGTGCGCCCTTACTCGA  
CACCACCACAGAGAACTTGATCTACGAAAAATGGTGGGCCACGCCAATAT  
GCTGGACAGGATCCTCGACGAAATAGACGAAATCGACAGCGAGGTAGTAC  
TGTGTGACGCTGCCGATGGTTCTTCTACTGCAGAAGCTCATTCCGCTTCC  
CCAGCATCCAGCGACTCTTCTCCTCTCACTAATAACATCCGGCCCATTAG  
CATTATGTGA

106/251

YJR115W, 169 aa (SEQ ID NO 236)  
MFTNTRTILIIYNSKVMNTHTHTHTHTHTHIYITGDQVSVRGRLLSLKFF  
KVLKLFPSPTSLATSHPLSSMSPYMTIPQQYLYISKIRSKLSQCALTR  
HHHRELDLRKVMVGHANMLDRILDEIDEIDSEVVLCDAAAGSSTAEHSAS  
PASSDSSPLTNNIRPISIM

YBL072C, 1103 bp, CDS: 501-1103 (SEQ ID NO 27)  
GTCCTACACACGAGCATCGCTGGGAAAGCTTGAGGGCTTTCTCTTACGCAGTGTTTCATGGTGTTACGGG  
ATGGAAGTGTTCATATACGTTATTTACAGGCCTATCTTAAAGTTATAGGAAATTACACTTGCCATTTG  
CTTTTTGGTACTCACAAGAAGACGTTATAAACACACCAGGACAAAAAGTATGTGCTATGGTCATATGAG  
TAATGGAAGTACATATTATTTTGAATGCTACAGGACCTCTCTTTGAATGGAATAGATAGTGGAAAAAGT  
AAACTTAACTAAAAGGGATGATATAAATTGTGACAGGAGCAGTGCACTAAACTGAATCCTTTGTGTACC  
CCAAAAATCAAGCCTCTTATGAAACGCCGAGTTTTCACAAGAAGAGATGAAAAGAAACCAAAGCATAT  
TTCAAGATAAGAAAAAATTCCGCAACTTTTGTACGTTCTTTATTTTACTAACAAGCGTCATTAAATTT  
TCTATTACAGTTACAAAATGGGTATTTCTCGTGATTCTCGTCACAAAAGATCCGCTACCGGTGCCAAGC  
GTGCTCAATTCAGAAAGAAGAGAAAGTTCGAATTAGGCCGTCAACCAGCCAACACCAAGATCCGGTGCTA  
AGAGATTTCACTCTGTTAGAACTAGAGGTGGTAACAAGAAATACAGAGCTCTAAGAATTGAAACCGGTA  
ACTTTTTCTTGGGCTTCTGAAGGTATCTCCAAGAAGACCAGAATTGCTGGTGTGTTTACCATCCATCCA  
ACAATGAATTGGTTAGAACTAACACTTTGACCAAGGCTGCCATTGTCCAAATTGATGCTACTCCATTCA  
GACAATGGTTTGAAGCTCACTACGGTCAAACCTTGGGTAAGAAGAAGAACGTCAAGGAAGAAGAACTG  
TTGCCAAGAGCAAGAACGCTGAAAGAAAGTGGGCTGCTAGAGCTGCTTCTGCCAAGATCGAATCTTCCG  
TTGAATCTCAATTCAGCGCCGGTAGATTATACGCTTGTATCTCTTCCAGACCAGGTCAATCCGGTAGAT  
GTGATGGTTACATCTTGAAGGTGAAGAATTAGCTTTCTACCTAAGAAGATTGACTGCTAAGAAATAG

YBL072C, 200 aa (SEQ ID NO 28)  
MGISRDSRHKRSATGAKRAQFRKKRFELGRQPANTKIGAKRIHSVTRGGNKKYRALRIETGNFSWAS  
EGISKKTRIAQVYHPSNNELVRTNTLTAAIVQIDATPFRQWFEAHYGQTLGKKKNVKEETVAKSKN  
AERKWAARAASAKIESSVESQFSAGRLYACISSRPGQSGRCDGYILEGEELAFYLRRLTAKK

YBL092W, 893 bp, CDS: 501-893 (SEQ ID NO 33)  
TACTGGAGAAGAGTGTGTTGATTCCAGCAGAAGGTAATACGCACCTTTCTCATCTATTTGCAGAATCGTT  
TTATTAAATACTTTTAAAGAATTTAGATTTTGATAATTAGTTCATTCTCTTTTACAAAGATAATCACC  
AAACAGGGACAATACTGAACGATAAAAGTATGTGACATAGAATGCTAGAATGAATAGCCTAGACT  
GCATTGTTATGAGAGCAACGTTTGATATTTGTGGCGATTGGAACAAACATAGTACATGCCAAAATGAGA  
TGAAATGTCCAATTTGAAC TGATTAACATACACGCGCAAGCTCGTATTTGTTTACTGGTACACCTAGAG  
TTAGCCGATCAAAGAGACAGTGGCAGATATATGGGAAAATTTTCTCCGGAAGATTGCATGCGAGAGTCT  
CATAACCAGTCATTTCCCAAGATACAATTCTCGGAGCTGTTATACTAACAACTTTTAATTTTCATTTT  
TTTTTTTTTTTTGATTAGATGGCCTCCTTACCTCACCCAAAGATTGTCAAGAAGCACACCAAGAAGTTCA  
AGCGTCATCACTCTGACCGTTACCACAGAGTTGCTGAAAACCTGGAGAAAGCAAAGGGTATTGACTCTG  
TTGTTAGAAGAAGATTGAGAGGTAACATCTCTCAACCAAGATCGGTTACGGTTCTAACAAGAAGACCA  
AGTTTTTGTCAACCATCTGGTCACAAGACTTTCTTAGTCGCTAACGTTAAGGATTTGGAAACCTTGACCA  
TGCACACCAAGACTTACGCCGCTGAAATTGCTCACAACATCTCCGCTAAGAACAGAGTTGTCATTTTGG  
CTAGAGCTAAGGCTTTGGGTATCAAGGTCACCAACCCAAAGGGTCGTTTGGCTTTGGAAGCTTAA

YBL092W, 130 aa (SEQ ID NO 34)  
MASLPHPKIVKKHTKKFKRHHS DRYHRVAENWRKQKGIDSVVRRRFRGNISQPKIGYGSNKKTKFLSPS  
GHKTFVLVANVKDLETLTMHTKTYAAEIAHNISAKNRVVILARAKALGIKVTNPKGRLLALEA

YBR009C, 812 bp, CDS: 501-812 (SEQ ID NO 37)  
GAAAAATCGCCCGGGCATTTCTGTTATCTTCCACGCTAAAAGTCAAGGAGAGATATTACGGCCAGGATCG  
CAAAGGTGCAGAGCAAGGAAATGTGAGAAATTGTGAGAACGATAATGTATGGGACAATGCGAAAATGTG  
AGAACGAGAGCAAAAATCTTTTTTGTATCTCCCCGCCGAATTTGGAAACCGCGTTCTGAAAACCTTCGCA  
TCTTCACATAGTAAAACCTGTTCCGAGCGCTTCTCCCCATAATGGTTAGTGGTAAAAACCGAAGTTGTTT

107/251

ACTTTAGCAAATGCCCGGAATACGGTGGTAAATTGCCACCCCCCTTCCCCATTTCATTGGGTAAAGAC  
CAATTTGATGGATAAAATTGGTTGTGGAAAAGGTCTAATTTCTTTTCTATAAAATACCGAGATATTTTTT  
CTATATGATGGTTTCCGTCGCATTATTGTAATCTATAGTACTAAAGCAACAAACAAAACAAGCAACAA  
ATATAATATAGTAAATATGTCCGGTAGAGGTAAAGGTGGTAAAGGTCTAGGTAAAGGTGGTGCCAAGC  
GTCACAGAAAGATTCTAAGAGATAACATCCAAGGTATTACTAAGCCAGCTATCAGAAGATTAGCTAGAA  
GAGGTGGTGTCAAGCGTATTTCTGGTTTGATCTACGAAGAAGTCAGAGCTGTCTTGAAATCCTTCTTGG  
AATCCGTCATCAGAGACTCTGTACCTACACCGAACACGCCAAGAGAAAGACTGTTACTTCTTTGGATG  
TTGTTTATGCTTTGAAGAGACAAGGTAGAACCTTATACGGTTTCCGGTGGTTAA

YBR009C, 103 aa (SEQ ID NO 38)

MSGRKGKGLGKGGAKRHRKILRDNIQGITKPAIRRLARRGGVKRISGLIYEEVRAVLKSFLESVIRD  
SVTYTEHAKRKTVTSLDVVYALKRQGRITLYGFGG

YBR189W, 1501 bp, exon1: 501-507, intron1: 508-920, exon2: 921-1501  
(SEQ ID NO 59)

TGGCTTCTTCTTTGCCTGTTTTGCCAGCTGGTTGATACGGGCACGTAAGTGAATTAATTTCTTGGTCC  
TTTCTAGTGATAAATCTCGCAGAGAGGGCATACTGGTTGTAAAAAGTAGTCGCAACAAGTAAGTCGTAA  
AAAAGTAGATGTAATGGAAGGCTTTGAAGGAACGGCTAGCCAGCTTTTCTGTATCATTCTAGCCTAAT  
TGACAGCATCTTGACCTTCTAGTATGGAACTTTCAATTTAGAAAGCGGTGTTCCCGCTGCGACGAT  
TTAATCCGTACATTTACACATCTGTACATTTTTCATATTCGCAAAACAAAGGTTACTTGAAAAAATCAT  
AAAGTTGGCGGCTTCAGGTGGACGCGCTTCACTCATGTAGCTTAACATTCAATCCCATTAAAGCATTATG  
CATAAATTTTCATGAAGTTTACTTAATAAAATTGTTTCATTTGCATAGACAAGAAAGAAAGCAACAAGACA  
ACTAAGACTAAGCAACAATGCCAAGTACGTATTAGACTATATCGAAGAGGAGGGAAATTCTTCACTCTG  
ACTCGTTGATTTTGAAAGAGGTTCCGGTCCCTCATAAATATTTGAGAATATGAAATTCATAATAGTATA  
CCTTCATTGAGTAGCACGACAACAGCCTGAATTACTATCCATATTATGAATATCTTTATTTACACTGAA  
CTCCCGACACTTCAGTTAAACAGGGATACATTAGAGATCAAGGTGATCTAATAGGGAACATCTCTCTCG  
TAACAATGGGACAGTATTTTATTTTCCAAGGCGGATACCTAATTATGCGTTTTTAATCATATCTCTACA  
ATATTTATGAGCACTTACTTGGGCCCTTGCAGACTTTTGTTCGGGAAAACTTTTGACTAACAAGAATC  
CAATTTTACTTTTTTTTTTTTAGGAGCTCCAAGAACTTACTCTAAGACTTACTCTACACCAAAGAGACC  
TTACGAATCTTCTCGTTTGGACGCAGAATTGAAGTTGGCCGGTGAATTCGGTTTGAAGAACAAGAGAGA  
AATTTACAGAATTTCTTTCCAATTGTCTAAAATTCGTCGTGCTGCCAGAGACTTGTTAACTAGAGACGA  
AAAGGACCCAAAGAGATTGTTTGAAGGTAATGCCTTGATCAGAAGATTGGTTAGAGTTGGTGTCTTGTCT  
CGAAGACAAGAAGAAGTTGGATTATGTTTTGGCTTTGAAGGTTGAAGATTTCTTGGAAGAAGATTGCA  
AACTCAAGTCTACAAGTTGGGTTTGGCCAAGTCTGTCCACCACGCCAGAGTTTAACTCACTCAAGACACA  
CATTGCTGTTGGTAAGCAAATCGTCAACATCCCATCTTTTCATGGTCAGATTGGACTCTGAAAAGCACAT  
TGACTTCGCTCCAACCTTCTCCATTCCGGTGGTGCTAGACCAGGTAGAGTTGCTAGAAGAAACGCTGCTAG  
AAAGGCTGAAGCTTCCGGTGAAGCTGCTGAAGAAGCCGAAGACGAAGAATAA

YBR189W, 195 aa (SEQ ID NO 60)

MPRAPRTYSKTYSTPKRPYESSRLDAELKLAGEFGLKNKREIYRISFQLSKIRRAARDLLTRDEKDPKR  
LFEGNALIRRLVRVGVLSDDKKLDYVLALKVEDFLERRLQTQVYKLGLAKSVHHARVLITQRHIAVGK  
QIVNIPFSFMVRLDSEKHIDFAPTSFPGGARPRVARRNAARKAEASGEAAEEAEDEE

YBR191W, 1371 bp, exon1: 501-511, intron1: 512-899, exon2: 900-1371  
(SEQ ID NO 61)

AATCCTTATTGTGAGAAATTGAAGCCGTTAATATTTAAAGGCTAATTCTCCATGCCATCTTGCATTAC  
TTTGGTATATCTCTTGACCTCAATATATCTCGATAATATAAATCGCAATATTATACTTGTTAGTCTG  
ACAGTTTTACACCTGTACATCTTCAACATCACCACACCTTTTTTACTGGAGGCAAGGATGAGTTTGAA  
TATCGCCTTTTTCCAGCCGCTAGAACATGCTCAGAACCGAGGAAAGCACCCTGCCCCAACCTCCTTT  
GATGTGTTGGCCACCGCTACTAGTGGCCGTGCTGGAAGCCAGGAGCGGTGGGGCCACAATACGAG  
AGCTGGAAGGTAAACGGTCTCTGCGCTCTGTGAAATTTTATCACCATGGAGTGTATGTCTGGTAA  
AGATAATATAGAAAGTAGTGTGCAATTTAGGCATTACCGATTGAACTTTGGAATAAGAGAACCAAGAC  
AAAAATAACTAGCAACAATGGGTAAATCGTATGTCAATTTAATCCTATGAATCTACAGCACGAACGAATC  
ATGGTATCTCAAACCGAACATATCGTCACAGAAATAAAAGATTAAAGACGTGTCTAGTGTGAATAAA  
GCAAACATATCATTAGAGCAAAATATTGGGCAGATAAGATGATGCTACACTGATTCTGAGAAAATTACG  
TGACATGATAGGCTTTTAACGGGCTGTAAGTCATTAGTTTACAGTCGTTGCTTTGAAAATTAGTTCAAC



108/251

ATTAGAAGTGTAGTAATTACAAGCCCTTTTTCCAAACATTTCGGTTATGTGCTGGGACGCATCTCAGAAA  
CTCGCAAAACAATAGAATACTAACATGATTTCTTATAAATCTTAATTTTGATTTATTTCTTTATAATAC  
AGACACGGTTACAGATCTCGTACTCGTTACATGTTCCAACGTGACTTCAGAAAGCATGGTGCCGTCCAT  
CTTTCTACTTACTTGAAGGTCTACAAGGTTGGTGACATTGTCGACATCAAAGCCAATGGTTCTATCCAA  
AAGGGTATGCCACACAAGTTTACCAGGTAAGACCGGTGTTGCTCTACAACGTTACTAAGTCTTCTGTT  
GGTGTATCATCAACAAGATGGTCGGTAACAGATATCTAGAAAAAGATTAAACTTAAGAGTTGAACAC  
ATCAAGCACTCCAAGTGTAGACAAGAATTTTTGGAAAGAGTTAAGGCCAATGCTGCTAAGCGTGCTGAA  
GCTAAGGCTCAAGGTGTTGCTGTTCAATTGAAGAGACAACCAGCTCAACCAAGAGAATCCCGTATCGTT  
TCTACTGAAGGTAACGTTCCCTCAAACTTTGGCCCCAGTCCATACGAAACTTTCATCTAA

YBR191W, 160 aa (SEQ ID NO 62)

MGKSHGYRSRTRYMFQRDFRKHGAHLSTYLKVYKVGDIVDIKANGSIQKGMPHKFYQGKTGVVYNVTK  
SSVGVIINKMVGNNRYLEKRLNLRVEHIKHSKRQEFLEVRKANAAKRAEAKAQGVAVQLKRQPAQPRES  
RIVSTEGNVPQTLAPVPYETFI

YCL035C, 833 bp, CDS: 501-833 (SEQ ID NO 65)

CCGAAAGAAACCCCATGTTCTTGTTTTGCCTGCCCTCCAAATGCTTTATCACTCTCTCACACTGTCACAAT  
CGTGTGTGCTTTCATCCTTAGAAAGGATACCACATTGATAAACAACATATATAAAGTTTAACTATTACCT  
TGATCACTTTACACGTCAAGGTCAAACAGTTTCATAGTTATCACCTTGAAGTATGGCTCCATCATCTA  
TAAACATGAACCTCATGCACAAGTGAGCTGTCTACAGATAACGAGCAGCCGCAACGGCGTTTTCCAGAT  
TGCGATGCTTGTTTTCTTTATCTACTACTGCCTTACTACCCCCCTTGCGCCTCCTGATTACGATGATGT  
GGGAATTTTGTCTTGAAAGGAGTAAATATATAAAATAAATGAAAAGTTTATATAATATAAAAAGGGACT  
TTAGCATAAAATAAAGAACTTCGTGCAGTACTTATACGAGCATTCGCATAATTATACAAATAGACAAAA  
CCTCAGAAGGAAAAAAATGGTATCTCAAGAACTATCAAGCACGTCAAGGACCTTATTGCAGAAAACG  
AGATCTTTCGTGCGATCCAAAACGTACTGTCCATACTGCCATGCAGCCCTAAACACGCTTTTTGAAAAGT  
TAAAGGTTCCCGAGTCCAAAGTTCTGGTTTTGCAATTGAATGACATGAAGGAAGGCGCAGACATTCAAG  
CTGCGTTATATGAGATTAAATGGCCAAAGAACCCTGCCAAACATCTATATTAAATGGTAAACATATTGGAG  
GCAACGACGACTTGCAGGAATTGAGGGAGACTGGTGAATTGGAGGAATTGTTAGAACCATTCTTGCAA  
ATTAA

YCL035C, 110 aa (SEQ ID NO 66)

MVSQETIKHVKDLIAENEIVASKTYCPYCHAALNTLFEKLVPRSKVLVLQLNDMKEGADIQAALYEI  
NQRTVPNIYINGKHIGGNDLQELRETGELEELLEPIAN

YDL004w, 983 bp, CDS: 501-983 (SEQ ID NO 81)

ATAAACATAAGATATAATAGTTTTTAAAATGGTCAACGTATGCGATGCACAACATAAAAGGTACCAATTC  
ATTAAATATATATAATATTTACTTCTTACTATTACACGAAAGACAAGTGTGAAATGCCTAGGAGATTGAT  
GATTGACAAGCTCTGGCCTTGCAATAAAAATACTTATACACAACCTTCAAATAATATAGAAAAGAAAGAA  
GACTATAAGCTAAAAATGTAGACAACCTCATTTAAATATTTATCTTAGGACTTGGTAATAATAGCTAAT  
TTGTATATTATTCACCTCGGTCACCGCCTGTAATCACCTTTAACGAAAATAGATGCCAGCCAATCAAA  
GCGCATTATGGAGTCGCTTAGGAAGGGGCCGTCCTCATTTGTAAAAGTTTCATGTTAAATTAGATGGAG  
GATAACAATAAAGGTATCGTACACACACTGCTAAAAGAGCCTCAATCAATTTGTGAAGGTATAACTGTA  
GCCGTGAGGATAGGAAAATGTTACGTTCAATTATTGGAAAGAGTGCAATCAAGATCATTTGAATTTCTGTCG  
CTAAGCGTTTCATATGCAGAAGCTGCTGCCGCATCATCAGGTTTGAAGTTACAATTTGCTCTACCACACG  
AACTTTTATATAGTGGCTCCGAAGTTACTCAAGTGAACCTGCCCTGCTAAGTCAGGACGTATTGGTGTAT  
TGGCCAACCATGTTCCACCGTTGAACAATTACTACCAGGTGTCGTTGAAGTTATGGAAGGCTCTAACT  
CTAAAAAATTTCTTTATATCAGGTGGATTTGCAACAGTTCAACCAGACTCGCAGTTATGTGTAAGTCAA  
TTGAAGCTTTTCCATTGGAATCCTTTTCAAGAAAATATAAAAAATTTGTTGGCAGAAGCTAAGAAGA  
ACGTTAGTTTCATCTGATGCCAGGGAAGCCGAGAGCTGCAATTCAGTAGAAGTTTGTAGAAAACCTAC  
AATCCGTATTGAAATAG

YDL004W, 160 aa (SEQ ID NO 82)

MLRSIIKGSASRSLNFVAKRSYAEAAAASSGLKLQFALPHETLYSGSEVTQVNLPAKSGRIGVLANHVP  
TVEQLLPGVVEVMEGSNSKKFFISGGFATVQPDSQLCVTAIEAFPLESFSQENIKNLLAEAKKNVSSSD  
AREAAEAAIQVEVLENLQSVLK

109/251

YDL075W, 1263 bp, exon1: 501-557, intron1: 558-978, exon2: 979-1263  
(SEQ ID NO 85)

ACTATATTTTGTTCCTCCCGAACCTCTCCCTTCTGGGCCCTTTTCCATTATTTCACAATATTTTCATAC  
CTTTACCTCCGTACACCAATCTTTATTTTACCCCATACCTTTGTATTCTGAAATTGAGAAATGATTT  
GTGGTGCCTTTTGGACAATCTGCCTTCGTGGACAGTTTGAACGCTAGGCGACAGTTTGGCAA  
CGGAAGGAAGTGGGAGAGCCAGAAAGGCTTCTCTCGATGGTGGATCATTCTTGCAGGCGGAGGAT  
GGGAAAGCTCCGTTTCAGGTTTGCAGGCTTTCTTCTTCTGGCATTTTCTGTTCTCCCAACTGCGCAGGCAGAC  
ATAGCTTGACTTTACTCATGCTCGCATTAGGCGGGTTGAATCTCATAGCTTGAAAGATAGTATTGAATT  
ATATTGAAGATTTTATAACTAGTGATAATTTTCAATCAAGTTTTAAAGAAAGAATTAATAAGCAAACAGA  
ACTCAATCAAAGGAAAAATGGCCGGTTTGAAGACGTTGTCACTCGTGAATACACCATTAACCTTGCACA  
AAAGAGTATGTGAAAGAATAAAAAATATAATGCCCAAGGGCTTGTCACTTGAATGGTTAATTAAGAAGAT  
ATTTCTATAGTCAAGGAATACAATATCAAGAATTTGTACCACAGAAACCTATCAACAAAGATCATTTGAT  
CAAGATATATTTTATAATACGGAATTTGAAGACCATAATCAATATTATAACATCCAAGAGGGGAAAGAT  
ACACTTCGGCTGGACTTAAAGAGCGATGAAGACAGAAATAGTTATCTTAAATAGTGGAAATCCTTAGATTT  
TAAGTCGACAATTTATCCATATCCCAAGTTTGACTAAATATGAATCAGAACAATTTGGGTCTCCAATATA  
CAAAACCATTCATCAAGATTACACTAATATTAAAAATGAACAATCGTTACTAACAAAAAATTTACCATT  
TATTTTAAATAGTTGCACGGTGTCTCCTTCAAGAAGAGAGCTCCAAGAGCTGTCAAGGAAATTAAGAAG  
TTCGCCAAGTTACACATGGGTACTGATGATGTCCGTCTAGCTCCAGAATTGAACCAAGCTATCTGGAAG  
AGAGGTGTCAAGGGTGTGAATACAGATTGAAGTTGAGAATTTCCAGAAAGAGAAACGAAGAAGAAGAC  
GCCAAGAACCCATTTGTTCTCCTACGTTGAACCTGTCTTAGTTGCTTCTGCCAAGGGTCTACAACTGTT  
GTTGTCTGAAGAAGATGCTTAA

YDL075W, 113 aa (SEQ ID NO 86)

MAGLKDVVTREYTLNLHKRLHGVSFKKRAPRAVKEIKKFALHMGTDVRLAPELNQAIWKRGVKGVEY  
RLRLRISRKRNEEDAKNPLFSYVEPVLVASAKGLQTVVVEEDA

YDR064W, 1495 bp, exon1: 501-521, intron1: 522-1060, exon2: 1061-1495  
(SEQ ID NO 89)

TGACGGTCGTTTCACAGGAATGGAAGATGCTTTATGCCGGCGCATTAGAAATGATCAGAGAGGAGTGCG  
GTACTTTTAAATTGATAGAGGTTTCTTCAGGTTTGGAGGATGACTCAGACGTTGAAGAATTGAGGGAGC  
AATTAGAAAAATTGTTAGTATAGTCTATCTTAAACACTAACTACCTCCTATAATCATGTAGTGACTTT  
AAACATTTTTTTATCTTTCATAGCAATAATATAAGCCTTTTACCACCCATAAACCATAAAGTAGACCCAA  
ACATTTTTTAAAAAAATTTTACGTTATAATTTTTTTCTTTGTCTGTTTCTTGAGCGCGCAAAGTAGCGGT  
GAAATTTTGATACGAATGAGATTTCCACTTCTGTACAGATGGAAATTTATGTTGGCCGACATATATCAC  
AGTCGTGATTGAATTAACAATTTCTTTCTCATTAATATTTATTTCTAAACGGTTAACCACATAATCAATC  
AACAACAATCAGTCAAAATGGGTGCTATGCACAGTGCCGTATGTTTATTAACACCATAGCGAGATATTA  
ATGCAAAAGTTGCATTGAATAGTTTCGCTAAATCAGATGACACTCTAATGTGGAATTCAAAAGTGGATTT  
CTAATATAATTTGTCTCTGTCTCGGATCACAATTTCTATTACAAGTTCCGGTGTGTACACAGGTATAGTTTA  
TACTGGAGAGTAGTTTCTACTCGCTGTACATTAGCTGGGTGATTCCAATTTCTTTTACAAATATGTTGC  
ATTAGTTTAAACAGGTTATACTATCTGCCGTTTCTCAGTATAATTTACGCCGGAATAATTTACTGATGGCTA  
GCCGCCCTTTATGAATTAGTTTTCACAAAGCTCATAACATAACACGTTAACCTATCGGAGGAGAACCAAG  
ATTGAAGAATCACCCGGAATAGTTATACTTTAATGGAATTGTATGGTCTGAACGAGGAAATATGTCATG  
ATACACTTTTCTTCAAGCCATATGAATCTTCATGTTACTAACATTTCGATAAATTTTTTGGAAATATCCAA  
TTCCACTAAATATTACTTTTAAACAGGGTAAAGGTATTTCTTCTTCTGCTATTCCATACCTTAGAAATGC  
TCCAGCTTGGTTCAAGTTGTCTCTGAATCTGTCAATGAACAAATGTCAAGTACGCGAGAAAGGGTTT  
GACTCCATCTCAAATGGTGTCTTGTGAGAGATGCTCACGGTGTACCCAAAGCTCGTGTATCACTGG  
TAACAAGATCATGAGAATCTTGAAGTCCAATGGTTTGGCTCCAGAAATCCAGAAAGATTGTACTACTT  
GATTAAGAAGGCTGTCTCTGTGTTAGAAAGCACTTGGAAAGAAACAGAAAGGACAAAGACGCTAAGTTTCA  
ATTGATTTTGATCGAATCTAGAATTCACAGATTGGCCAGATACTACAGAACTGTTGCTGTCTTACCACC  
AAACTGGAAGTACGAATCCGCCACTGCCTCCGCTTTGGTCAACTAG

YDR064W, 151 aa (SEQ ID NO 90)

MGRMHSAGKGISSAIPYSRNAPAWFKLSSESIVIEQIVKYARKGLTPSQIGVLLRDAHGVTVQARVITGN  
KIMRILKSNGLAPEIPEDLYYLIKKAIVSVRKHLERNRKDKDAKFRLLILIESRIHLARYYRTVAVLPPN  
WKYESATASALVN

110/251

YDR099W, 1322 bp, CDS: 501-1322 (SEQ ID NO 93)

TTGTTACGACCAATCCGTAATTCAAGCGTGGGTATTCATATGACCAGAGATAATAATACAGCGAATACT  
ATTGAAATCGTCCCTTTTTTGTAGGGAAGAACGACAAATCGGTCGTCTGCTCGAAATGATTAGTAGT  
GTGTCACCCGGATCAGCAAAATGACACACAGAAATACGAGGAAAAAGTCGGTCGAAAGGGGCAAATGT  
TATTATAAGTCCCTCCAGTAGTCTTTTTTTTCAAATATTCATCATCAAAGGTTACGAAATCTTTTGA  
GCTATCTTAAACATTCGTTCTTTTTATCAAATTTCAATTACTAACTTATTTTTTCAAAAAAATTGCCCT  
CTCCCGGTTTTTAATCATTATTTTTTTCGATTGATTAAGGGGAAAAGCAAAGAACGAGAAAACCTTGGA  
CAGAAGGTAAATACTCTGACAATTTCAAACGAAGTAAAAAGAAAAATTATCAAATCAACAAAAAGTAC  
CCGTTACAACAAAAAATGTCCCAAACCTCGTGAAGATTCTGTTTACCTAGCTAAATTAGCTGAACAAG  
CCGAACGTTATGAAGAAATGCTCGAAAACATGAAGGCCGTTGCTTCATCAGGTCAGAGCTTATCTGTCTG  
AAGAACCGGAATCTATTTGTCGGTTGCTTACAAGAACGTCATCGGTGCTCGCCGTGCTTCATGGAGAATAG  
TTTCTTTCGATCGAACAAAAAGAAGTCAAAGGAGAAATCTGAACATCAAGTTGAATTAATCCGTTCTT  
ACCGTTCTAAAATTGAAACTGAATTGACCAAAATCTCTGACGACATTTTATCTGTGTTAGATTCTCATT  
TAATCCCTTCTGCTACTACTGGTGAGTCTAAAGTATTTTACTATAAGATGAAGGGTGACTACCACCGTT  
ATTTAGCTGAATTTTCCAGCGGAGATGCAAGAGAAAAGGCAACCAACTCCTCTTTGGAGGCTTATAAAA  
CCGCTTCCGAAATCGCCACAACCTGAATTGCCTCCAACCTACCCAATTCGTTTAGGTCAGCTTTGAATT  
TCTCCGCTCTTCTATTACGAAATTCAAAACCTCTCTGATAAGGCTTGCCACTTGCCAAACAAGCCTTG  
ATGATGCTATTGCTGAGTTAGATACTTTATCTGAAGAATCATACAAGGATAGCACTTTGATCATGCAAT  
TATTAAGGGACAACCTTGACCTTATGGACCTCTGATATTTCTGAATCTGGTCAAGAAGTCAACAACAAC  
AACAACAACAGCAACAGCAACAGCAACAACAGCAACAACAAGCTCCAGCTGAACAACTCAAGGTGAAC  
CAACCAAATAA

YDR099W, 273 aa (SEQ ID NO 94)

MSQTREDSVYLAKLAEQAERYEEMVENMKAVASSGQELSVEERNLLSVAYKNVIGARRASWRIVSSIEQ  
KEESKEKSEHQVELIRSYRSKIETELTKISDDILSVLDShLIPsATTGESKVFYKMKGDYHRYLAEFS  
SGDAREKATNSSL EAYKTASEIATTELPPTHPIRLGLALNFSVFYIEIQNSPDKACHLAKQAFDDAIAE  
LDTLSEESYKdstLIMQLLRDNLTLWTSdISESGQEDQQQQQQQQQQQQQQQQAPAEQTQGEPTK

YDR134C, 701 bp, CDS: 501-701 (SEQ ID NO 97)

GGAGTTTTCTATTTTCAATTTGATGGCTGGGTTTGGAGCTGCAGGACACGCTGCAGTGGGGAAGCCCTTT  
TAAATCCGCGAGTCCGGTCCGTGCTCACTTTTAGACGCGTGTCCATCGGCGTTCCGATGGTTTCCAGT  
GAGAAAAGGGGCTACGCGTATGGTCCGTAGTCCCTTTTCAGGGACCAGTGCAGAGGGTGAATCAACGGCC  
CCTTCACAGAAACCGCGCAGGAATTTTCTGGTGTTGTATTTTTTTTCTTTGACTTATGCTCACTTT  
TTCTTTTCTAACTATTTTTTTTGAATTTTTTGTGTACACTTTCCACAACATATAGGATGTTTAGT  
CATCTCTCGAAGTATATAAACCGTTGCTGGATCGTGGTTGTTCTTCATCGACTTCTCTCTGTAGACTC  
TCTTTTTTAAAAATTTTTTTCATAGAATAAAAAACCAAGGATAACAAACATCTTCTTTTCGTTTCGCTTCAA  
ATAACTACAAATTAATAATGCAATTTCTTACCGTCGCTTCTATCGCTGCTATTGCCGCTGTTGCCCTCCG  
CCGCTTCTAACATTACCACTGCTACTGTACAGAGAATCTACCACTTTGGTCACTATCACTTCTTGTG  
AGGACCACGTTTGTCTGAAACAGTTTCCCCAGCTTTGGTTTCCACTGCTACCGTCACCGTAAATGACG  
TTATCACTTAA

YDR134C, 66 aa (SEQ ID NO 98)

MQFSTVASIAIAAVASAAASNITTATVTEESTTLVTITSCEDHVCSETVSPALVSTATVTVNDVIT

YDR171W, 1628bp, CDS: 501-1628 (SEQ ID NO 103)

CTGGGGTTGGGTAAACAAGTGAGCAAGGGAAGTGAACATTTTAAGAAGAACAATAAAATAGCAAGAG  
ATGGAATGGTAATGCTTGGCTCTCGAGAAGAGTAGCATAAAACGAGACTTGTTTAAACAGGATATGAC  
ATACTTCAATTCAGCTTTCCCTATCAGCCGCTCGAGCAGTTATATAGGTGTGTTGCCGGAGTAATTTGG  
CGGAGGCCAACAGTGGCTAGGCGGCAACGCCGGAACACGCGCTTAAAAGTTCTGGAAGGTTCCGGAAT  
TGAGAACTGCTCAGGGGCGAATACAGGGGCGGCTTGGCGGCAGGGGGGAGGCCTCTGTGAAGTTAGTT  
ATATAAGATACTGCTGTCATCGTTTTTTTGTATCCCGGCAGGAACCTATCTTTTATTCTCATACATACGGTC  
AAGAAGTATAATTATACATAACATAGGGACAGTTTCAGGCAATTGTCCATATCCACACAAATTAAGAT  
CATACCAAGCCGAAGCAATGAGTTTTTATCAACCATCCCTATCTTTTATGACGTTTTGAACGCATTAT  
CCAACCAAACCTGGCCAGAGAGGGCAGCAAGGATATCCTCGCCAACCACAAAGGCCACAGAGATACCATC  
CCCATTATGGACAAGTGCACGTTGGCGGGCATCATCTCGTCATCATCCATTGTATAGCAGATACAATG

111/251

GTGTTCCCTAATACCTATTACTACCAGTTCCTGGACAAGCCTATTACTATAGTCCTGAATACGGTTATG  
ATGACGAGGATGGTGAAGAAGAGGACCAAGACGAAGATATGGTGGGTGACAGCGGCACTACAAGACAGG  
AAGATGGTGGCGAGGACAGCAACTCGAGAAGATATCCATCATATTACCATTGTAATACTGCCAGGAATA  
ATAGGACCAACCAACAGGCAAACAGTTTAAACGACTTATTAACCGCGTTAATAGGTGTTCCACCATATG  
AAGGCACTGAACCAGAAATTGAAGCAAATACCGAACAGGAGGGCGAAAAGGGAGAAGAAAAGGATAAGA  
AGGATAAGTCTGAAGCACCCAAAGAGGAAGCTGGCGAAACCAACAAAGAAAAACCTTTGAATCAGCTGG  
AGGAATCGTCGAGACCACCATTAGCCAAAAAATCTTCATCGTTTCGCTCACCTACAAGCGCCTTCCCCAA  
TACCTGACCCGTTACAAGTATCCAAGCCTGAAACGAGAATGGACTTACCATTTTCACCAGAAGTGAATG  
TCTATGATACCGAGGACACTTACGTAGTTGTTCTTTCGCTTACCAGGTGCTAACTCTAGGGCTTTCCACA  
TTGATTACCATCCATCTTCTCATGAGATGCTCATCAAGGGTAAGATCGAAGACAGAGTGGGCATTGATG  
AAAAATTCTTGAAGATCACGGAATAAATATGGTGCCTTTGAGAGAACCCTTAAATTTCCCGTGCCTGC  
CACGCATTAAGGACGAAGAAATTAAAGCTACTTACAACAACGGTCTACTACAAATTAAGGTGCCTAAAA  
TTGTCAATGACACTGAAAAGCCGAAGCCAAAAAGAGGATCGCCATTGAGGAAATACCCGACGAAGAAT  
TGGAGTTTGAAGAAAATCCCAACCCTACGGTAGAAAATTGA

YDR171W, 375 aa (SEQ ID NO 104)

MSFYQPSLSLYDVLNALSNTGTGQRGQQGYPRQPQRPHYQVHVGGHHPRHPLYSRYNGVPNTY  
YYQFPQAYYYSPEYGYDDEDGEEEDQDEDMVGDSGTTTRQEDGGEDSNSRRYPSYHNCNTARNNRNTNQ  
ANSLNDLLTALIGVPPYEGTEPEIEANTEQEKEGEEKDKDKSEAPKEEAGETNKEKPLNQLEESSRP  
PLAKKSSSFAHLQAPSPIPDPLQVSKPETRMDLPFSPEVNVYDTEITYVVVLALPGANSRAFHIDYHPS  
SHEMLIKGKIEDRVGIDEKFLKITELKYGAFERTVKFPVLPRIKDEEIKATYNNGLLQIKVPKIVNDTE  
KPKPKKRIAIEEIPDEELEFEENPNPTVEN

YDR399W, 1166 bp, CDS: 501-1166 (SEQ ID NO 129)

TCGTTTATCCTTTTTTGAAGTGCATCTGGCATCGTTAACAGTAAGGCCATCTGGAACATCAAGCAAGCAC  
TCCACTTTTACGTCACAACCATAGTTGGTTAACTAAGAAAAGACAGTACATATTTCCCTTCCGAGTCAC  
TTATTTTTTTTTTCTTCTGAAAAAATTAATTAGATTAATTTCAATTAATATCATTTCGCTTATCTGAC  
TTCTTTTCATTTTTTTTCTCTATATTTTCGCGTTTACTAGGAAAGAAAAGGAAAAAATTTTTCCCCCTC  
CATCTGTCCCAAATCGGGTAGCGATGAGCTGCTATAGAATTTTCTATTTAAACATGTTTGATAAGCCCA  
ATTTCCGTTAGATTTTGTTCCTTTCGAGTTTGGTTTGCCGTAACTTTTTTATTTTAGTCTCCATCT  
AGCTGGAGTAATACGATGTAGTGCCTTGTAATCTTTCTTATTTTTATATTACCGTTCGTGTTTATTATA  
TCCATTACGTTCCCATATGTCGGCAAACGATAAGCAATACATCTCGTACAACAACGTACATCAACTAT  
GTCAAGTATCCGCTGAGAGAATTAAGAATTTCAAGCCGGACTTAATCATTGCCATTGGTGGTGGTGGTT  
TCATTCCTGCTAGGATCCTACGTACGTTCTTAAAGGAGCCCGCGTGCCAACCATCAGAATTTTTTGCTA  
TTATTTTGTCTTTGTACGAAGATTTGAACAGTGTAGGCTCAGAAGTTGAGGAAGTTGGTGTAAAGGTTA  
GCAGAACACAATGGATTGATTACGAGCAATGTAAATTAGATCTAGTCGGCAAGAAGCTTCTTATCGTTG  
ACGAAGTCGATGACACCCGTACCACACTTCATTACGCTTTGAGTGAATTGGAAAAGGATGCAGCTGAAC  
AGGCAAAGGCTAAAGGTATCGATACGAAAAGTCTCCAGAGATGAAAACAACTTCGGGATTTTTGTTC  
TACACGATAAGCAAAAACCAAAGAAAGCAGATTTGCCTGCCGAAATGTTGAATGACAAGAACCCTTATT  
TTGCAGCTAAACTGTTCCAGACAAGTGGTATGCATATCCATGGGAATCTACTGACATTGTTTTCCATA  
CTAGAATGGCTATTGAACAGGGCAATGACATCTTTATTCCTGAGCAGGAACACAAGCAATGA

YDR399W, 221 aa (SEQ ID NO 130)

MSANDKQYISYNNVHQLCQVSAERIKNFKPDIIAIGGGGFIPARILRTFLKEPGVPTIRIFAILLSLY  
EDLNSVGSEVEEVGVKVSRTQWIDYEQCKLDLVGKNVLIVDEVDDTRTTLHYALSELEKDAAEQAKAG  
IDTEKSPMKTNFGIFVLHDKQPKKADLPAEMLNDKNRYFAAKTVDPKWYAYPWESTDIVFHTRMAIE  
QGNDIFIPEQEHKQ

YDR418W, 998 bp, CDS: 501-998 (SEQ ID NO 131)

TGCACTGTGGATGTTTGGGTTGTGTATTTTGCCTTTCATAACATACAGATATTTTGTTTAAGGAAGTGAA  
ATAAACAATATCATAAAACAGGTACTTCATAGACCATAAAGCATAACCCAGATTATCCTCTTAGATAGC  
AATGCTAATGTAAACAGAGATCCGTTTGCCTGACTTTATACTAATATGATATGCTACTTCGCTTTGTG  
TTCGAGCAGCCTGGCAGTCCCCCTCTAGCCGCTTTTTTCCCTTTCCGAAGGTTTCCGCCTAAGCCCCCTG  
GCTCTAGGCCGAGAAAATGTTAATGCTCCTTCTACGAGAAAATGCTTGTGCGCCACACCAGGACAGGTGC  
TCGACGACGCTTCCGCTAATCTTTCTCAATGTTGTATCTTCTTTGGCGGTACATTACTAGTATGAAAAT  
GGAATAAAAACAGTACCTAAATTATTTACTTACTTCCCGTTAAAGCAACCCCAAGTGCCCAATAGAAGG

112/251

ATAAATCAATAGTCAATATGCCTCCAAAGTTTGTATCCAAATGAAGTTAAGTACTTGTACTTGAGAGCTG  
TCGGTGGTGAAGTTCGGTGCTTCCGCCGCTTGGCTCCAAAGATCGGTCCATTGGGTTTATCCCCAAAGA  
AGGTTGGTGAAGATATCGCCAAGGCCACCAAGGAATTCAAAGGTATCAAAGTTACTGTCCAATTGAAAA  
TCCAAAACAGACAAGCTGCTGCTTCTGTTGTTCCATCTGCTTCTCTTTGGTCATTACTGCTTTGAAGG  
AACCACCAAGAGACAGAAAGAAGGATAAGAACGTCAAGCATAGCGGTAACATCCAATTGGATGAAATTA  
TTGAAATTGCCAGACAAATGAGAGACAAATCCTTCGGTAGAACTTTGGCTTCCGTTACTAAGGAAATTT  
TGGGTACTGCTCAATCTGTCGGTTGTCGTGTTGATTTCAGAACCCTCATGACATCATTGAAGGTATTA  
ACGCTGGTGAATTTGAAATTCAGAAAACTAA

YDR418W, 165 aa (SEQ ID NO 132)

MPPKFDPNVYLYLRAVGGVGVGASAAAPKIGPLGLSPKKVGEDIAKATKEFKGIKVTVQLKIQNRQA  
AASVVPSSASLVITALKEPPRDRKDKNVKHSNIGLDEIIIEIARQMRDKSFGRTLASVTKEILGTAQS  
VGCRVDFKNPHDIIIEGINAGEIEIPEN

YDR513W, 932 bp, CDS: 501-932 (SEQ ID NO 133)

TCTCCCTCTCCTGCCATATAACCCCACTGGTATTTTCCAATGCCTTATTGTTGGAAACCTGATCTTTAT  
ACCATTCCTGCACCTTTCACAGGGTCATTGCCGTGGATAATACAAAACCTGAATTTGGACACCTGCTTGT  
CACATGATGTAAATCTCCATATCTGTAATAGCTTCTAAATTGCCCTCCAATCGAATAGCAACTCGTCA  
GTTGATCAAATGCCTCTCGGCAACTCATCGTTGTCGGATATTTTGTACTCATCCTTTCCTGTTTCTTCC  
TCAAGCTGCTCTCTTTTACCCTAATAGAACCATCGCCTCCCTCTTGATTTATGCTAATACCACATCCAA  
TAGCAGAACTATTACTAAGATCCGATATTTTCGGCCCCCTTCGCAAAGGGGGCCCGCCGCACTTTCTTCAT  
GAATTTTCATATAAAAAGTCCCAGGACGCCAAGAAAAGGTGCCCTCTTGATTAACGGACACTCCAATA  
CTGTTATATATTGTTTCATGGAGACCAATTTTTCCTTCGACTCGAATTTAATTGTTATTATCATTATCA  
CGTTGTTTGCACAAGAATTATTGCTAAAAGATTTTATCTACTCCAAAATGGTATCCCAGGAAACAG  
TTGCTCACGTAAAGGATCTGATTGGCCAAAAGGAAGTGTTTGTTCAGCAAAGACATACTGCCCTTACT  
GTAAAGCTACTTTGTCTACCCTCTTCCAAGAATTGAACGTTCCCAAATCCAAGGCCCTTGTGTTGGAAT  
TAGATGAAATGAGCAATGGCTCAGAGATTCAAGACGCTTTAGAAGAAATCTCGGGCCAAAAAAGTGTAC  
CTAACGTATACATCAATGGCAAGCACATTGGTGGTAACAGCGATTTGGAACTTTGAAGAAAAATGGCA  
AGTTAGCTGAAATATTGAAGCCGGTATTTCAATAG

YDR513W, 143 aa (SEQ ID NO 134)

METNFSFDSNLIVIIITLFIATRIIAKRFLSTPKMVSQETVAHVKDLIGQKEVFVAAKTYCPYCKATLS  
TLFQELNVPKSKALVLELDEMSNGSEIQDALEEISGQKTVPNVYINGKHIIGNSDLETLLKNGKLAIEIL  
KPVFQ

YEL009C, 1346 bp, CDS: 501-1346 (SEQ ID NO 139)

AGTTTCACTAGCGAATTATACAACCTACCAGCCACACAGCTCACTCATCTACTTCGCAATCAAAACAAA  
ATATTTTATTTTAGTTTCAGTTTATTAAGTTATTATCAGTATCGTATTAAAAAATTAAAGATCATTGAAA  
AATGGCTTGCTAAACCGATTATATTTTGTGTTTTAAAGTAGATTATTATTAGAAAATTATTAAGAGAATT  
ATGTGTTAAATTTATTGAAAGAGAAAATTTATTTTCCCTTATTAATTAAAGTCCTTTACTTTTTTTGAA  
AACTGTCAGTTTTTTGAAGAGTTATTTGTTTTGTTTACCAATTGCTATCATGTACCCGTAGAATTTTATT  
CAAGATGTTTTCCGTAACGGTTACCTTTCTGTCAAATTATCCAGGTTTACTCGCCAATAAAAAATTTCCCT  
ATACTATCATTAATTAATCATTATTATTACTAAAGTTTTGTTTTACCAATTTGTCTGCTCAAGAAAATA  
AATTAAATACAAATAAAATGTCCGAATATCAGCCAAGTTTATTTGCTTTAAATCCAATGGGTTTCTCAC  
CATTGGATGGTTCTAAATCAACCAACGAAAATGTATCTGCTTCCACTTCTACTGCCAAACCAATGGTTG  
GCCAATTGATTTTTGATAAATTCATCAAGACTGAAGAGGATCCAATTATCAAACAGGATACCCCTTCGA  
ACCTTGATTTTGATTTTGCTCTTCCACAAACGGCAACTGCACCTGATGCCAAGACCGTTTTTGCCAATTC  
CGGAGCTAGATGACGCTGTAGTGAATCTTTCTTTTCGTCAAGCACTGATTCAACTCCAATGTTTGAGT  
ATGAAAACCTAGAAGACAACCTCTAAAGAATTGACATCCTTGTTTGACAATGACATTCCAGTTACCACTG  
ACGATGTTTCAATTGGCTGATAAGGCAATTGAATCCACTGAAGAAGTTTCTCTGGTACCATCCAATCTGG  
AAGTCTCGACAACCTTCACTTACCCACTCCTGTTCTAGAAGATGCTAAACTGACTCAAAACAAGAAAGG  
TTAAGAAACCAAAATTCAGTCGTTAAGAAGTCACATCATGTTGGAAAGGATGACGAATCGAGATGGATC  
ATCTAGGTGTTGTTGCTTACAACCGCAAACAGCGTTTCGATTCCACTTTCTCCAATTGTGCCCGAATCCA  
GTGATCCTGCTGCTCTAAAACGTGCTAGAAACACTGAAGCCGCCAGGCGTTCTCGTGCGAGAAAGTTGC  
AAAGAATGAAACAACCTGAAGACAAGGTTGAAGAATTGCTTTTCGAAAAATTATCACTTGGAAAAATGAGG  
TTGCCAGATTAAAGAAATTAGTTGGCGAACGCTGA

113/251

YEL009C, 281 aa (SEQ ID NO 140)

MSEYQPSLFALNPMGFSPLDGSKSTNENVASASTSTAKPMVGQLIFDKFIKTEEDPIIKQDTPSNLDFDF  
ALPQTATAPDAKTVLPIPELDDAVVESFFSSSTDSTPMFEYENLEDNSKEWTSLFDNDIPVTTDDVSLA  
DKAIESTEEVSLVPSNLEVSTTSFLPTPVLEDAKLQTRKVKKPNSSVVKSHHVGKDDESRDLHLGVVA  
YNRKQRSIPLSPIVPESSDPAALKRARNTAARRSRARKLQRMKQLEDKVEELLSKNYHLENEVARLKK  
LVGER

YGL123W, 1264 bp, CDS: 501-1265 (SEQ ID NO 163)

TGGCTTATTCACTAAGGATTCCTTAAGGTTTTCTTAATAGTTTTCTACGTCGGCATGCGATTGTTTGGTT  
TAGAAGACTGCTTTCTAAATATGGTTGGGTGTATTTAAGCTAGACCCATACACCCGCTCTATGGGATTA  
TTTACTTGTGTTGAATTTTAAGATTTGTGATAATGGAAGTGGACGCAAAACATTTGATGGAAAACGCATGT  
CATCATTAACGAGGTAACGTAGGTATCTGTCTGCTTGTAGTATTGCACGCAGCTTCCCAGGACGCCTAG  
CTATTTTTTTCATCTATTTCCCTCTGTAGTAACGTAAGAGTTTTCAAGTTTTTAATTCAGACTTTCTCTT  
CCTTTGTTTCCAATTTCCCTTCTTACTGCTTGATACCTTTTCAATCCCAAAGAAACCGTGTCTTTATA  
TATTGTCGATTGAAAGTTACCTACATCAACTTTCCGTGTTCATTCGACTATAACAAACAACCAATAA  
GCTCAACTAATTAAGTAATGTCTGCTCCAGAAGCTCAACAACAAAAGAGAGGTGGTTTCCGGTGGCCGTA  
ACAGAGGCCGTCCAAACAGAAGAGGACCAAGAAACACTGAAGAAAAGGGATGGGTTCAGTTACCAAAC  
TAGGTAGATTAGTCAAGGCTGGTAAGATTACCAGCTGAAGAAATCTTCTTGCCAGTCA  
AGGAATTTCCAAATCATTGACACTTTGTGTGCCAGTTTGCAAGACGAAGTCATGAACATCAAGCCAGTTC  
AAAAGCAAACAGAGCCGGTCAAAGAACCAGATTTAAGGCTGTTGTCGTTGTTGGTGACTCTAACGGTTC  
ACGTTGGTTTGGGTATCAAGACCGCCAAGGAAGTTGCTGGTGCCATCAGAGCTGGTATCATTATTGCCA  
AGTTGTCCGTTATCCCAATCAGAAGAGGTACTGGGGTACCAACTGGGTCAACCACATTTCTTTGGCCA  
CCAAGACCACTGGTAAGTGTGGTTCCGTCACTGTTAGATTGATCCCAGCCCCAAGAGGTCTGGTATCG  
TCGCTTCTCCAGCTGTCAAAAAGTTGTTGCAATTGGCTGGTGTGAAGATGTCTACACCCAATCTAACG  
GTAAGACTAGAACTTTGGAAAACACCTTGAAGGCTGCTTTCTGTTGCTATTGGTAACACATACGGTTTCT  
TGACTCCAAACTTGTGGGCCGAACAACCATTGCCAGTTTCTCCATTGGACATCTACTCCGATGAAGCTT  
CTGCTCAAAAGAAGAGATTCTAA

YGL123W, 254 aa (SEQ ID NO 164)

MSAPEAQQQKRGFGGRNRRGPRNREEKGWVPVTKLGRVLKAGKITTEEIFLHSLPVKEFQII  
DTLLPGLQDEVNLIKPVQKQTRAGQRTFRKAVVVVGDSNGHVGLIKTAKEVAGAIRAGIIIKLSVIP  
IRRGYWGTLNQGPHSLATKTTGKCGSVTVRLIPAPRSGIVASPAVKLLQLAGVEDVYTQSNKTRTL  
ENTLKAFAIGNTYGFLTPNLWAEQPLPVSPLDIYSDEASAQKKRF

YGR209C, 815 bp, CDS: 501-815 (SEQ ID NO 187)

AACATCCAGACTTTTACGGGTGGCAACGGAACCAACGTATTTAGAGATTGTTTTTTGGTCAAGCGAGGA  
ACCCCTGTTGGCAAAGTTGCCAGGTATATCATGGGTGGCGAGGTCACCATTGCAAGCATTGAAACCGTT  
GGCGGCGTGAGAGTCAGTGAAGAAAGTCTTGTGAGCCCGTAAGAATGACATACTCGGCTTCAAGATC  
GCTCCAAGATCAGCATAACTTGAGTGCCAGTGAATATTAAGTAATCATCAAAGTATATGTGTAATTGTT  
TATACTCTTAGTAAAGGATGCTCCCTACAAGGTGGCTCTTTTCTTACTAAGCGCGTTCAGTTTCCAGCC  
AGCCGAAAGAGGGATATCAGTATATAAGAAAGCCATTGGGGGATGAAAAGCTGACAAGAGAATAACGA  
GGACCAGTTTTTTATTTGTTGTCTAGCAAGAATTATACACGCACACATACACGAGAGTCTACGATATCTT  
TAAATAACACATCAATAATGGTCACTCAATTAATCCGCTTCTGAATACGACAGTGCTTTAGCATCTG  
GCGACAAGTTAGTCGTTGTTGACTTTTTTGCCACATGGTGTGGGCCATGTAAAATGATTGCACCAATGA  
TTGAAAAGTTTGCAGAACAATATTCTGACGCTGCTTTTTTACAAGTTGGATGTTGATGAAGTCTCAGATG  
TTGCTCAAAAAGCTGAAGTTTCTTCCATGCCTACCCTAATCTTCTACAAGGGCGGTAAGGAGGTTACCA  
GAGTCGTCGGTGCCAACCCAGCTGCTATCAAGCAAGCTATTGCTTCCAACGTATAG

YGR209C, 104 aa (SEQ ID NO 188)

MVTQLKSASEYDSALASGDKLVVVDFATWCGPCKMIAPMIEKFAEQYSDAAFYKLDVDEVSDVAQKAE  
VSSMPTLIFYKGGKEVTRVVGANPAAIKQAIASNV

YHR039C-B, 1007 bp, exon1: 501-503, intron1: 504-665, exon2: 666-1007  
(SEQ ID NO 197)

GTACATGCACCATTCGCTTCAACTGCGTCAGATAGTTGTAGTCCCTCTGGACATAAGCATTTCGTTCTGT  
GCTTGTCTGTCGTCGCCCTGTTTCAACGCCTCACTCGATATATACTCCTTAGGATCATGTGTTTGACCTG

114/251

AGCAATTGTCCCTTGTCTTGTGCTTCTTGGAACTCCAAAGAGCAAGTTTGACACCAAACATCTTGGAC  
ACTTGTATTTGAACTCTTTTATTCCGCATACACCACACAACACCGCCATACCTTGCAAATTGCCACACCC  
TTCCCTATTAAGTGGACTCCTATTCCAGCTCATCTCATGAATATGAACTTTGACATCCACTATTATTA  
CCGCGAATTTTTTTTTTTTTTCAATTTGTTACCCTGCCTTGGGTATCAAAAATTTTCATCTCTAAAAGGGA  
GCGTGATAGATAAAGCAATCACACCTTAAACAATACATTTTTTTTTTTTCTGCAATCTCCAAAGTGTGC  
AAGGTATACAAAGCAGAATGGTATGTGCCATTACATTACGTGTCAACACTTCTGTCTCTAACAAGCGTT  
CTTACTAACATGAAAACTTTTTTAAACTGTGCTCTCTTGTGGACTGGTACCTCGTGACAAAGGTAT  
TGGTTTTTTCATTGTTGCTCAGAACTATGTAATATTCTCTTTAGTCCCAAAAAACGGAATTGCCACCC  
TACTACAAGCTGAAAAGGAAGCCCACGAAATAGTATCAAAGGCTAGAAAAGTACAGACAAGATAAGTTGA  
AGCAAGCCAAGACTGATGCAGCCAAGGAAATCGACTCATACAAAATTCAAAAAGACAAGGAATTGAAGG  
AGTTTGAACAAAAGAATGCCGGTGGTGTGGTGAATTGGAAAAGAAAGCAGAGGCTGGTGTGCAAGGTG  
AATTAGCTGAGATTAAAGAAAATTGCAGAGAAGAAAAGGATGACGTTGTCAAATTTTGATCGAGACTG  
TCATCAAGCCTTCTGCTGAAGTCCATATCAATGCCTTGTA

YHR039C-B, 114 aa (SEQ ID NO 198)

MSQKNGIATLLQAEKEAHEIVSKARKYRQDKLQAKTDAAKEIDSYKIQKDKELKEFEQKNAGGVGELE  
KKAEGVQGELAEIKKIAEKKDDVVKILIETVIKPSAEVHINAL

YHR053C, 686 bp, CDS: 501-686 (SEQ ID NO 199)

AACTTCAACGATTTCTATGATGCATTTTATAATTAGTAAGCCGATCCCATTACCGACATTTGGGCGCTA  
TACGTGCATATGTTTCATGTATGTATCTGTATTTAAACACTTTTGTATTATTTTTCTCATATATGTGT  
ATAGGTTTATACGGATGATTTAATTATTACTTCACCACCCTTTATTTTCAGGCTGATATCTTAGCCTTGT  
TACTAGTTAGAAAAAGACATTTTGTCTGTCAGTCACTGTCAAGAGATTCTTTTGTCTGGCATTTCTTCTA  
GAAGCAAAAAGAGCGATGCGTCTTTTCCGCTGAACCGTTCCAGCAAAAAGACTACCAACGCAATATGG  
ATTGTCAGAATCATATAAAAGAGAAGCAAATAACTCCTTGTCTTGTATCAATTGCATTATAATATCTTC  
TTGTTAGTGCAATATCATATAGAAGTCATCGAAATAGATATTAAGAAAAACAACTGTACAATCAATCA  
ATCAATCATCACATAAAATGTTTCAGCGAATTAATTAACCTTCCAAAATGAAGGTCATGAGTGCCAATGCC  
AATGTGGTAGCTGCAAAAATAATGAACAATGCCAAAATCATGTAGCTGCCCAACGGGGTGTAACAGCG  
ACGACAAATGCCCCTGCGGTAACAAGTCTGAAGAAACCAAGAAGTCATGCTGCTCTGGGAAATGA

YHR053C, 61 aa (SEQ ID NO 200)

MFSELINFQNEGHECQCQCGSCKNNEQCQKSCSPTGCNSDDKCPCGNKSEETKKSCCSGK

YHR055C, 686 bp, CDS: 501-686 (SEQ ID NO 201)

AACTTCAACGATTTCTATGATGCATTTTATAATTAGTAAGCCGATCCCATTACCGACATTTGGGCGCTA  
TACGTGCATATGTTTCATGTATGTATCTGTATTTAAACACTTTTGTATTATTTTTCTCATATATGTGT  
ATAGGTTTATACGGATGATTTAATTATTACTTCACCACCCTTTATTTTCAGGCTGATATCTTAGCCTTGT  
TACTAGTTAGAAAAAGACATTTTGTCTGTCAGTCACTGTCAAGAGATTCTTTTGTCTGGCATTTCTTCTA  
GAAGCAAAAAGAGCGATGCGTCTTTTCCGCTGAACCGTTCCAGCAAAAAGACTACCAACGCAATATGG  
ATTGTCAGAATCATATAAAAGAGAAGCAAATAACTCCTTGTCTTGTATCAATTGCATTATAATATCTTC  
TTGTTAGTGCAATATCATATAGAAGTCATCGAAATAGATATTAAGAAAAACAACTGTACAATCAATCA  
ATCAATCATCACATAAAATGTTTCAGCGAATTAATTAACCTTCCAAAATGAAGGTCATGAGTGCCAATGCC  
AATGTGGTAGCTGCAAAAATAATGAACAATGCCAAAATCATGTAGCTGCCCAACGGGGTGTAACAGCG  
ACGACAAATGCCCCTGCGGTAACAAGTCTGAAGAAACCAAGAAGTCATGCTGCTCTGGGAAATGA

YHR055C, 61 aa (SEQ ID NO 202)

MFSELINFQNEGHECQCQCGSCKNNEQCQKSCSPTGCNSDDKCPCGNKSEETKKSCCSGK

YHR056C, 2999 bp, CDS: 501-2999 (SEQ ID NO 203)

ATGTATAGTTAAAGGTAAATTAAC TAGAGAACGTGGGAACAGTTCCGCAC TGTGACCACCGGAACGTAC  
GTCTGGTTAGCGCAGCATTAGTCCCAGTTACATCCGATTCAAAATGCAACAGCAAGTATTAATTGGGGA  
AATCATATCATTTTGAATATAACCTTGGCGTCTACTAAGGATGGTTATACATCCTAGCTCGTGTAGTG  
TGATATTTTGCAGGAATGATGCAAAGAGAGGAAGAACAAGAAGAGAGTTGTTGTTTTTAATGTATCTTA  
GCAATTTATGAGAGGAGCATTTGTCGTTGTCTGCTGTGACTAGTGCGTAGCTTTGCCGTTTGTTTTTAAT  
CATGATGGACATGCAAGTGAGAAAAGTGAGGAAGCCGCCTGCTTGCACCCAATGCAGGAAGAGAAAGAT  
CGGGTGCGACAGGGCCAAAACCGATATGTGGGAATTGCGTCAAGTATAACAAGCCGACTGTTTTTATC

115/251

CAGATGGACCTGGTAAGATGGTCGCTGTGCCCTCTGCGTCCGGGATGTCCACGCACGGCAATGGCCAAG  
GTTCCAACCATTTTAGTCAGGGAAACGGTGTAATCAGAAAAACGTAATGATTCAAACGCAGTATCCGA  
TTATGCAAACGTCGATAGAGGCATTCAACTTCTCGTTCAACCCCTCTGTGGATACTGCGATGCAGTGGAA  
CCAAGGCCGCTAGCTACCAGAATAATAACACCAATAATAACTGCTCCTCGTCAGAATAGTAGTACCG  
TTAGTAGTAATGTTTCATGGAAACACTATTGTGAGAAGCGATAGTCCAGATGTGCCCTCCATGGATCAGA  
TTAGAGAATATAACACACGATTACAACCTGGTTAACGCTCAAAGTTTTGACTATACAGATAACCCATACT  
CTTTTAATGTTGGTATCAATCAAGACTCGGCCGTTTTTCGATCTAATGACTTCTCCGTTTACTCAAGAGG  
AAGTATTAATCAAGGAGATAGACTTTTTAAAAAACAAATTGCTTGATTTACAAAGCTTGCAACTGAAAA  
GTTTGAAAGAAAAATCGAATTTAAATGCCGACAATACCACGGCAAACAAAATTAACAAAACAGGTGAGA  
ATTCTAAGAAAGGCAAGGTTGACGGTAAAGAGCCGGATTTGATCATCAGACTTCAAGGACTTCTCAGT  
CCTCACAAAAATACTTTACAGCGCTCACAATAACAGATGTGCAAAGTTTAGTCCAAGTGAAACCGTTGA  
AGGATACCCCCAACTACCTTTTCACTAAAAACTTCATCATTTTTTAGAGATCATTATCTTTTCAAGTTCT  
ATAATATTTTGCACGATATCTGCCATATTAATCAGTTCAAAGTAAGTCCTCCTAACAATAAAAAATCACC  
AACAATATATGGAAGTTTGCAAAGTTAACTTCCCACCAAAGCAATAATTATTGAGACACTAAACTCTG  
AATCCCTTAACAATCTGAATATTGAAGAATTTTGCCAATCTTTGACAAAACCTCTTACTAGAATTTG  
TTCATAACTCTTTTCCAAATGGTGATACCTGTCTTCATTCTCAACGGTCGATCTTCTTTTATCTCAAC  
TGACCAAACTAGGCGAATTAAGTGTGCTTCTACTGTTGTTAAACGATTCAATGACCTTATTCAATAAGC  
AGGTATTAATAACCATGTTTTCGGCATTAAATGAATAATTGAGGTTGATTGCAAGGCCAAATCACATTTGA  
TAAACCTGGAATATTATGACCAAGAGACAATCAAATTTATTGCCATCACAAAATTTTATGAATCTCTGT  
ACATGCATGATGATCATAAATCAAGTTTAGACGAAGATTTGAGCTGTCTGTTAAGCTTCCAGATAAAAAG  
ATTTCAAGTTATTCCATTTTTTGAAAAAATGTATTACTCAAGACATTCGCTTCTAGGTCAGTCTTCAT  
TCATGGTACCCGCTGCTGAAAACCTATCTCCGATACCTGCCTCTATTGATACGAACGACATTCCTTTAA  
TTGCTAACGATTTAAAATTACTGGAACGCAAGCAAAATTGATAAATATTCTGCAAGGTGTTCTTTCT  
ACTTGCCAGTAAATTTAACCAAAATTGAAAGTCTGTTAGAAACCTTGACTATGGGCGTGAGTAATACAG  
TAGACTTATATTTTCATGACAACGAAGTCAGAAAAGAATGGAAGACACTTTAAATTTTATCAATACCA  
TTGTTTATACAAATTTTTCTTTTTGTTCAAACGAATCCTCTTTGTCCATGGCAGTTCAACATTCTT  
CTAACAACAATAAGACCTCGAACTCTGAAAGATGTGCAAAGGATCTGATGAAATTATTTCTAATATGC  
ACATTTTTTACTCAATAACATTTAATTTTATCTTCCCCATAAAGTCGATAAAGTCATTTTCAAGCGGCA  
ATAATCGCTTTCATTCTAATGGTAAAGAATTTTTATTTCGCAAATCATTTTATTGAAATCTTACAGAATT  
TTATAGCAATCACATTTGCTATTTTCCAACGTTGTGAAGTAATATTATATGACGAATTTTACAAAAATC  
TTTCAAATGAGGAGATTAATGTTCAATTGCTATTGATTTCATGACAAGATTTTGGAATTTTAAAAA  
TAGAAATTATCGTATCCTTTTTACGAGATGAAATGAATAGCAACGGAAGTTTCAAATCTATTAAAGGTT  
TCAACAAGGTTTTGAATCTGATTAAATATATGCTGAGATTTAGCAAGAAAAACAAAATTTTGCGAGAA  
ACTCTGATAACAATAATGTTACAGATTATAGTCAGTCGGCGAAGAACAATAATGTTCTCTTGAAATTCC  
CCGTTAGTGAAGTGAACAGAATCTATTTAAATTTAAGGAGATTTAGATTTTAAATGGAAGAGAAG  
TTGTCCAAAGGAGTATAATTATTGACAAGGATTTGGAATCTGATAATCTGGGTATTACTACGGCAAAC  
TCAACGATTTCTATGATGCATTTTATAATTAG

YHR056C, 832 aa (SEQ ID NO 204)

MVAVPSASGMSTHGNGQGSNHSFQNGVNVQKNVMIQTQYPIMQTSIEAFNFSFNPSVDAMQWTKAASY  
QNNNTNNNTAPRQNSSTVSSNVHGNTIVRSDSPDVPSMDQIREYNTRLQLVNAQSFQDYTDNPYSFNVGI  
NQDSAVFDLMTS

PFTQEEVLIDFLKNKLLDLQSLQLKSLKEKSNLNADNTTANKINKTGENSEKKGKVDGKRAGFDHQ  
SRTSQSSQKYFTALTITDVQSLVQVKPLKDPNYLFTKFNIIIFRDHYLFKFYNILHDICHINQFKVSP  
NNKNHQYMEVCKVNFPPKAIIEITLNSSESLNNLNIEEFLPIFDKTLLEFVHNSFPNGDTCPSFSTVD  
LPLSQLTKLGELTVLLLLLNDMSMTLFNKQAINNHVSALMNNLRLIRSQITLINLEYDQETIKFIAITK  
FYESLYMHDDHKSSLDEDLSCLLSFQIKDFKLFHFLKKMYSRHSLGQSSFMVPAENLSPIPASIDT  
NDIPLIANDLKLLETQAKLINILQGVPFYLPVNLTKIESLLETLTMGVSNVTVDLYFHDNEVRKEWKDTL  
NFINTIVYTNFFLVQNESSLSMAVQHSSNNNKTNSERCADLMKIIISNMHIFYSITFNFIFPIKSIK  
SFSSGNNRHFHNSNGKEFLFANHFIEILQNFIAITFAIFQRCEVILYDEFYKNLSNEEINVQLLLIHDKIL  
EILKKIEIIVSFLRDEMNSNGSFKSIKGFNKLNLIKYMLRFSKKKQNFARNSDNNNVTDYSQSAKNKN  
VLLKFPVSELNRIYLFKEISDFLMEREVVQRSIIIDKDLESDNLGITANFNDFYDAFYN

YJL138C, 1688 bp, CDS: 501-1688 (SEQ ID NO 223)

CTGTTGAATCATGGTAAAAGAGAAAATCAAAGCACGTTGACCTGGATATAACCTCAGTAGATCGAAAT  
GCTTCGCAGAAGAGTACTGCAGAGAAACATGATATTGAGAAACCGACATCTAAGCCGCAATCTGCTTTT



116/251

AAATTTGATTGGGAGTCTACGGATTATTTAGACCGCGTCCAAAGAGCATTCCCAAAGCCTGATACCTGA  
TGCCATCCCTCTACCTCTTAGCTATCAATCATTCAACTAACTACTACATAGTATACATTAGCTGTACA  
GTCGTACATCAGACGAATACAAAAGGCCGGGTGAAAGCGTTGATTTTGCGTACCTTTTTCTTTTTTC  
GAAATTTTTTTATTTTTTTTTTCAGCATCATATATAAAAGAAATCTCATCTCAAGGAGAAGGAAACAGCA  
GATCCCAATACACATAGTAGGAAAAAAAAGGTTTCGCTAAACAAAGGACTGGTGTGTACAAGAACTAA  
TAAATAGTAATTGCAATATGTCTGAAGGTATTACTGATATTGAAGAATCCCAAATTCAAACCAACTATG  
ACAAGGTCGTCTACAAGTTCGATGATATGGAATTGGACGAAAACCTGTTAAGAGGTGTTTTCGGTTACG  
GTTTCGAAGAACCATCTGCCATTCAACAACGTGCCATCATGCCTATTATTGAAGGTCACGATGCTTTGG  
CTCAAGCTCAATCTGGTACTGGTAAGACCGGTACTTTCTCCATTGCTGCTTTGCAAAGAATTGACACCT  
CTGTCAAGGCTCCTCAAGCTTTGATGTTGGCTCCAACCTAGAGAATTGGCTTTGCAAATCCAAAAGGTTG  
TCATGGCTTTGGCTTTCCACATGGACATCAAGGTCCACGCTTGTATCGGTGGTACTTCCTTTGTTGAAG  
ACGCTGAAGGTTTGAGAGATGCTCAAATCGTCGTTGGTACTCCAGGTCGTGTTTTGACAACATCCAAA  
GACGTAGATTTCAGAACTGACAAGATCAAGATGTTTCATCTTAGATGAAGCTGATGAAATGTTGTCTTCTG  
GTTTCAAGGAACAAATCTACCAAATTTTCACCTTACTTCCACCAACCACTCAAGTTGTTCTATTGTCCG  
CCACCATGCCAAATGACGTCTTGGAAGTTACCACCAAATTTATGAGAAACCCAGTTAGAATTTTGGTTA  
AGAAGGATGAATTGACTTTTGAAGGTATCAAACAATTCTACGTTAATGTTGAAGAAGAAGAATACAAAT  
ACGAGTGTGTTGACCGATTTATACGACTCTATCTCCGTTACTCAAGCTGTCATCTTCTGTAACACCAGAA  
GAAAGGTCGAAGAATTGACCACTAAGTTAAGAAACGACAAATTTACCGTTTCTGCCATCTATTCTGATT  
TACCACAACAAGAAAGAGACACCATCATGAAGGAATTGAGAAGTGGTTCTTCCAGAATTTTGATCTCCA  
CTGATTTGTTGGCTAGAGGTATCGATGTTCCAAGGTTCTTTGTTGTTATTAACCTACGACTTACCAGCTA  
ACAAAGAAAACTATATTTACAGAATCGGTAGAGGTGGTTCGTTTCGGTAGAAAAGGGTGTGGCCATCAACT  
TTGTTACTAACGAAGACGTTGGCGCTATGAGAGAACTAGAAAAGTTCTACTCCACTCAAATTTGAAGAAT  
TGCCATCCGACATTGCTACCTTGTGTAACCTAA

YJL138C, 395 aa (SEQ ID NO 224)

MSEGITDIEESQIQTNVDKVVYKFDDMELDENLLRGVFGYGFEEPSAIQQRAIMPIIEGHDVLAQAQSG  
TGKGTGFSIAALQRIDTSVKAPQALMLAPTRELALQIQKVMALAFHMDIKVHACIGGTSFVEDAEGLR  
DAQIVVGTPGRVFDNIQRRRFRDQIKMFI LDEADEMLSSGFKEQIYQIFTLPLPPTQVVLVSATMPND  
VLEVTTKFMRNPVRILVKKDEL TLEGIKQFYVNVEEYKYEC LLDLYDSISVTQAVIFCNTRRKVEEL  
TTKLRNDKFTVSAIYSDLPQQRDTIMKEFRSGSSRILISTDLLARGIDVQQVSLVINYLDPANKENYI  
HRIGRGRFRGRKGVAINFVTNEDVGAMRELEKFYSTQIEELPSDIATLLN

YKL060C, 1580 bp, CDS: 501-1580 (SEQ ID NO 239)

TGGGTCATTACGTAAATAATGATAGGAATGGGATCTTCTATTTTTCTTTTCCATTCTAGCAGCCGT  
CGGGAAAACGTGGCATCCTCTCTTTTCGGGCTCAATTGGAGTCACGCTGCCGTGAGCATCCTCTCTTTCC  
ATGTTAACAACCTGAGCAGTAACCAATGGAAGCAAGCTTAGAGCTTAGCGTTGCTCCAAAAAAGTATTGGA  
TGGTTAATACCATTGTCTGTCTCTCTTCTGACTTTGACTCCTCAAAAAAATAATCTACAATCAACAG  
ATCGCTTCAATTACGCCCTCACAAAAACTTTTTTCTCTTCTTCTTCTCGCCACGTTAAATTTTATCCCTCA  
TGTTGTCTAACGGATTTCTGCACTTGATTTATTATAAAAAGACAAAGACATAACTTCTCTATCAATT  
TCAGTTATTGTTCTTCTTCTGCGTTATTCTCTCTGTTCTTCTTTTCTTTTGTTCATATATAACCATAACCA  
AGTAATACATATTCAAAATGGGTGTTGAACAAATCTTAAAGAGAAAGACCGGTGTCATCGTTGGTGAAG  
ATGTCCACAACCTATTCACTTACGCTAAGGAACACAAGTTTCGCTATTCCAGCTATTAAACGTCACCTCTT  
CTTCTACTGCCGTCGCTGCTTTAGAAGCTGCTAGAGACAGCAAGTCCCAATCATTTTGCAAACCTCTA  
ACGGTGGTGCTGCTTACTTCGCTGGTAAGGGTATCTCTAACGAAGGTCAAAATGCTTCCATCAAGGGTG  
CTATTGCCGCTGCCCACTACATCAGATCCATTGCTCCAGCTTACGGTATCCCAGTTGCTTTACACTCTG  
ACCACTGTGCCAAGAAGTTGTTGCCATGGTTGATGGTATGTTGGAAGCTGATGAAGCTTACTTCAAGG  
AACACGGTGAACCATTATTCTCTCCACATGTTGGATTTGTCTGAAGAAACCGATGAAGAAAACATCT  
CTACTTGTGTCAAGTACTTCAAGAGAAATGGCCGCTATGGACCAATGGTTAGAAATGGAAATCGGTATTA  
CCGGTGGTGAAGAAGATGGTGTAAACAACGAAACGCTGACAAGGAAGACTTGTACACCAAGCCAGAAC  
AAGTTTACAACGTCTACAAGGCTTTGCACCAATCTCTCCAACTTCTCCATTGCTGCTGCTTTTCGGTA  
ACTGTCACGGTTTGTACGCTGGTGACATCGCTTTGAGACCAGAAATCTTGGCTGAACACCAAAAGTACA  
CCAGAGAACAAGTTGGTTGCAAGGAAGAAAAGCCATGTTTCTTTGGTCTTCCACGGTGGTTCGGTCTTA  
CTGTCCAAGAATTCCACACTGGTATTGACAACCGTGTGTTCAAGGTCAACTGGACACTGACTGTCAAT  
ACGCTTACTTGACTGGTATCAGAGACTACGCTTTGAACAAGAAGGACTACATAATGTCCCCAGTCGGTA  
ACCCAGAAGGTCCAGAAAAGCCAAACAAGAAGTTCTTTCGACCCAAGAGTCTGGGTAGAGAAGGTGAAA  
AGACCATGGGTGCTAAGATCACCAAGTCTTTGGAACTTTCCGTACCACCTAACACTTTTATAA

117/251

YKL060C, 359 aa (SEQ ID NO 240)

MGVEQILKRKTGVIVGEDVHNLFTYAKEHKFAIPAINVTSSSTAVAALAAARDSPKSPIILQTSNGGAAY  
FAGKGISNEGQNASIKGAIAAAHYIRSIAPAYGIPVVLHSDHCAKLLPWFDMLEADEAYFKEHGEPL  
FSSHMLDLSEETDEENISTCVKYFKRMAAMDQWLEMEIGITGGEEDGVNNENADKEDLYTKPEQVYNVY  
KALHPISPNSIAAAGFNCHGLYAGDIALRPEILAEHQKYTREQVGCKEEKPLFLVFHGGSGSTVQEFH  
TGIDNGVVKVNLDTDCQYAYLTGIRDYVLNKKDYIMSPVGNPEGPEKPNKKFFDPRVWVREGEKTMGAK  
ITKSLETFRTTNTL

YKL097W-A, 779 bp, CDS: 501-779 (SEQ ID NO 245)

AGCTCCGAAGGGCAATTCCACAGGCACTCCGCGGGGGCCCGCCAAGGCCAAAAGGCGTGGAATATGCC  
CGTTTTGGGGCCATAACACCCAGTACCACGGCCGGAACGGGCCATATAATAAGTTTTTCACTCTCAAGA  
ATGGTAAACGTAAATAGGAACATCCCACTACCTAGAAATTGCGGAAATTTTCGCGCTTATCATTAGAAA  
ATCTGGAACCGTCCTTTTTCTCTCTTCTTGCAATTTCCCTTTCCGTATTATTGCCATTCTTTAACTGCAT  
TTGGGGAACCGTAGACCAAAAGCCAAACAGAGAAATGTAACGTTCTAAAAAACAACGAAAAAATT  
GAAAAATAAGATACAATAATCGTATATAAATCAGGCTTCTTGTTCATCATTTTCAATTCTCTTCTTGCC  
ATCCCTTTTCTTATCTTTTGTCTTTTCTTCTCATAATCAAGAATAAATAACTTCATCACATTCTGCTACA  
CATCAACAAGAAAAAATGCAATTCTCTACTGTCTGCTTCCGTTGCTTTCTGCTGCTTTGGCTAACTTTG  
TTGCCGCTGAATCCGCTGCCGCCATTCTCAATCACTGACGGTCAAAATCCAAGTACTACCACTGCTA  
CCACCGAAGCTACCACCACTGCTGCCCATCTTCCACCGTTGAAACTGTTTCTCCATCCAGCACCGAAA  
CTATCTCTCAACAACTGAAATGGTGTCTGCTAAGGCCGCTGTCTGGTATGGGTGCCGGTGCTCTAGCTG  
CTGCTGCTATGTTGTTATAA

YKL097W-A, 92 aa (SEQ ID NO 246)

MQFSTVASVAFVALANFVAAESAAISQITDGIQATTTATTEATTTAAPSSTVETVSPSSTETISQQT  
ENGAAKAAVGMGAGALAAAML

YKL150W, 1409 bp, CDS: 501-1409 (SEQ ID NO 249)

CCCATCACATCGCATCACATCACATCACTCCCTATTCTGCCCTTTACAGCGCAAAGGAGTCGTGTGTGG  
GTGTGTGCTCCTTTTGACGATCATAAGAGTCCATTTCTAGTATGCAAGCTGGTAACAATAGGTGAATGA  
ATTAGGTTCAATTTGCGATGACCTTCAGTATCCCTCCACGCAATGCTAAACTATCCCCCTCATTATGACG  
CCTATATCGTATAAGGAACCTGTTACCCCTGACAATTCAAACCTCAAAGGTCTAAGACCAACAAGCGT  
AGGAACATTCGCTCGGAGTGTTTCTCCGTTTGAAGAAAGAGAGAAATAAGGGCCCTTGATTGGTGTCT  
TGTCGAGAGAGGTACGTATATAAGAATGCAGTTTGTCTCGCAATGCCGCTTGTGTTAAGTACTCTTACC  
TTTTCCCTCAATACTAACGTTTTGAAGCAGCCAAACTAACAATAGTATAACGTATATAGGTTAAATAA  
TATTCGAAGTCAAAAACATGTTTTCCAGATTATCCAGATCTCACTCAAAAGCATTACCGATTGCTTAG  
GTACAGTTGCTATAGCAGCTGCTACCGCATTCTATTTTGCAAACCGTAACCAACATTCCTTTGTCTTCA  
ATGAATCTAATAAAGTGTTCAAAGGTGATGACAAATGGATCGACTTGCCAATATCTAAATAGAGGAGG  
AATCCCACGACACCAGAAGGTTTACTTTTAAGCTGCCTACCGAAGACTCAGAAATGGGGTTGGTCTTAG  
CATCTGCTCTGTTTGTCTAAATTTGTACACCAAAGGGATCCAATGTGGTGAGACCATACTCCTGTGA  
GTGATCTTTCCCAGAAGGGTCACTTCCAGCTGGTCTGCAAGCATTATGAAGGTGGTAAATGACCTCAC  
ATTTATTTGGTCTTAAACCAATGACACCGTTTCTTTCAAGGGTCTTATTATGAATGGAAGTGGAAC  
CTAATCAGTTCAAGTCAATCACCTTGTTAGGTGCCGGTACCGGTATCAACCCTCTGTACCAATTAGCTC  
ATCATATAGTTGAAAACCCAAACGACAAGACCAAAGTTAACTTGCTATATGGGAACAAGACTCCTCAGG  
ACATTTTACTAAGGAAGGAAGTGGATGCGTTGAAGGAAAAGTATCCTGACAAGTTCAATGTTACTTACT  
TTGTTGACGACAAGCAAGATGACCAAGACTTTGATGGTGAATTAGTTTCATCTCCAAAGATTTTATTC  
AGGAGCATGTTCCAGGTCCAAAGGAAAGCACATTTGTTTGTCTGCGGTCCCCCACCATTTATGAACG  
CTTACTCAGGTGAGAAGAAGTACCTAAGGACCAAGGTGAATTGATCGGTATCTTGAACAATTTGGGCT  
ACTCCAAGGACCAAGTTTTCAAATTTTAA

YKL150W, 302 aa (SEQ ID NO 250)

MFSRLSRSHSKALPIALGTVAIAAATAFYFANRNQHSFVNESNKVFKGDDKWLDPISKIEEESHDR  
RFTFKLPTEDESEMGLVLASALFAKFVTPKGSNVVRPYTPVSDLSQKGHFQLVVKHYEGGKMTSHLFLK  
PNDTVSFKGPIMKWKWQPNQFKSITLLGAGTGINPLYQLAHHIVENPNDKTKVNLLYGNKTPQDILLRK  
ELDALKKEYPDKFNVTYFVDDKQDDQDFDGEISFISKDFIQEHVPGPKESTHLFVCGPPPFMNAYSGEK  
KSPKDQGELIGILNLLGYSKDQVFKF

118/251

YKL156W, 1099 bp, exon1: 501-503, intron1: 504-853, exon2: 854-1099  
(SEQ ID NO 251)

CGAAAGGTTTCGATCAAAGTTTGGCTCAATCACTGGACACTATTACTTCGAAAGCGCAGTGGGGTTAAC  
AGAGACCGTGATGTCGTCAACAAGTATTTGAAGGAAAATGGTTACTATTAAGAAAAATCTCTTTTCTA  
GCCATTTTGCCTTTTATATAGTCAAGTATCTATATGTGACAAATACTTCTTCTAAGCTTGGCCTTCTG  
ATAGGCTTAGCTTGCAGTGGTTGCAACATACATAAATCAACAAAAAGTACGGCTTAAAATTTTGGTA  
TTCATTTATTTCAACCCGTGCACACTGGAAATAAATCTGTACATAACAGCATATTTTGTTTTGAAGAAA  
ATTTCTGTGTTTCTCCGATGTGGGAAGAATTTTAGGATCGGCTAAATTTTCGTAAAGTATCAGTAACCTG  
GTATCTCTGTATAAGCGGAGTCTAATTTTCGATAACAAGCAACTTCATCGTAACACCTTCCAACAAAGCA  
AAGATAGATATCCCAAAATGGTATGTTAGTATCCAATAAATGCAGCGCAACTGGACCAGTGAATAGAAC  
AATACATATAGATAAGTCGCAAAAGAAAAGAATACATGTGGTGGAAAATTTTGCACCAAGAGAGGCAAG  
AACTATGAAGAAAGACTTTTGAATATTTCAAGCGGTGGCTACATATAGTGGATAAGATTTCAGGATGGA  
CGTATGAGCTTACAGTTCATTGTAGGGGAATATAAAATTTCTGATGATGGCGAACTTCATTCCCAGCAAC  
TCAAGCTATTGTTATTTTCTATTCTGCACCGAGATGAGGAGAAAAAGGAAGTTTACTAACAGTTAGA  
TTTATTTCTTATTCTGTCTACAACAGGTTTGTAGTTCAAGATTTATTGCACCCAAGTGCAGCTTCTGAAGC  
AAGAAAGCACAAATTAAGACATTAGTCCAAGGTCCAAGATCGTACTTCCTAGACGTTAAGTGGCCAGG  
TTGTTTGAACATCACTACAGTTTCTCACACGCCCAAACTGCAGTTACCTGCGAATCCTGCTCAACAAT  
TTTGTGCACCCCAACTGGTGGTAAGGCAAGCTTTCTGAGGGTACATCTTTCAGAAGAAAGTAA

YKL156W, 82 aa (SEQ ID NO 252)

MVLVQDLLHPTAASEARKHKLKTLVQGPRSYFLDVKCPGCLNITTVFSHAQTAVTCECSTILCTPTGG  
KAKLSEGTSFRRK

YLR029C, 1115 bp, CDS: 501-1115 (SEQ ID NO 265)

TCGACACTTACTTAATATGTTTTGCCGCCCTTCATAAGAGGGTGTTCATAAAATTTATTGGGCAAGAAT  
GAGATGGACTCGCACCCCTACATGACGTTTAAATATTTAGTGTTAAGGTTTCAGAACATGCACCAGGTGCG  
ACATGTGTTGCGATTATCATGACAATGTCTCTATCCGAGATGCATTTGTAGTATCAATTGATGCGTATT  
ATGACATGATTTACATAGCATACATCGTCAACATGATATTATATCTTTTTTGTATAAATGTACGGAT  
TTAAAGCTGTGCAATATATTTTCTGAAATTTCTTGGAGCTGACGCAAAATTTTCAAAGGTGCTAAAAT  
TTTCAAGATTTCTCACTTTTGCTTGGTAACAAAGAATGATGGCATTGCATTTTACCACCGGTACATTT  
AAGTCTATTTCTCACGTTTCTTTCCCTATCCTTAAGTAATTCTTTTACAATCTAAGAAAACACGATC  
AAACAAATAAATCAGCAATGGGTGCCCTACAAATATTGGAAGAATTGCAAGAAGAAGCAAGATCTGATG  
TTTTGAGATTTCTTGCAAAAGAGTCAGAGTCTGGGAATACAGACAAAAGAATGTCAATCACAGACCGCTA  
GACCAACTAGACCAGACAAGGCTAGAAGATTGGGTTACAAAGCTAAGCAAGGTTTCGTTATCTACCGTG  
TCAGAGTTAGACGTGGTAACAGAAAGAGACCTGTTCCAAAGGGTGCTACTTACGGTAAGCCAACCTAACC  
AAGGTGTCAATGAATTGAAATACCAAAGATCCTTGAGAGCTACCGCTGAAGAAAGAGTTGGTCGTCGTG  
CCGCTAACTTGAGAGTCTTGAACCTCTACTGGGTTAACCAAGATTCTACTTACAAGTACTTCGAAGTTA  
TCTTGGTCGACCCTCAACACAAGGCTATCAGAAGAGATGCTCGTTACAACCTGGATCTGTGACCCAGTTC  
ACAAGCACCGTGAAGCTAGAGGTTTACTGCCACTGGTAAGAAATCCAGAGGTATCAACAAGGGTCACA  
AATTCACAACACCAAGGCTGGTAGAAGAAAGACCTGGAAGAGACAAAACACTTTGTCCTTGTGGAGAT  
ACAGAAAATAA

YLR029C, 204 aa (SEQ ID NO 266)

MGAYKYLEELQRKKQSDVLRFLQVRVWVEYRQKNVIHRAARPTRPDKARRLGKAKQGFIYRVRVRRG  
NRKRPVPGKATYGKPTNQGVNELKYQRS LRATAEERVGRRAANLRVLNSYWVNQDSTYKYFEVILVDPQ  
HKAIRRDARYNWICDPVHKHREARGLTATGKKS R GINKGHKFNNTKAGRRKTWK RQNTLSLWRYRK

YLR038C, 752 bp, CDS: 501-752 (SEQ ID NO 267)

GGAAAGCAAAGCTCTAAATGATAACTCTACAAAAAGTCAGAGAAATCTGTCACTAATTTATTGAAGGA  
TGAAGAATTAATGCTTAAAGTCTTAGAGCTTTTGGTGACAAGTGCTGCAACGCCACAGACCCAATTAA  
AGCTACCGATTTCGTGGGACATGTGTTTCCAATTAATACGCTTACTCAAGGAATTAGACAGAGAAAAACA  
CACACAATTGGTTCAAAAAGCACTCGAGAGATTCAAATAAATCTATATGACACCATGTATTCTTTACCA  
TATAGCTTCATAACATTGACCAATCAATTTTTCAGAAATGCGTCGCGCGTAGTTTTGCCCGATATCCCCA  
TCCCTTCAGGATCTTTAAAAGGTGATGAAAGATGCACCAGATAGAAAAGTTGCATTAAAATGATTAGCA  
GAGATATACAAATATTTTAGTAAGAATACATAAAGTATCTTTGCTTTCACAAATAGGAACAAGCACATA  
AATACAGTATAATAGACATGGCTGATCAAGAAAACCTCTCCACTACATACAGTTGGTTTCGATGCTAGAT

119/251

TTCCCCAACAAACCAAACAAAGCATTGTTGGCAATCTTATGTGGATTATCACAAGTGTGTTAATATGA  
AGGGCGAAGATTTTGTCTCCGTGCAAGGTCTTTTGAAGACCTATAACGCCTTATGTCCCCTAGACTGGA  
TCGAAAAATGGGATGATCAAAGAGAAAAAGGTATTTTCGCAGGTGATATCAACTCAGACTAA

YLR038C, 83 aa (SEQ ID NO 268)

MADQENSPLHTVGFDFARFPQONQTKHCWQSYVDYHKCVNMKGEDFAPCKVFWKTYNALCPLDWIEKWDD  
QREKGIFAGDINS

YLR312C, 1697 bp, CDS: 501-1697 (SEQ ID NO 285)

CATCAATTAGGGCAAACCTTGAATAGTCAGCTAGGTCATATATTTAAATCAATTAGCCCTATGACTACA  
TTAGGTTTATTGTTAGGTCTTTACGGCTGCATATTTGCTTTTCGCCGTTTCGGCGGGGTCTGCGACGATT  
TCTGCGCGGTCTTGTATGGGTGGAGTTGACAGTTAACCCTCCGGACCCCTACCCCGGTGTGCCCCGG  
TCCATCTATCCATTTTGCAGTAACCCCTTTGCGCGACAGCTGCTTATCAAGGTACCTGGATCGAGCCAT  
AAAAATTGATCTACACAGATGAGATGGGGCATTGGGATATATTATTAGTCGGAGTATCATTATAGTTAT  
TCAGTTTATGCAGGTTACTGGCCAAACGTTTTTCTTCATTTGGAATAATCGTTTAGGAGCTACTGTTTC  
CGGTATAAAGTAACAAGCACAGTAGCAGAGTAATACGCAGTGACGATAATAGAGACTAGTAAAAACAGTC  
GAGTTGTCTGGACCTAAAATGTCAGAAGAAGCAGTATCGAAGTCAGAAATATCTTTGGATAGTTTGCATGAAAGCTCCT  
TTGCGAGGAGAGGACGACGAGGACTTCGATGCAGATGTCCTATCGAACACTAGCAGTGAAGAGTCTGCAC  
AGATGAATCGTATTTACGATTTTAGAACATCTAATGAATTTAGTAATGCTGGAGTTAATATTGATCAAA  
CTGGAGTTCCCCTATTTTACAGAGTCATTTGATACTTTGTCCGGCTCAAATGTTGGCGGAACGGTATTGC  
CAAGTATGGAGGGGTGAAACTGAAGGATAGTACGATAAGGAATCTAGCACACTATCGGATCATATCA  
TAGATAAAAGTGAGGGTAAATCTGCTAAATTGAAGATGTGGCATGTTATCATGCTATCTTCATTGCTTT  
CCATGACCTTTTCATACCTCGCCCTCGAATATTCCCTGACTGGTGATGTGTTGGCAGGTTTTAAATCAC  
AACAGTCATTACGTAATAATGAAAGGAAGCTGTTGTACGGCAATATCGATTTTGTGATAAAAAATCTT  
ACGATTCATCAAGTGACTCTTTAAGTCAGTGGGCTCCTTCAGGAAAATACTACGTCGACTTCGACAATC  
ATATTGCATACCCATTAAAGGATGATGACCTAATGGGCTGGAGACGATACAAAACAGACTTAGTTATTT  
TATGGTATACAACAAAAGCTCGAATGAAAGACGGTTGGCACAAGAGAATTAACAAAATAAACGGAGGAA  
GAATAAAGTTACACCTATTTCTCAAGAATCTTTTAAATCCGCTCAAGAAAGTTTAAAGGTATTGCATA  
AAGAACAGAAACGCCGCTGGAAAAGGCTCTTTGTGCTACTTCATAATAAATACAGGCAATTTTCTCCAC  
ATATTAAGGTATTTTCGATCATTCTTGCCAAAAAGCAAAACAATGTTGGTCGGGATCCAGATTGCAGT  
TGCGCAAGCTTCGTTTCAAGTCAATGAAACCATTCCGAGTTTTTCAGTTTAAAGGTTTCGCAAAGATACCA  
ACTGGTTTGTAAAGCAGCTGAAACGGTTCCGATTGAAATTACAGCATTTCGAGGATGTATAAAGCGATGT  
CAGAATGCAGGAAAAAAATTTATTTAAGTGCAACACTAG

YLR312C, 398 aa (SEQ ID NO 286)

MSEEDDHWNLVRLRLRKREGEEQSSKSEISLDSLHESSFAGEDDEDFDADVLSNTSSEESAQMNRIY  
DFRTSNEFSNAGVNIDQTVPTISESFDTLSGSNVGGTVLPSMEGSKLKDSTIRNSSLSLSDHIIDKSEG  
KSAKLKMWHVIMLSSLLSMTFSYLALEYSLTGDLVLAGFKSQSLRNNERKLLYGNIDFVDKSYDSSSD  
SLSQWAPSGKYVDFDNHIAIYPLKDDDLMGWRRYKTDLVILWYTTKARMKDGWHKRINKINGGRIKLHL  
FLKNSFKSAQESLRVLHKEQKRRWKRLFVLLHNKYRQFSPHIKRYFDHSCQKAKQCWSGSRQLRLKRF  
KSMKPFVRVQFKVRKDTNWFVKQLKRFGGLKLQHSRMYKAMSECRKKNYFKCKH

YLR414C, 1292 bp, CDS: 501-1292 (SEQ ID NO 293)

TAGTCAGCCACACATTGACGTACACTGTGAACAGCCTATTTCTTTCCATGTATCTCAGTGCCAGCTTA  
TGAGAACTGTACAGCCTCCCACTTGACCCTCAGAGCCCTCTCCACTCCCCCTCTTTCAACATCGCC  
AGATAGCCCGCGTTGAATGGTGCAGGACAACCCGGCTGGCCTGGCCAGGCAAAAAAGGACGCAGCAGC  
CCTCGAGCGTTATTTCCAAATCGGGCGTACTATCAGCCAAGCCAGCTCGGTATTTTTCAGCGTTCTCG  
CAGGAAAATTGGCTGAGAAATATATACGCGAGAATGTTGCTCTTCCATGTCTCAGTAGTCAATGAGT  
GTCCAGTGGTGTTCATTCTGGACCAGTTGTTTGGAAAGTAGAACTAAAAGAACTAGATCAAGATCATA  
CAACGCTGCGCAGTAGTGAACCTGATTAAAGCAATAGAGAACTATTAAGAAAAAACAAACACATCAT  
CGAAGGACGCTATAAGCATGAGGAATTTTTTACAGTTATTTTTTTCAGCTATATTTTTCGCTAGGAGCAC  
TTATATTAGCCATTGTTGCTATGCGCAGGATCAACGAAAAATTACAGTCCCATAAAATAAAATTTACTGTG  
CAGAATTGGATCTGTGCGCAGATGAAGGTATCGACGGTGCTCCCTCTTTGAGTTCTGCTACGCTATCTT  
CGTTGGGCTGCCCTCATATATAAATATAGGGCTTTGGTCGTACTGTACAGTGGACTCCTCGCATAACA  
TCCAATCATGTTCTTCGCCCTCACGGTATCCAGAATTTTAACTATCGTCATTAGTGATGACAATATCA

120/251

ACAACAATGAGGCTCTGGAGCTTATGGATTCCGTGGCCAGTGTGTGTTTTGCCCGAAAACTAAAAAGTA  
AAATGACATACTACAACAATTTGGTCAAGTGTATGTTTCATTACCATTCTTATTGGTATTGTCTTGACCT  
TTGTGAATCTAGTGTTCACGTATTGCGCTGGATCATCCACATAAGGCCGCTAACGTGGTTTGGTGCCCT  
TTTTTTTCATTTTTTCGCCTTTGCCGCCCTATTAGTCAGTATAGGTTTCGTGTTTGGGCACTTACTCATACA  
TCAAATACATCCTAAAGCATAACTATAGTGATTACGGTATTTCAATGAGCATTGGTAGGAACCTACCAGG  
GTTTGATGTGGGGGGCTGTCGTGGAGCATTACTGAATTTTCATTCTATGGTGTAGCGTGAGATCGAGGC  
CCACCGTCATCTATGCGAACGCTCCAATTGAGGAAAAACCATTGATTGTA

YLR414C, 263 aa (SEQ ID NO 294)

MRNFFTLFFAAIFSLGALILAIVACAGSTKNYSPINKIYCAELDLSQMKVSTVLPSSLSSATLSSSLGLPS  
YINIGLWSYCTVDSSHNIQSCSSPHGIQNFNLSSLVYDNNINNEALELMDSVASVVLPEKLKSKMTYYN  
NLVKCMFITILIGIVLTFVNLVFNVLRWIHIRPLTWFGAFFSFFAFAALLVSIGSCLGTSYIKYILK  
HNSYDYGISMSIGRNYQGLMWGAVVGALLNFILWCSVRSRPTVIYANAPIEEKPLI

YMR251W-A, 680 bp, CDS: 501-680 (SEQ ID NO 317)

ATCCCGTTGAAGCAACCGCACTATGACTAAATGGTGCTGGACATCTCCATGGCTGTGACTTGTGTGTAT  
CTCACAGTGGTAACGGCACCGTGGCTCGGAAACGGTTCCTTCGTGACAATTCTAGAACAGGGGCTACAG  
TCTCGATAATAGAATAATAAGCGCATTTTTGCTAGCGCCGCCGCGCGCCCGTTTCCCAATAGGGAGGC  
GCAGTTTATCGGCGGAGCTCTACTTCTTCTATTTGGGTAAGCCCTTTCTGTTTTCGGCCAGTGGTTG  
CTGCAGGCTGCGCCGAGAACATAGTGATAAGGGATGTAACCTTTCGATGAGAGAATTAGCAAGCGGAAA  
AAAATATGGCTAGCTGGGAGTTGTTTTCAATCATATAAAAGGGAGAAATTGTTGCTCACTATGTGAC  
AGTTTCTGGGACGTCTTAACCTTTTATTGCAGAGGACTATCAAATCATAACAGATATTGTCAAAAAAAAA  
AAGACTAATAATAAAAAATGAAGTTATCTCAAGTTGTTGTTTCCGCCGTGCGCTTCACTGGTTTTAGTAA  
GTGCTGCTAACAGTTCTAACAGCTCAAGCTCAAAGAATGCTGCCCAACCAATTGCCGGTTTAAACAACG  
GTAAGGTTGCAGGCGCCGCTGGTGTGCTCTAGCTGGTGCTTTGGCCTTTTTGATTGTA

YMR251W-A, 59 aa (SEQ ID NO 318)

MKLSQVVVSAVAFTGLVSAANSSNSSSSKNAAQPIAGLNNQKVAGAAGVALAGALAFLLI

YNL030W, 812 bp, CDS: 501-812 (SEQ ID NO 323)

GTTTTGACACCGAGCCATAGCCGTGATTGTGCGTCACATTGGGCGATAATGAACGCTAAATGACCAACT  
CCCATCCGTAGGAGCCCCCTTAGGGCGTGCCAATAGTTTCACGCGCTTAATGCGAAGTGCTCGGAACGGA  
CAACTGTGGTCGTTTTGGCACCGGAAAGTGGTACTAGACCGAGAGTTTCGCATTTGTATGGCAGGACGT  
TCTGGGAGCTTTCGCGTCTCAAGCTTTTTCGGGCGCGAAATGCAGACCAGACCAGAACAAAACAAGTAC  
AAGAAGGCGTTTAATTTAATATGTTGTTCACTCGCGCTGGGCTGTTGTTATTTCGGCTAGATACATACG  
TGTTTGTGCGTATGTAGTTATATCATATATAAGTATATTAGGATGAGGCGGTGAAAGAGATTTTTTTTT  
TTTCGCTTAATTTATTCTTTCTCTATCTTTTTCTCTACATCTTGTTCAAAGAGTAGCAAAAAACAACA  
ATCAATACAATAAAATAATGTCCGGTAGAGGTAAAGGTGGTAAAGGTCTAGGAAAAGGTGGTGCCAAGC  
GTCACAGAAAGATTCTAAGAGATAACATTCAAGGTATCACTAAGCCAGCTATCAGAAGATTAGCTAGAA  
GAGGTGGTGTCAAGCGTATTTCTGGTTTGATCTACGAAGAAGTCAGAGCCGTCTTGAAATCCTTCTTGG  
AATCCGTCATCAGGGACTCTGTTACTTACACTGAACACGCCAAGAGAAAGACTGTTACTTCTTTGGATG  
TTGTTTATGCTTTGAAGAGACAAGGTAGAACCTTATATGGTTTCGGTGGTTAA

YNL030W, 103 aa (SEQ ID NO 324)

MSGRGKGGKGLGKGGAKRHRKILRDNIQGITKPAIRRLARRGGVKRISGLIYEEVRAVLKSFLESVIRD  
SVTYTEHAKRKTVTSLDVVYALKRQGRPLYGFGG

YOL109W, 842 bp, CDS: 501-842 (SEQ ID NO 343)

GGAGGTCTGCTTCACGAGCGCGGTGTGCGCCTAGTATTGCCCCGACGGTCCGGGTGCCTATCCCTAGAT  
TTCGTGCTGCCCCGACCCAAATAGTTAAACGTGTGGTTTATGGGTGCACCAGGGCTTTATCGTGTTTTA  
TATCGATGGCGATTTGTGCCCTCCAGTGTATTTTTGTATATCCAATTAAGGTTTCTTACCTAATTTTATT  
TTTATCATCTTTAGTTAATGCTGGTTTGCTCTGTTTCTGCTGCTTTCTGTGCGGTTCTCCTCTTCTCTT  
GTTTCTTTCGTGTTGTCCCCATCGCCGATGGGCTTATATGGCGTATATATATAGAGCGAGTTTTTACGT  
CGAAGATCATCTCAGTTTGCTTGATAGCCTTTCTACTTTATTACTTTTCGTTTTTAACCTCATTATACTT  
TAGTTTTCTTTGATCGGTTTTTTTTCTCTGTATACTTAAAGTTCAAATCAAAGAAACATACAAAACCTAC  
GTTTATATCAATTAATAATGTCTGAAATTCAAACAAAGCTGAAACTGCCGCCCAAGATGTCCAACAAA

121/251

AGTTGGAAGAAACCAAAGAATCTTTGCAAAACAAGGGCCAAAGAAGTAAAGGAACAAGCTGAAGCTTCTA  
TCGACAACCTAAAAATGAAGCTACTCCAGAAGCTGAACAGGTGAAGAAGGAAGAACAAAACATTGCTG  
ATGGTGTGCAACAAAAGAAGACCGAAGCTGCCAACAAAGTTGAAGAACTAAGAAGCAAGCTTCCGCCG  
CCGTCAGTGAGAAGAAGGAAACCAAGAAGGAAGGCGGTTTCTTGAAGAAATTGAACCGTAAAATTGCTT  
CCATTTTCAACTAA

YOL109W, 113 aa (SEQ ID NO 344)

MSEIQNKAETAAQDVQKLEETKESLQNKQVEVKEQAEASIDNLKNEATPEAEQVKKEEQNIADGVEQK  
KTEAANKVEETKKQASAAVSEKKETKKEGGFLKKLNRIASIFN

YOR285W, 920 bp, CDS: 501-920 (SEQ ID NO 365)

ACTAGCAAGATGATCGTCAGATATGGTGATTTATTTCCCTGTGCATTGTACTTCAAAGATCATACAGCA  
TACTAAGCGCTTTCCAGGGACACCTTCTGTGCGAAAAATATCAGAATTTTCTTGATTAAACGCAGCATA  
TTGAGTATATGAAATTAACGGGACACTGTGTGAAAAATTTGTAGTTGTACTTTTGTATCCCCTTTG  
GTAGACATATGGACGAATTACTACTAAGATTGGCTTCCATAAGGCCCAAATCCAGATATCACCTACGGT  
ATGTCCTTTTCCCTACTTTGCAATGACAAATAATTTGTATTATCTTGGAACCTATATAAGTTACATCTG  
ATTGCTTTTGTATTTTGGGAGAAATATTATACCGCGGGGAAGGAAGTAAGGGGAGAATTTTGTAG  
GTGTATAAAAGAGAGTGGAGGCTTAATCAATCAAAGAATCTTTCTCGTTTATTTTCAGGGTTTGTGAC  
TAAGAAACGATATTAAAAATGTGGAAGGCCGTGATGAATGCTTGGAATGGAACCGAGAGTCAAAGTAAGA  
ATGTTTCAAATATTCAATCTTACAGTTTGAAGACATGAAAAGAATCGTTGGAAGCATGATCCTAATG  
TGGTTTGGTAGATGTTAGAGAACCATCTGAGTACTCGATTGTTTCATATTCCTGCTTCCATCAATGTGC  
CATATAGATCGCACCCCTGACGCATTTGCCCTTAGATCCTTTAGAATTTGAGAAACAGATTGGCATCCCAA  
AACCTGACAGTGCCAAGGAGCTAATATTTTATGTGCTTCTGGCAAACGCGGGGAGAAGCTCAAAAAG  
TCGCCTCCTCACATGGATATTCAAACACCTCACATATCCTGGCTCTATGAATGATTGGGTTTCTCATG  
GGGTGATAAACTTGACTTATAG

YOR285W, 139 aa (SEQ ID NO 366)

MWKAVMNAWNGTESQSKNVSNIQSYFEDMKRIVGKHDPNVVLVDVREPSEYSIVHIPASINVPYRSH  
DAFALDPLEFEKQIGIPKPSAKELIFYCASGKRGEAQKVASSHGYSNTSLYPGSMNDWVSHGGDKLD  
L

YOR327C, 848 bp, CDS: 501-848 (SEQ ID NO 369)

GTGTATTATTAAATACGAACAAAATAAAAAATATGCCGACCAATTCTGTAGTAGTACTGTACTATATTGAA  
TATTAAGGGTTTTTCTGGTCTTAGCGTATCCCTTTATCAGTCCGTGGAACAAAGCCACGGGCGGCTGTA  
ACAATGACCATGGAATCATTCAGTCGCCCCATAAAGCGCATTCCACGGAGCGTTTTATAGTGATCTTGGTC  
ACATGATATACGCGTGACTTTTTTTTTATTTTTTCTCCCTGTCTTCCGCAAAAGTGGCTCAAAATTCCTT  
CGGATTTTGGCATTATAGCGCAATGGTGCAGCGCAACCAAAACAAACACCAGTTGTGCGACCCAAAAGA  
TGCAAAAGCGGGAGCCAGTTAGTTTTCTTCAAGTTTGGTTGAAACAGCCTTTAATATTTTATAGAA  
AGGTAACTATCTGCTCAGTGAATAGTATCTGTAAGTCAGGCATACATTCGAAACACTTCCAAATACAA  
AATAAGAACGCGCAACGATGTCGTCATCAGTGCCATACGATCCATATGTGCCTCCAGAGGAGAGTAACT  
CAGGCGCAAAACCCAAATTCCCAAAACAAGACTGCTGCTTTGAGACAAGAGATTGATGACACGGTGGGAA  
TAATGAGAGATAATATCAACAAGGTTGCTGAACGTGGTGAAAGGCTAACATCCATTGAGGACAAAGCTG  
ATAACTTGGCTATCTCCGCACAAGGATTCAGAGAGGCGCCAACAGGGTCAGAAAGCAAATGTGGTGGGA  
AAGATCTAAAAATGAGAATGTGTTTATCTTAGTTGTTATTATTTTACTAGTGGTAATTATCGTTCCCTA  
TCGTGCTCCATTTTCAGCTAA

YOR327C, 115 aa (SEQ ID NO 370)

MSSSVPYDPYVPPEESNSGANPN SQNKTAALRQEIDDTVGIMRDNINKVAERGERLTSIEDKADNLAI  
S  
AQGFKRGANRVRKQMWKDLKMRMCLFLVVIILLVVIIVPIVVHFS

YPL037C, 974 bp, CDS: 501-974 (SEQ ID NO 377)

TCACGGCTGCTCTTCCCTCTTTTTTCGCATATTCTATTTTATCATCGACTTCCCTAATTTCGCACTCGTACC  
AAAATGTTAAGCAGTATGGCGAAGAACGTGGCGCGCTGGAGTCGTGAATGTTTGGGTCTTGTATGATGG  
ACTACGGTAGTAAGTATGTAGTAGTTGCAACTTCATATGTTCACTTCTGATCCAAGGAAGAGCGGTTAT  
GAATTAATCTCTTGGCATGAGCGGACGGGTAAGGGGACACCGCCTTTCTTCGATGGGAATCAGGGTAA

122/251

TGGTATATGATGGATTATTGTGGAATCATTTAGTACGGCAGATGTTGAAAAAAAAAGCAGAAAATTTTT  
GAATTTTTTTTCGTTGACATTGGAAGATTTCTAGTGGAAACAGCTGCAATTGCTTGTTAAGTAGTAACC  
CCTCCTTTGTGACAAGAGAGCGAATATTCTTTCTAGGGAGGTTAAGAAATAGAATCTCACACCAGAC  
GCGACTCATAATTCATAATGCCAATTGACCAAGAAAAATTAGCTAAGCTACAAAAGTTGTCTGCTAACA  
ACAAAGTTGGTGGTACTAGAAGAAAGCTTAACAAGAAGGCAGGCTCTTCTGCCGGTGCCAACAAGGATG  
ACACCAAGTTGCAAAGTCAATTAGCTAAGTTGCACGCTGTCACCAATTGACAACGTCGCCGAAGCCAAC  
TTTTCAAGGACGACGGTAAGGTCATGCACCTCAACAAGGTCGGTGTCCTAAGTTGCTGCTCAACACAACA  
CTTCTGTATTCTACGGTCTACCACAGGAAAAGAACTTGCAAGATTTGTTCCCAGGTATTATCTCTCAAT  
TGGGCCCTGAAGCCATCCAAGCCTTGTCTCAATTGGCTGCCCAATGGAAAAGCACGAAGCCAAGGCTC  
CAGCTGATGCTGAAAAGAAGGATGAAGCTATTCCAGAGTTAGTTGAAGGTCAAACTTTTGATGCTGACG  
TCGAATAA

YPL037C, 157 aa (SEQ ID NO 378)

MPIDQEKLAQLQKLSANNKVGGRRLNKKAGSSAGANKDDTKLQSQLAKLHAVTIDNVAEANFFKDDG  
KVMHFNKVGQVAAQHNTSVFYGLPQEKNLQDLFPGLIISQLGPEAIQALSQLAQMEKHEAKAPADA  
KDEAIPELVEGQTFDADVE

YPL079W, 1404 bp, exon1: 501-511, intron1: 512-932, exon2: 933-1404  
(SEQ ID NO 381)

AAATAGGACGAAGAACTTTTTATATACGAGCATTTCCTAATTAGTAGGAAGCGGAAAATAATAATATAA  
GAAAGTAAACGCAAAAGATAGGCTGACTGCCCTTCAATTCGACTAGGAGGTGAGGCGACATATTTGTCACC  
ATTCAAGTTACCGAGATGGTAGAGAGGTGGATGGCTCGGGTGAGCTTGATTGTACACTGCAGCAACGAT  
GCTTTTTCTACCCATTTTATGAAGTTTAACATCCGTACCTTTCCACCTCCAAACATTTTTTGTAACTTC  
GTCCTTTGAAAAATCAAGAAGTAATAGGTGTGCAGTATAGGGCCGCTTGAGCGCGCAATATCGGTGAGT  
GAGGTAAGATCCATCCATACCTTAGCAAAATATGGTAGTGAGGAGGCCAACTGTATTGCGTTAAAGGCAA  
AAGGATTGGTATATACGAATGATTGGTAATTTGAAAAGTAGGTTTCGAATCAAAGAACTGAGACAGTC  
AAGGACACTAAACAAAAATGGGTAAATCGTATGTCCATATAACTTCAAAATGAAAATATAGCAGTTGAA  
ACATATCAATTAATTCATTATACATCTCCAATAAACATGTATGCAAGAGGAAAGCGTAAATATCTTCGA  
TTTCGACAATACTTTGTCTACTGAACTAAAAATGAAAATGAAGTTGAATTTCTCAAAGGAATGTGATGCAA  
GTTTCGTTAATTAATATGGTTTGTAGTGGAATTATCATAGTTTGTGATAGATACACACGAGGAGTAGTGA  
GCAAAGCAAGTGCAACAGCAATGATATGTTAGCAGGAAATAATATTATAAATTGGATATTGTGTGTTTT  
TTTGATATATGTTTGTGCGAAGCTAATACAGAATGATTACTAACTGGAATTTAAAGCACAAATCATGCTC  
TTGGATGATTGATCTATTAAAAAATTATAAACAGACATGGTTACAGATCTCGTACACGTTACATGTTTC  
CAACGTGACTTCAGAAAGCATGGTGCCGTTCCACATGTCCACCTACCTGAAGATCTTACAAGGTTGGTAC  
ATTGTGCGACATCAAAGCCAAATGGTTCTATCCAAAAGGGTATGCCACACAAGTTCTACCAAGGTAAGACC  
GGTGTGCTCTACAACGTTACCAAGTCTTCTGTTGGTGTATCATCAACAAGATGGTCGGTAACAGATAC  
TTGGAAGAGAGATTGAACTTGAGAGTTGAACACATCAAGCACTCTAAATGTAGACAAGAATTTTTTGAA  
AGAGTTAAGGCCAATGCTGCTAAGCGTGCTGAAGCCAAGGCCCAAGGTGTGCTGTCCAATTGAAGAGA  
CAACCAGCTCAACCAAGAGAATCCCGTATTGTCTCTACTGAAGGTAACGTTCCCTCAAACCTTTAGCTCCA  
GTTCCATACGAAACCTTCATTTAA

YPL079W, 161 aa (SEQ ID NO 382)

MGKSHGYRSRTRYMFQRDFRKHGAVHMSYLYKIKYKVGDIVDIKANGSIQKGMPhKFYQGKTGVVYNVTK  
SSVGVIIINKMVGNRYLEKRLNLRVEHIKHSKRQEFLEVRKANAAKRAEAKFAQGVAVQLKRQPAQPRE  
SRIVSTEGNVPTLAPVPYETFI

YBL109W 836bp CDS: 501 836 (SEQ ID NO 35)

CATCGCTTGATTTCGGCCTGCAAAAATAAAGTAGTCGGTACGTACTTTTCGTTTTCAATTTCCATGGTG  
CACAGTATCTTAACTATCTGCTTAGTCGAGGAGAACCAAGGATTCTGTTTCGTTGCTCAGCCGCTTCGTGG  
ATATTCTCTTGGATACCTTAAACATGGACCTACGTTCCGCTCTCGAAAAGACCAATATAATAAAAAGTT  
ATAAATTACATTTCCCTTATTAGGTATACGACCTCGCGCTTCGAAGTAGAGGAGCCCTTTTTGGCGTACC  
TACATATGGCGCGTCAGACAGACAACTTCCCCCAAAAATGTATTACCCCGCCGAATAAGAAAACAGAC  
CCATTCAACCCACGACGTATCAAGTTACTTCCCTTGGTGCAATGTCCCACTATAAAAAAATTCCTTGACGC  
TAGATCGTTGGACTAAAATCTGCGTCACAATCGCCTAAACAGGAAATATTGCCATTTTTCGTACAAGGT  
TACTTCTTAGATGCTATATGTCCCTACGGCCTTGTCTAACACCATCCAGCATGCAATACAGTGACATAT  
ATATATACCTTAACACTACCTTAACCTTACCTTATTTCAACCTTCCAACCTGTCTCTCAACTTACCT  
CACATTACCTTACCTCTCCACTTGTACCCTGTCCCATTCACCATACCTCCCAACCACCATCCATC

123/251

CCTCTACTTACTACCACCAATCAACCGTCCACCATAACCGTTACCCTCCAATTAGCCATATTCAACTTC  
ACTACCACCTTACCCTGCCATTACTCTACCATCCACCATCTGCTACTCACCATACTGTTGTTCTACCCCTC  
CATATTGA

YBL109W 111aa (SEQ ID NO 36)

MSLRPCLTPSSMQYSIDIYPNTTLLPYFNPSNLSLNLPSHYPTSPLVTLSSHSTIPLPTTIHPSTYYH  
QSTVHNNRYPPISHIQLHYHLPCHYSTIHHLLLTILFYPPY

YHR094C 2213bp CDS: 501..2213 (SEQ ID NO 205)

GCATTGAGTCAAAAGTTTTTCCGAAGTGACCCAGTGCTCTTTTTTTTTTCCGTGAAGGACTGACAAAT  
ATGCGCACAAAGATCCAATACGTAATGGAAATTCGGAAAACTAGGAAGAAATGCTGCAGGGCATTGCCG  
TGCCGATCTTTTGTCTTTTCAGATATATGAGAAAAAGAATATTTCATCAAGTGCTGATAGAAGAATACCAC  
TCATATGACGTGGGCAGAGACAGCAACGTAAACATGAGCTGCTGCGACATTTGATGGCTTTTATCCG  
ACAAGCCAGGAACTCCACCATTATCTAATGTAGCAAAATATTTCTTAACACCCGAAGTTGCGTGTCCC  
CCTCACGTTTTTAATCATTTGAATTAGTATATTGAAATTATATATAAAGGCAACAATGTCCCCATAATC  
AATTCCATCTGGGGTCTCATGTTCTTTCCCCACCTTAAATCTATAAAGATATCATAATCGTCAACTAG  
TTGATATACGTAAATCATGAATTCAACTCCCGATCTAATATCTCCTCAGAAATCCAATTCATCCAAC  
CATATGAATTGGAATCTGGTCTGTTCAAAGGCCATGAATACTCCAGAAGGTAAAAATGAAAGTTTTACG  
ACAACCTTAAGTGAAAGTCAAGTGCAACCCCGCTTGCCCTCCAAACACCCGAAAAAGGTGCTACGTAA  
CGGTTTTCTATCTGTTGTGTTATGGTTGCTTTCCGGTGGTTTCATATTTGGATGGGATACTGGTACCATT  
CTGGTTTTGTGCTCAAACCTGATTTTCTAAGAAGATTTGGTATGAAGCACCACGACGGTAGTCATTACT  
TGTCCAAGGTGAGAACTGGTTTAATTGTCTCTATTTTAAACATTGGTTGTGCCATTGGTGGTATCGTCT  
TAGCCAAGCTAGGTGATATGTATGGTCGTAGAATCGGTTTGATTGTGCTGTTGTAGTAATCTACACTATCG  
GTATCATTATTCAAATAGCCTCGATCAACAAGTGGTACCAATATTTTCATTGGTAGAATTATCTCTGGTT  
TAGGTGTCCGGTGGTATCACAGTTTTATCTCCCATGCTAATATCTGAGGTGCGCCCCAGTGAAATGAGAG  
GCACCTTGGTTTTCATGTTACCAAGTCATGATTACTTTAGGTATTTTCTTAGGTACTGTACCAATTTTG  
GTACCAAGAATTACTCAAACCTCTGTCCAATGGAGAGTTCCATTAGGTTTGTGTTTTCGCTGGGCCTTAT  
TTATGATTGGTGGTATGATGTTTGTTCCTGAATCTCCACGTTATTTGGTTGAAGCTGGCAGAATCGACG  
AAGCCAGGGCTTCTTTAGCTAAAGTTAAACAAATGCCACCTGACCATCCATACATTCAATATGAGTTGG  
AAACTATCGAAGCCAGTGTGGAAGAAATGAGAGCCGCTGGTACTGCATCTTGGGGCGAATTATTCAGT  
GTAAACCAGCCATGTTTCAACGTACTATGATGGGTATCATGATTCAATCTCTACAACAATTAACCTGGTG  
ATAACTATTTCTTCTACTACGGTACCATTGTTTTCCAGGCTGTGCGTTTAAGTGACTCTTTTGAAACTT  
CTATTGTCTTTGGTGTGCTCAACTTCTTCTCCACTTGTTGTTCTCTGTACACCGTTGACCGTTTTGGCC  
GTCGTAACGTGTTGATGTGGGGTGCTGTGCGGTATGGTCTGCTGTTATGTTGTCTATGCCTCTGTTGGTG  
TTACCAGATTATGGCCAAACGGTCAAGATCAACCATCTTCAAAGGGTGCTGGTAACTGTATGATTGTTT  
TCGCATGTTTCTACATTTTCTGTTTTCGCTACTACCTGGGCCCCAATTGCTTACGTTGTTATTTTCAAGT  
GTTTTCCATTAAAGAGTCAAATCCAAGTGTATGTCTATTGCCAGTGCTGCTAAGTGGATCTGGGGTTCT  
TGATTAGTTTTCTTACCCCATTTATTACTGGTGCCATCAACTTCTACTACGGTTACGTTTACGTTGGCT  
GTATGGTTTTTCGCTTACTTTTACGTCTTTTTCTTTCGTTCCAGAACTAAAGGTTTATCATTAGAAGAAG  
TTAATGATATGTACGCCGAAGGTGTTCTACCATGGAAATCAGCTTCTGGGTTCAGTATCCAAGAGAG  
GCGCTGACTACAACGCTGATGACCTAATGCATGATGACCAACCATTTTACAAGAGTTTGTTTAGCAGGA  
AATAA

YHR094C 570aa (SEQ ID NO 206)

MNSTPDLISPKSNSNSYELESGRSKAMNTPEGKNESFHDNLSESQVQPAVAPPNTGKGVYVTVSICC  
VMVAFGGFIFGWDGTISGFVAQTDFLRRFGMKHHDGSHYLSKVRTGLIVSIFNIGCAIGGIVLAKLGD  
MYGRRIGLIVVVVIYTIIGIIIIQIASINKWYQYFIGRIISGLGVGGITVLSPLMISEVAPSEMRGTLVSC  
YQVMITLGIPLGYCTNFGTKNYSNSVQWRVPLGLCFAWALFMIGGMMFVPESPRYLVEAGRIDEARASL  
AKVNKCPDPHPYIQYELETIEASVEEMRAAGTASWGELFTGKPMFQRTMMGIMIQLQLTGDNYFFY  
YGTIVFQAVGLSDSFETSIVFGVWNFFSTCCSLYTVDRFGRNCLMWGAVGMVCCYVVYASVGVTRLWP  
NGDQPSKSGAGNCMIVFACFYIFCFATTWAPIAYVVISECFPLRVKSKCMSIASAANWIWGFLISFFT  
PFITGAINFYGYVFMGCMVFAYFYVFFVFPETKGLSLEEVNDMYAEGVLPWKSASWVPVSKRGADYNA  
DDLMDHDDQPFYKSLFSRK

YBL099W 2138bp CDS: 501..2138 public: 1..2138 (SEQ ID NO 693)

CCCCGGGTGATGCAGTTGCGGCCGGCCCTGGCCAATCAGATCCCTTTAAAAATGGGCCCGGTGCGCTTCT  
ACCCCTTCACGCCTTTTACGCCTTTTTCGAATCTTGTATTTATTGTAATTATTAAACATTGGTCATATC  
AAATTACATCAGACTTCAATTTTTCAATTCACTTTCTGAATAAGAGCCCTTCCCTTCATACAAGTAGA  
GATATTATACTGTATAGCTCTTTCAATTGGTCTTATTAGATTGTCTCCATCTTTCCCATTTGACGTTGT  
TACTCCCTCTCTTTTTTCGTTTTTAACTGATTTCTCATATATTCCCAAACAGGCATATATACTCGACGT  
CAAGAAAGAAAAGAAAAGAAAACCCCTCATAAAAAATATAATCGAGAAGTTTTTTTCTCATCGCGAACC



124/251

ATTAGTATAACAGATTGATCGTTTCAGCTCTCATAACTATCGCAAGAACAGTAACAAAATAAATAAAAAA  
AACACGCACATATAATAATGTTGGCTCGTACTGCTGCTATTTCGTTCTCTATCGAGAAGCTCTAATTAAGT  
CTACCAAGGCCGCAAGACCTGCCGCTGCTGCTTTGGCTTCCACCAGAAGATTGGCTTCCACCAAGGCAC  
AACCCACAGAAGTTTCTCCATCTTAGAGGAAAGAATTAAGGGTGTGTCCGACGAGGCCAATTTGAACG  
AAACTGGTAGAGTTCTTGCAGTCGGTGATGGTATTGCTCGTGTGTTTTGGTTTGAACAACATTTCAGGCTG  
AAGAATTGGTCGAGTTCTCCTCTGGTGTAAAGGTATGGCTTTGAACTTGGAGCCTGGTCAAGTCGGTA  
TCGTTCTTTTTCGGTTCCGATAGACTGGTTAAAGAAGGTGAATTGGTCAAGAGAACCAGTAATATTGTTG  
ATGTCCCAGTCGGTCCAGGCCTTTTGGGTAGAGTTGTCGACGCTTTAGGTAACCCATTGATGGTAAAG  
GTCCTATTGACGCTGCCGGTTCGTTCAAGAGCTCAAGTCAAAGCACCAGGTATTTTGCCAAGAAGATCTG  
TCCATGAACCAGTTCAAACCGGTTTGAAGCCGTTGACGCCTTGGTCCCTATCGGTAGAGGTCAAAGAG  
AGTTGATTATTGGTGATCGTCAAACAGGTAAGACTGCTGTGCGCTTAGACACCATCTTGAATCAAAAGA  
GATGGAATAACGGTAGTGACGAATCCAAGAACTTTACTGTGTTTACGTTGCCGTTGGACAAAAAGAT  
CTACCGTTGCTCAATTGGTCCAACTTTTGAACAACATGACGCCATGAAGTACTCTATTATTGTTGCAG  
CTACTGCATCTGAAGCCGCTCCTCTACAATACTTGGCTCCATTACTTGCCGCATCCATTGGTGAATGGT  
TCAGAGATAATGGAAGCACGCTTTGATCGTCTATGACGATTTGTCCAAGCAAGCCGTGGCATAACCGTC  
AATTATCTTTGTTGTTGAGACGTCCTCCTGGTCGTGAAGCCTACCCTGGTGATGTCTTTTACTTGCATC  
CAAGATTGCTAGAAAGAGCCGCTAAGCTTTCTGAAAAGGAAGGTTCTGGTTCTTTAACTGCTTTGCCTG  
TTATTGAAACCCAAGGTGGTGATGTCTCCGCTTATATCCAACCAATGTTATTTCCATTACCGTAGGTC  
AAATATTCTTTGGAAGCTGAATTATTTCTACAAGGTTATCAGACCTGCCATTAACGTTGGTTTGTCCGTTT  
CTCGTGTGCGTTCCGCTGCTCAAGTTAAGGCTTTTGAAGCAAGTCGCTGGTTCTTGAATATTGTTTTTGG  
CTCAATACAGAGAAGTCGCTGCTTTTGTCTCAATTCCGTTCCGATTTAGATGCCTCCACCAAGCAAACCTT  
TGGTTAGAGGTGAAAGATTGACTCAATTGTTGAAGCAAAACCAATATTTCTCTTTGGCTACAGAAGAAC  
AGGTTCCATTGATTTATGCCGGTGTAAATGGTCATTTGGATGGTATTGAACTATCAAGAATTGGTGAAT  
TTGAGTCTCTCTTTTGTCTATCTAAAATCCAATCACAATGAGCTTTTGACCGAAATTAGAGAAAAGG  
GTGAATTGTCTAAAGAATTGTTGGCATCTCTAAAGAGTGCTACTGAATCATTTGTTGCCACTTTTTAA

YBL099W 545aa public: 1..545 (SEQ ID NO 694)

MLARTAAIRSLRSLINSTKAARPAALASTRRLASTKAQPTVSSILEERIKGVSDKANLNETGRVL  
AVGDGIARVFLNLIQAEELVEFSSGVKGMALNLEPGQVGVIVLFGSDRLVKEGELVKRTGNIVDVPVGP  
GLLGRVVDALGNPIDGKGPIDAAGRSRAQVKAPGILPRRSVHEPVQTGLKAVDALVPIGRQORELIIGD  
RQTGKTAVALDITLQKRWNNGSDESKLYCVYVAVGQKRSTVAQLVQTLQHDAMKYSIIIVAATASEA  
APLQYLAPFTAASIGEFWRDNGKHALIVYDDLQKQAVAYRQLSLLRRPPGREAYPGDVFLYHPRLLER  
AAKLSEKEGSGSLTALPVIETQGGDVSAIYPTNVISITDGGIFLEAEFYKGIKIRPAINVGLSVSRVGS  
AQVKALKQVAGSLKFLAQYREVAFAQFGSDLDASTKQTLVRGERLTQLLKQNYSPATEEQVPLIY  
AGVNGHLDGIELSRIGEFESSFLSYLKSNNHLLTEIREKGELSKELLASLKSATESFVATF

YDR504C 884bp CDS: 501..884 public: 1..884 (SEQ ID NO 695)

TAAAAGCCTTGCATATTGCTCAGAGTAAATTACAAGCGTTAAATGATAATTCAAATCTCAAATACAA  
ATGACAGTTCTTCCAATAATTTTACGAATGCTGCAACTTATTCAAAGCCTAAATGAATATCAAGATTT  
TAAACGCAGAATTCCAATTTGATAGAAAGGAATTAACGTTTACTACGTTTGTGAGGAGAGAAATGATT  
TTAGAGACTTGATAAAAGAGCTGTTCAAATATTACAAGACAAGAATTTGGTTGTGTGCCATCCCGAATA  
ATCTGTCTATTGATTCTAAGTATTATGATAAACAACAAAAGAGCTGAAATTATATCAAACATAGTAA  
AAAATTACAATGCTGAAGATTTAATGAATGTCAATGAGTTTTTCGCAGAACAGGGGGAATAACAGAGTTA  
ATTTTGCACCTCCGTTGAACGAAATGAACGACAACTTTTCAAGATTGCTGTGTATGAAGAATTAGTTC  
ACGAATTATTTTCAATTAATGATCTGTTATTTCTTGTGTAACATATAAATTTTCTAAAAGAAAAGACAA  
CCATTGGCCATTATTTTGTAAACATTTTTTCAATGTTTTTGTGTTTTGTTTTGTTTTGTTTTGTTTTA  
TTTTTGTCTACTTTTTTTTATGTTATTTTGTGTTTTATCGTTTCTGTTTCGTTGTTTACCTATTTTCTGCCA  
ATTCAATTTGGTACTATCTTTCTATTATCAATATTTCTTTCCCTTATGTTTTTTTCTATATGAAAAC  
TCACAGGGAGAAATAGAAGAAATGTTTATTCTGTTTAACTTTGATAAAAATTACTTATACGTCTC  
CCAATCATGGTTTCATGGTCACTGGTAAGGAAAAATTCGAAAAACTACGGGACTAA

YDR504C 127aa public: 1..127 (SEQ ID NO 696)

MICYFLVVTINFLKEKTTICHYFVNIFSLFLFVVFVIFVFFYVILFYRCSLFTYFPANSIWY  
LSIINIFFPLCFFLYENFTGRNRRKCSLFLCLTIKITYTSPNHGFMVTGKEKFEKL RD

125/251

YEL032W 3416bp CDS: 501..3416 public: 1..3416 (SEQ ID NO 697)  
TATCTACCGGCTGCAAGCAGCCGGTTCGGTGGCAAATCCGGCGCTTCCCCCTCAAAAAAAAAAAAAAAAAA  
AAAAAAAAAGGGAACCTCAGAACGGGGGAGGTTGAAGAGCAGGCCAAGGGAAATATTAGTTTTGACCTA  
TGTGGGAAACAGAATTTCAATGAGTTATGGCAACTTGGCCGAGTGGTTAAGGCGAAAGATTAGAAATC  
TTTTGGGCTTTGCCCCGCGCAGGTTTCGAGTCTGTCAGTTGTCGTTATTTTTCTCTTTTTTTTCAATTTCC  
CTTGTTCGTCAGATCGAGGCGGTAGAAGAAACAATTACTTTTCCCTAAATGGGTAAAACTCGTGTTTTA  
GGAAAAAAAAAGAAAAATTTGGTCAAACTCGAAAGATAGGTTCTTAATCTTCTTTCAAGTTGAAAAGGC  
CTACGCTCTTTTTCCCTTGAAGCATTTTTCATCCTACTGCTCGTATTGAACCTCCACTATAAGCGCACCAAAA  
AGATACAAACGTCAATTATGGAAGGCTCAACGGGATTTGATGGAGACGCTACTACTTTTTTTCGCTCCAG  
ACGCTGTGTTTTGGTGACAGAGTGGCGAGATTTCAAGAGTTTTTAGATACTTTTCACCTCATACAGAGACT  
CTGTAAGGTCCATACAAGTTTACAACAGCAATAACGCGGCCAACTACAACGATGATCAAGATGACGCAG  
ACGAACGAGATTTGCTAGGTGATGACGACGGTGATGATCTTGAAGGAAAAAGAAAGCAGCATCGTCCA  
CCTCATTGAATATACCTCCCTCACAGGATTATCATCTCGCTTGATGACTTGAGAGAATTCGACAGGTCGT  
TCTGGTCGGGCATTTTAGTCGAACCAGCATACTTCATCCCGCCTGCCGAAAAGGCGCTTACTGACCTAG  
CAGATTCATGGACGATGTTCCACATCCCAATGCCCTGTCAGTATCGTCTCGCCATCCTTGGAAGCTTT  
CGTTCAAAGGCTCATTTGGTGCACACGCATTGTCCTCGTACTCTAACGGCACAACATTTAAACAAAC  
TGGTCTCTGTTGAGGGTATCGTAACCTAAGACTTCGTTGGTCAGGCCAAAGCTTATCAGATCTGTCCACT  
ACGCGGCAAAGACTGGTAGATTCCATTACAGAGATTATACAGATGCTACTACAACCTCACCACCCGCA  
TCCCAACGCCTGCCATCTATCCAACGGAGGACACTGAAGGTAACAACTAACACCAGGAATGGGTATA  
GTACGTTTCATAGACCATCAGCGTATCACTGTGCAAGAAATGCCCGAAATGGCCCCCGCTGGCCAACTTC  
CCAGGTCCATTGACGTCATTTCTCGATGACGACCTTGTGGACAAGACCAAGCCAGGTGACAGAGTTAACG  
TTGTGCGGGTATTCAAGTCGCTTGGTGTGTTGGTCATGAACCAAGTCCAACCTTAATACATTGATCGGGT  
TCAAACTCTGATCCTAGGTAATACGGTGTATCCTCTCCACGCCAGATCCACGGGTGTCGCTGCGAGAC  
AAATGTTGACAGATTTTCGATATAAGAAATATCAATAAACTATCCAAAAAAGGACATTTTCGATATCT  
TGTCTCAATCTTTAGCGCCTTCTATTTATGGACATGACCATATAAAGAAAGCCATTTTATTGATGCTCA  
TGGGAGGTGTGGAGAAAAATTTAGAAAATGGCTCGCATTTAAGAGGTGACATCAATATCCTAATGGTGG  
GTGATCCATCCACTGCCAAGTCCCAATTGCTAAGGTTTTGTGTTGAATACAGCATCACTGGCAATTGCTA  
CTACTGGTAGAGGTTCTTCCGGTGTGGTTTTGACCGCAGCGGTCACTACTGATAGGGAAACAGGTGAAA  
GAAGACTAGAGGCTGGTGCCATGGTTCTTGCTGACCGCGGGGTTGTATGTATTGATGAATTTGATAAGA  
TGACAGATGTGGATAGAGTCGCCATTTCATGAAGTAATGGAACAACAACCGGTGACGATTGCCAAAGCAG  
GTATTCACACAACATTAATGCTCGTTGTAGTGTTATTGCTGCCGCAAATCCCGTTTTTGGGCAGTACG  
ATGTCAATAGAGATCCACACCAAAACATTGCCCCTACCGGACTCGCTGTTGTCTCGTTTTGATTTACTAT  
TTGTTGTGACAGACGATATCAATGAAATCAGAGATAGATCCATTAGTGAGCATGTCTTAAGAACACACA  
GATATTTGCCTCCAGGTTATTTAGAGGGTGAACCTGTGAGAGAGCGTTTGAATTTATCATTAGCCGTTG  
GGGAGGATGACAGATATAAATCCGTAAGAGCATTTCAACTCCGGGGCTGGTGTAGAAAATGAAGGAGAAG  
ATGATGAAGACCATGTCTTTCGAAAAGTTCAACCCCTTATTACAAGCAGGTGCTAAGTTAGCAAAAAACA  
AAGGTAACATAACGGTACAGAAATTCCAAAGCTAGTCACCATCCCATTTCTTAAGAAAGTACGTTCAAT  
ATGCCAAGGAAAGGGTTATTTCCACAGTTAACACAAGAAGCCATCAATGTTATTGTGAAAAATTATACTG  
ATTTAAGAAACGATGATAATACCAAAAAATCGCCCATTACTGCAAGAACTTTGGAGACTTTGATCAGAT  
TAGCCACAGCTCACGCCAAAGTCAGGTTATCCAAACAGTCAACAAGGTGGATGCTAAAGTGGCTGCCA  
ATCTACTAAGGTTTTGCACTATTGGGTGAGGATATCGGCAATGATATCGATGAAGAGGAAAGTGAATACG  
AAGAAGCTTTGTGCAAGAGGTCTCCACAGAAATCACCGAAAAAAGACAAAGAGTCAGACAACCAGCAA  
GCAACTCTGGATCCCCAATCAAATCTACTCCAAGAAGGTCAACGGCATCTTCCGTTAATGCCACGCCAT  
CGTCAGCACGCAGAAATATTACGTTTTCAAGATGACGAACAGAACGCTGGTGAAGACGATAACGATATAA  
TGTCACCGCTTCCCTGCGGATGAGGAAGCTGAATTACAAAGAAGGCTTCAACTGGGGTTGAGAGTGTCTC  
CAAGACGTAGAGAACATCTTCACGCACCTGAGGAAGGTTTCGTGCGGACCTCTTACCGAGGTCCGTACTC  
CAAGATTACCTAACGTATCTTCTGTCAGGTGAGGATGATGAGCAACAACAGTCAGTTATTTCTTTTGACA  
ATGTGGAGCCTGGTACCATTTCTACTGGTAGATTGTCTTTAATCTCAGGTATTATTGCGCGTCTGATGC  
AAACAGAAATATTTGAAGAAGAAATCCTATCCTGTGGCCTCTTTGTTCGAAAGAATCAACGAAGAATACT  
CGGAGGAGGAAAAATTTCCGCTCAAGAATATTTAGCAGGTTTGAAGATCATGTGCGACAGAAATAACT  
TAATGCTTGCTGACGATAAAGTTTGGAGAGTCTGA

YEL032W 971aa public: 1..971 (SEQ ID NO 698)  
MEGSTGFDGDATTFPDAVFGDVRVRFQEFLLDTFTSYRDSVRSIQVYNSNNAANYNDQDDADERDLL  
GDDDGDDLEKEKKAASSTSLNLPRIIISLDDLREFDRSFWGILVEPAYFIIPPAEKALTDLADSMDD  
VPHPNASAVSSRHPWKL SFKGSFGAHLSPRTLTAQHLNKLVSVEGIVTKTSLVRPKLIRSVHYAAKTG

126/251

RFHYRDYTDATTTLTTRIPTPAIYPTEDTEGNKLTTEYGYSTFIDHQRTVQEMPEMAPAGQLPRSIDV  
ILDDDLVDKTKPGDRVNVGVFKSLGAGGMNQSNSNTLIGFKTLILGNTVYPLHARSTGVAARQMLTDF  
DIRNINKLSKKKIDIFDILSQLAPSIYGHDKKAILLMLMGGVEKNLENGSHLRGDINILMVGDPSTA  
KSQLLRFVLNTASLAIATTGRGSSGVGLTAAVTTDRETGERRLEAGAMVLADRGVVCIDEFDKMTDVDR  
VAIHEVMEQQTVTIAKAGIHTTLNARCSVIAAANPVFGQYDVNRDPHQNIALPDSLLSRFDLLFVVTDD  
INEIRDRSISEHVLRLTHRYLPPGYLEGEVVRERLNLSLAVGEDADINPEEHSNSGAGVENEGEDDEDHV  
FEKFNPLLQAGAKLAKNKGNYNGTEIPKLVITIPFLRKYVQYAKERVIPQLTQEAINVIVKNYTDLRNDD  
NTKKSPITARTLETLIRLATAHAKVRLSKTVNKVDAKVAANLLRFALLGEDIGNDIEEESYEALSK  
RSPQKSPKKRQVRVQPASNSGSPKSTPRRSTASSVNATPSSARRILRFQDDEQNAGEDDNDIMSPSPA  
DEEAELQRRLLQLGLRVSPRRREHLHAPEEGSSGPLTEVGTPLPNSVSSAGQDDEQQQSVISFDNVEPGT  
ISTGRLSLISGIIARLMQTEIFEESYPVASLFRINEELPEEEKFSAQEYLAGLKIMSDRNNLMVADD  
KVWRV

YGR146C 1136bp CDS: 501..1136 public: 1..1136 (SEQ ID NO 699)  
CTTTCAGTTGGGCATCTTTTTTTTTCACAATTAGGCCGCCCTTTTTTCCCAAATTGGCACTTGTTTGTA  
CGATCTTTAGCTAGAACTTGGAGACCTGAAACGTGGTGATTCTTATATTTAAAGGAATACCGATCTTTT  
CCGTTTTCAACACCCCAATTGTGAGAATTTTATTCTTGCAATTCGGAAAATTTAGATACATTCACATCC  
ATACTTGGACACATATATATACAATATAATCATTTGACACAGGCCATCGCCATTGAGTAAACTGTCTT  
TGAAGTGTCTAAAGAACTTAGAACTATAGTGTTGTCCCAAGAAGTTAAAAATTGAACACTTGTGAGAAT  
TATAAAACAGAGTAAGCAAAGAAAGAATAGAGAAACAATACTCCGCTACCGATTCTCCTTTTTTTCCTT  
ATAAAAAAAGCTCGAGAATAATTACTTTATTCTTATCCCTCCACTCCTTTCAGGTATTCTTTACCGATT  
TGCATATCAATCATATAATGAGCACCGCATTCAACGATTACTGCACTGTTTGTGATCGTCTCATTCCAA  
CATCTCCACAGAAAACGAACATTAATACCAGGAAGATCCAAAGGGACAATGAAACCAAGAGCAGTTTAC  
AATCAAATAAGTTATATTGCTCCGAAGATTGTAAGCTGAAGGATTGCAACCCTCTTAATGAGAAATTAT  
TATCCCACTTGCATAAAAAATCAAAAACCTTCTCATTGCGATAATCTCACTCCACCGCTTTCATATTCTA  
AAAATTTAACTGCATCAAACCTCTTCGAGCCGACTACCTCACTATCTTCATCTCCGACATCTTCAACTA  
TCCCCTTTGACGAGTTGGAGAAGCTAGAGTCCTTATTAATTTACCATTGCTGCTACCTCAGGATGGTA  
TAGTCAATCCTAAGCAGGAGTCTAATCCTTCTCGTGTTGACGAATATGATGAAAATGAACATTATTTGA  
ACTTAGCCGACTCTCTTAGACTCGATTCTAGTTACCAATTGCATTCAAAGGCACATTTGGGTTACGAAA  
ACAACCTGCCACGATCAAACGATCTAATTGATGATCATTGATCTCAGATCAGATCATTGAGAATAACT  
ACAACCTATGGTTTAGACTATCCTCCAGTTAA

YGR146C 211aa public: 1..211 (SEQ ID NO 700)  
MSTAFNDYCTVCDRLIPTSPQKTNINTRKIQRDNETKSSLQSNKLYCEDCKLKDSNPLNEKLLSHLHK  
KSKTSHSHNLTPPLSYSKNLTASNLFEPSTSLSSPTSSTIPFDELEKLESLLISPLLLPQDGI VNPQK  
ESNPSRVDEYDENEHYLNLADSLRLDSSYQLHKAHLGYENNLPRSNLDIDHLLISDQIIENNYNLWFR  
LSSS

YHR135C 2117bp CDS: 501..2117 public: 1..2117 (SEQ ID NO 701)  
AGAGTATAACGAGTACATTAATGAGAAAGATTCAAGTAGAGCGCAGCGTCAAAACGCTGCCGCCGTTTT  
AAGCAAGCTCGCCCATGACTTTTGGGAGAACGACTGTGTCAATTGACGAAGACATATTCGAAGATTGCTC  
TGACGAAGAACAATCATGATTGCATCTCTTAATCGTTACACATACATACCTTCTACCTCTGTACTGTTA  
CATATGCATTGACTTTACGATCTAATATAAATCCTTTTTGATGTTACCCCGCCTGTGGGCTCGTTCTCCT  
TTCGTTTCTTACGATTTTTTCGCCGGAACAAGAAAAACAGAACAAAACAAATCAGCGATCGTATACAT  
GGGTCTTTGATTTCTGCTTGCTTCTTACAAACAACAAACGCAAACCGTTTCAATTGAGTGCTCTGTGACTG  
GTTTTCATGTGGATGCCATAGTAGAGAAAAGACACATACAAAATTTTCGCGCATTGCTGGCCCTTTTC  
CTGCTCTCCTCTTCCCCATGTCCATGCCATAGCAAGTACCACTCTAGCAGTTAACAACCTCACCAATA  
TAAACGGAAGCAAAATTTTAACGTACAAGCAAACAACAACTCCACCACCAGGCTGTGCACTCGCCCG  
CAAGATCTTCGATGACCGCCACGACCGCCGCCAACTCCAACAGCAACTCTTCAGAGATGACTCTACTA  
TTGTGCGCCTACATTACAAGATCGGCAAAAAATAGGGGAAGGTTCTTTGGTGTGCTATTTGAAGGTA  
CTAATATGATCAATGGCGTACCCGTCGCGATCAAATTCGAGCCAGAAAAACGGAGGCCCTCAATTAA  
GAGATGAATATAAAACATATAAAATCTGAATGGCACTCCCAATATCCCCTACGCGTACTACTTCGGCC  
AAGAAGGTTTGCACAATATCTTGGTCATTGATCTTTTGGGTCCCTCTTTGGAAGATTTATTTGATTGGT  
GTGGAAGAAAATTTCTGTCAAACCGTTGTGCAAGTTGCTGTCCAAATGATTACTTTGATTGAAGACT  
TGCACGCACATGACTTGATATACCGTGATATCAAACCAGACAATTTCTTGATTGGAAGGCCCGGCCAAC  
CTGACGCAAACAACATCCATTTGATCGACTTCGGTATGGCCAAACAGTATCGTGATCCGAAAACATAAC

127/251

AGCACATCCCATATAGAGAGAAAAAATCACTCAGCGGCACTGCCAGATATATGTCCATTAATACTCACC  
TTGGAAGAGAGCAGTCCAGAAGAGATGATATGGAGGCCTTGGGTCACGTTTTCTTTTATTTCTTGAGAG  
GCCACTTACCCTGGCAGGGTTTAAAGCTCCAAACAATAAGCAAAAATACGAAAAGATTGGTGAAAAGA  
AAAGATCTACTAACGTTTACGATCTAGCTCAAGGCTTACCTGTGCAATTTGGCAGGTATCTAGAAATCG  
TCAGAAGTCTTTCTTTGAAGAGTGTCCCGATTATGAAGGCTATAGAAAATATTACTATCTGTACTGG  
ATGATTTAGGTGAAACCGCGGACGGCCAATATGATTGGATGAACTGAACGATGGCCGTGGTTGGGATC  
TTAACATAAAACAAGAAGCCAAATCTCCACGGATACGGCCATCCAAATCCACCAAACGAAAAATCGAGAA  
AACATAGAAAACAAACAGCTCCAAATGCAACAGCTCCAAATGCAACAGCTCCAACAACAGCAACAGCAAC  
AGCAATATGCTCAAAAAAAGTGGAGCAGATATGCGCAATTCTCAATATAAAACAAAGTTAGACCCTACTT  
CTTATGAAGCTTACCAGCATCAAACCCAGCAGAAATACCTGCAAGAACAACAAAAGAGACAGCAGCAAC  
AAAAACTTCAGGAGCAACAACCTTCAAGAGCAACAATTGCAACAGCAGCAACAGCAACAGCAACAGCTAC  
GTGCAACAGGCCAACCTCCATCTCAGCCTCAAGCGCAAACTCAATCTCAGCAGTTTGGCGCTCGTTATC  
AACCACAACAACAACCTTCTGCTGCTTTAAGAACTCCTGAACAGCACCCAAATGACGATAATTCAAGTC  
TAGCTGCTTCTCATAAGGGCTTTTTCCAAAAATTAGGTTGTTGCTAA

YHR135C 538aa pulic: 1..538 (SEQ ID NO 702)

MSMPIASTTLAVNNLTNINGNANFNVQANKQLHHQAVDSPARSMTATTAANSNSNSSRDDSTIVGLHY  
KIGKKIGEGSFGVLFEFTNMINGVPVAIKFEPRKTEAPQLRDEYKTYKILNGTPNIPYAYYFGQEGHLHN  
ILVIDLLGPSLEDLFDWCGRKFSVKTVVQVAVQMITLIEDLHAHDLIYRDIKPDNFIIGRPQPDANNI  
HLIDFGMAKQYRDPKTKQHIPYREKKSLSGTARYMSINTHLGREQSRRDDMEALGHVFFYFLRGHLPWQ  
GLKAPNNKQKYEKIGEKKRSTNVYDLAQGLPVQFGRYLEIVRSLSFEECPDYEGYRKLLLSVLDLGET  
ADGQYDWMKLNDRGWDNLNINKPNLHGYPHPNPNNEKSRKRNKQLQMQLQMQQLQMQQLQMQQLQMQQLQ  
TEADMRNSQYKPKLDPTSIEAYQHQTQOKYLQEQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQ  
PSQPQAQTSQQFGARYQPQQQPSAALRTEQHPNDNSSLASHKGFFQKLGCC

YJL060W 1835bp CDS: 501..1835 public: 1..1835 (SEQ ID NO 703)

TAGAGCAGATTGTTTTGAGTAGGATTTAGGAATCAAGACCTCCATCTTTGTGCGATTATTCTCTAAATGT  
AACGTAACCTCGTTTTGATAAGAGAATGTCTAATCGAAGAGAGTTAATAACTTAATAAGCTCTTTAAAAGA  
ACGATGGCATTATCGTCTCCTATGCCAAGATAATTACTGGCTCAAAATTGTTTCAGCGTTCATAAACT  
TTGATATCACTTTCTGGCGCACAAAGCTAACCTTTATGTAGTCTTACGTAGATTCTTTTTAGCAAGTGC  
CTGGTAGTGGTTATTACATAAATGTATCTTTTCATTTGATAACAATTTCTTCAGTAGCATGTCTGTCT  
AGCACGTGACGTAGAACTGTGGCTTTTTTGTGTGTCATTATGACAATCAAGATACCAAATTCAGTCATG  
TTTAAAAGGGGAAGGTACGATAGAGATATATAAAGTGTTCAATTTACTATAATTGCGTATAGAATCC  
ATTGTTACTTGCTCTCAATGAAACAACGATTTCATTGTCATTTACGAACCTAATGTCTACTTCGAGAC  
CGAAAGTTGTTGCCAACAAATATTTCACTTCTAACACTGCCAAAGATGTTTGGTTCGCTAACCAATGAAG  
CCGCTGCAAAAGCTGCCAATAACTCCAAAAACCAAGGCCGTGAACCTTATTAATTTAGGCCAAGGCTTTT  
TTTCATATTCCCCTCCTCAATTCGCCATTAAGGAGGCTCAGAAAGCCCTAGACATTCCAATGGTCAATC  
AATATTCTCCAACCTAGAGGTGACCTTCATTAATTAATTCCTTGATTAAAGTTGTATTCTCCTATTTATA  
ACACAGAATTGAAAGCGGAAAATGTTACCGTAACAACAGGTGCCAATGAAGGTATACTTTCTTGCTTGA  
TGGGGCTTTTGAACGCTGGCGACGAGGTTATTGTTTTTGAACCTTTCTTTGACCAATATATTCCAAATA  
TCGAACCTTTGCGGTGGTAAAGTTGTTTACGTCCCATAAATCCTCCAAAGGAATTGGATCAAAGGAATA  
CTAGAGGTGAAGAATGGACCATTGACCTTTGAGCAGTTTCGAAAAGCGATTACATCCAAGACAAAAGCTG  
TCATTATCAATACCCCTCACAACCCAATTGGTAAAGTTTTTCACGCGCGAGGAATTAACCACTTTAGGTA  
ACATTTGCGTCAAGCACAACGTTGTGATTATATCTGATGAAGTCTATGAACACCTTTACTTCACTGATT  
CTTTCACTAGAATTGCCACACTCTCTCCAGAAATTGGGCAACTAACCTTAACGGTTCGGTTCTGCCGGTA  
AATCGTTTGCTGCTACTGGTTGGAGAATTGGTTGGGTCTTATCCTTGAACGCAGAGTTGTTAAGTTATG  
CAGCTAAGGCACATACAAGAATTTGTTTTGCATCTCCATCCCCTCTACAGGAAGCTTGTGCAAACTCTA  
TTAACGACGCTTTAAAAAATTGGGTATTTTGAAGAAATGAGACAGGAATATATCAACAAATTCAAAATTT  
TCACATCGCTTTTGAATGAATTGGGACTACCATATACAGCTCCAGAGGGTACATATTTTGTCTCGTTG  
ATTTCTCTAAAGTGAAAATTTCCGAGGACTATCCCTACCCAGAGGAGATCCTGAATAAGGGAAAAGATT  
TTCGCATTTCTCACTGGTTGATCAATGAATTAGGTGTGGTTGCCATTCCACCAACTGAATTCATATCA  
AAGAGCACGAAAAGGCTGCTGAGAATTTGTTAAGGTTTGCAGTTTGTAAGATGATGCTTATCTAGAAA  
ATGCCGTAGAGAGATTAAACTACTCAAGGACTACTTATAA

128/251

YJL060W 444aa public: 1..444 (SEQ ID NO 704)

MKQRFIRQFTNLMSTSRPKVVANKYFTSNTAKDVWSLTNEAAAKAANNNSKNQGRELINLGQGFSSYSP  
QFAIKEAQKALDIPMVNQYSPTRGRPSLINSLIKLYSPIYNTELKAENVTVTTGANEGILSCLMGLLNA  
GDEVIVFEPFFDQYIPNIELCGGKVYVYPINPPKELDQRNTRGEEWTIDFEQFEKAITSKTKAVIINTP  
HNPIGKVFRTREELTTLGNICVKHNVVVISDEVYEHLYFTDSFTRIATLSPEIGQLTLTVGSAGKSFAAT  
GWRIGWVLSLNAELLSYAAKAHTRICFASPSPLQEACANSINDALKIGYFEKMRQYINKFKIFTSIFD  
ELGLPYTAPEGTYFVLVDFSKVKIPEDYPYPEEILNKGKDFRISHWLINELGVVAIPPTFEFYIKEHEKA  
AENLLRFAVCKDDAYLENAVERLKLKLDYL

YKL123W 881bp CDS: 501-881 public: 1..881 (SEQ ID NO 705)

AAAATTAATGGATGTAACACAAAATATTGGCATTGATCTTTTCATTGGAATTGGCGCGTTTAATGCCGC  
ATATACAAGAACATATACGAGGGATGGTCTATTGGAAGACCCGGATAATGTTAGCTTCCGTGAAGCTCT  
CTCTGAAGGCAAAGATATTGAAGTCGCCAAAGATCTTCAAAGAGTTCACGATCCACATGATGAAAGTGA  
TGAAATGACGTCAGATGAGGTGAATTACATGTTAATTTGGGCCAAGTTGGGTTCGTCTTTATAGAAGC  
CAATGTGAAAAAATATGCGTTTGGGAGTGTATTATGGCCAAATTGGAATTCCTCCTGCGTATAATGGAAC  
CGAGATCAAGAAGGATACTATTTTACAGAAAGGAGAAGAATTGCCACCAAGATATGCTGACACTGATAA  
TTTCTTTGGTAGTATGAAGGTAAAGAAGGGTCACTCTAGGATAACGGCGCAAACCTGAAGCCCCT  
GTGGTCTGTTGGGACGTATGAAAGAATCTCTTCTAACTTTGACAGAGAAAATAATGTTTACCACGACAG  
TCTTGAAACCGACGATAACAACACCGATAACAATGTTAATAACAACGATGAGAACGCTGGTTGCAATGA  
AAATTCGCCATTATTGGAAGATGATGGCAATAAAAGACCGGAAAATTCAAATACCCCCCGTGAAGTATC  
AGATGGAGCTATCAATAAGAACCCTAGAAATAAATCTACTAAAAACGTCAAAGAAACAGAGGCAAATC  
TTCTAAAAAGAAGAACAGATCGAGAAAATAAGAGACATTATGAATTTGGTTTTTTTTTACAATTTACGCA  
TACACAATATATACATTCTCTACTAGCTTTTTTTTTTCTTCAATTCGATAGTTTAG

YKL123W 126aa public: 1..126 (SEQ ID NO 706)

MKESLLTLTEKIMFTTTVLKPTITTPITMLITTMRTLVMKIRHYWKMMIAIKDRKIQIPPVKYQMELSI  
RTLEINLLKNVKETEANLLKRRTDRENKRHYEFGFFYNLRHNIYIPTSFFFFNISIV

YML028W 1091bp CDS: 501..1091 public: 1..1091 (SEQ ID NO 707)

GGTAAACGATAGGGTGATAACCGCTGTGATAAAGAACTTCGTGCTCTTTTGGGTACACTACTCCCCTA  
TGTGAAGGAGAAGCTGGATGATATTGTTGCACAGAGAGCAAGGGACCGTGAGCAACCGGCTCCATCTGC  
CCAACAGCAGGAAAACGAAGATGAGGCCCTCATAATCCCTGACGAGGAAGAACCACCGCCACAGGTGC  
GCAACCTCATCTCTACATTCTGATGAAGACTAATTCGAATGCGATGTGGCCACGTTATATAATGCGTT  
TAAGGTGTACGAAAACCCATGCTGTTCTGGCCCGTCGGGTTTTCTGACAAAATTGTCTTTAGGGATTTT  
TCGGTTTGGCTCGGGTTGGCAAAGTCGGCTGGCAACAAACCAGGACATATATAAGGGAGGTAATTCGT  
CAGATCAATGCCGAACCGTTCTCAACGGGCCTTCCCCTCGTTCAATTGCTCACAACCAACCACAACCTAC  
ATACACATACATACACAATGGTCGCTCAAGTTCAAAGCAAGCTCCAACTTTTAAGAAAACCTGCCGTGC  
TCGACGGTGTCTTTGACGAAGTCTCTTGGACAAATACAAGGGTAAGTACGTTGTCTTAGCCTTTATTC  
CATTGGCCTTCACTTTTCGTCTGTCCAACCGAAATCATTGCTTTCTCAGAAGCTGCTAAGAAATTCGAAG  
AACAAGGCGCTCAAGTTCTTTTCGCCTCCACTGACTCCGAATACTCCCTTTTGGCATGGACCAATATCC  
CAAGAAAGGAAGGTGGTTTGGGCCCAATCAACATTCCATTGTTGGCTGACACCAACCACTCTTTGTCCA  
GAGACTATGGTGTCTTGATCGAAGAAGAAGGTGTCGCCCTTGAGAGGTTTGTTCATCATCGACCCAAAGG  
GTGTCATTAGACACATCACCATTAACGATTTGCCAGTCGGTAGAAACGTTGACGAAGCCTTGAGATTGG  
TTGAAGCCTTCCAATGGACCGACAAGAACGGTACTGTCTTGCCATGTAACCTGGACTCCAGGTGCTGCTA  
CCATCAAGCCAACCGTTGAAGACTCCAAGGAATACTTCAAGCTGCCAACAAATAA

YML028W 196aa public: 1..196 (SEQ ID NO 708)

MVAQVQKQAPTFFKKTAVVDGVFDEVSLDKYKGKYVVLAFIPLAFTFVCPTETIIAFSEAANKFEEQGAQV  
LFASTDSEYSLLAWTNIPRKEGGLGPINIPLLADTNHSLSRDYGVLIEEGVALRGLFIIDPKGVIRHI  
TINDLPVGRNVDEALRLVEAFQWTDKNGTVLPCNWTPGAATIKPTVEDSKEYFEAANK

YOL052C-A 686bp CDS: 501..686 public: 1..686 (SEQ ID NO 709)

TGGCCACTGAAAATTCCTGGCCAGACCACCCCTGAGCTAAGGGAGTTTAGCCGCTCAAGCTTTTTATTTC  
CTCTGATGTAATATATCACACACCCAGACACGGTTGCCAAGGCCCTGACGGAAGGCCGCTTCAAGGGAC  
GGGGCAGTGGCTATCAGAAATACCTTAATATCATCAATATTTTTCATCAATCGCAAGGTGTCAAACATC  
AATAAAGGATGATGCTCAAAGGTTTATGCCCGATGTTCTTCTAATCCCCTTTCTCTCTAAATAATCC

129/251

TTTTTTTACTCTTCTTTTCCCCTGTTTCCATTTTGTCTTTTCTCACCCCTTATGGGACATCAATA  
ATGCAAGTATGTTTATACATTTTATATAAATGTATATATAAATGCCATTTCTTACACATAACCTCCAT  
TCTTTGGTTAATTCTTTCTTCATTCTTTTTTTTTTTCATTCTGAAAAGCCCTCCAAGCAAGCACGCTAAT  
TTAATATCGATTTAAACATGAAAGTATCACAAGTTTTTCTGCCATCTCTGTCTTCGGCCTCGCTA  
CTAGCGTAAATGCTCAAAACGCATCCAACACCACGAGTAACGCTGCTCCTGCTTTGCACGCTCAAAATG  
GTCAACTACTAAACGCCGGAGTCGTCGGTGCTGCTGTTGGTGGTCTTTGGCCTTTTTGATTTAG

YOL052C-A 61aa public: 1..61 (SEQ ID NO 710)

MKVSQVFISAVISVFLATSVNAQNASNTTSNAAPALHAQNGQLLNAGVVGAAVGGALAFLI

YOL099C 992bp CDS: 501..992 public: 1..992 (SEQ ID NO 711)

TGTCCAAATATGTTGATGAATTCTGTTTGCAAAGGGGAACAACTTCAATGAATTGTATTTGGAAAGGT  
TGCAGAATGTTACCAAAACAGATCTGAAAAATGCCATGCAGAAATATTTTGTCAACATGTTTGATTCCA  
ATAAAAGCGTTGCCTTTGTGAGCTGTCATCCAGCTAAATTGGAATCAGTTCAAGAATCTTTGAAACTC  
AAGGTTTCACTGTGCAAAATAGAAGAGCTAGAAGATGACGATGACGAAATTGATAGTGAAGAAGACGAAA  
ATGCGTGAGTACATGACCTCCATTTTCAGCTTCACCTTTCAACACAGAAACAGTGCCTATTATCTGCATTC  
AATAAATAGCAAAAGGAGCATTGTCTCATTCTTTTTCGAATTCTGGGATTCTGCCTTACGGCGCTCTTTC  
ATTTGATTGATCGAGAATTATTATTATTTATATGAGTACTTGAAATTCCTCATATATTTATTTTAG  
AGTATTTAAGTAGCTTGATGAAAACATTAGATAAAATTACTAATTACGACCTCTTCGATTTTGCAGATG  
AGTTTTTGAAATTTGTTCTGTGTTTAGACCTAATCCCACGGTAACTTGTCTTTTGGCAATCCGTTAA  
CTAATTTACTGGTTAACGGTACTGGAGCAGCGTGTTTTTTGAATTTTGTTCCTGGCATTGATAAAGG  
TTTCAAAAATTCTGCTTGATCTGTTGCTCTTAGCGCTATTAATCGATTGAGAAAACGAATTGTGCTTTG  
AAATTGATGGAGATTGGCTATGCGTCCTGGGTTTTGGCGAAGGAGACTTGAAGTTGGAAGATCTTTAG  
GTATGGCTCTTCCGGATGATGATGTTCTTCTTTCAATTACCTTTTGGTTTCTTTGCAACAGTTCTTTCT  
CTATTTTATTTGTATTGCAATTAAGAATTTTTTTGAGAACAGTAAACAATTTGCTCGTGGTTTTTTTAT  
CAGTGCTCAAAAGAAATGACTTGTA

YOL099C 163aa public: 1..163 (SEQ ID NO 712)

MKTLDKITNYDLDFDAEFLKFVPVFRPNPTVTCLFGNPLTNLLVNGTGAACFFEFCSLALIKVSKILL  
DLLLLALLIDSENELCFEIDGWLCLVGFGEGLLEVGRSLGMALPDDVLLSITFWFLCNSSFSILFV  
ELRIFLRTVNLLLVFLSVLKRNDL

YOL100W 3746bp CDS: 501..3746 public: 1..3746 (SEQ ID NO 713)

TTAACGATCGACTCGACACATTGTTGATGGAATAATTGGTCCCTAGTTAAACAGCGGAGAAATAGCCGC  
CCAGGATAATCGGAGAAAAGTCACGTGCAAAAAGAAATCATATTCGACGAAATAAACTAGAATAACTTT  
TGACGTTTAGCAATAATAACCCCAATGGAAGCGAACATTTCCCGATCCTTTTAGTTTTCTTTAAGGCG  
CTATTGGCATTATCTTCAAAGCTTCCGCAACACAGAAATTATATATTACATTTCTGAGGCAGAGAAT  
AGTTTTGACAACGAACTGTTAATATTTTACTCCAGTTACCGCCTTTGAAGTCTGATATTGGTGTACA  
AAGGTACTTAGGGGTATTTAAGAACAAGAACTACATAAAATAGTTGAAAAGGGGAAAACAAAAGTAAC  
ATCTTGATGAACCGAGAAGCCACTAAGTATTTTTTAAAGCAAAAGAAATTAATCTCTCTTTTTTT  
TTTTTCATTTCAACCAATGTATTTTGATAAGGATAATTCATGAGCCCTAGGCCGTTATTGCCAAGTG  
ATGAGCAGAAGCTAAACATTAATCTTCTAACGAAAAGGAGAAATCTCGCATTTAGACCCCCATTATG  
ACGCAAAAGCCACTCCACAAAAGCACTTCGAATAGAAACGTTGGCGATTTACTTTTGGAAAAAGAA  
CCGCTAAGCCTATGATTCAAAAGGCCTTGACGAATACGGATAATTTCAATTGAAATGTACCATAATCAGC  
AGAGAAAAAATCTTGATGATGACACTATTAAAGAAGTAATGATTAATGATGAAAACGGAAAAACTGTGC  
CTAGTACCAACGACGGCAGATATGACAACGATTACGATAATAACGATATTAATGACCAAAAAACTTTGG  
ATAATATAGCGGGAAGTCCCCACATGGAAAAAATCGAAACAAAGTAAAGATTGAACATGACTCTTCAT  
CTCAAAAACCAATAGCTAAAGAGTCATCCAAAGCCCAAAAAATATAATCAAAAAGGGAATCAAGGACT  
TTAAATTTGGTAGTGTAAAGGTGATGGCGCGTATTCTACTGTAATGTTAGCGACGTCGATTGATACCA  
AAAAGAGGTACGCCGAAAAGTACTAAACAAAAGAAATTTAATACGCCAGAAGATCAAAATACGTC  
GCATAGAAAAAACCGCCCTTCAAAGCTCAATAATTCTCTAGTGTTGTGCGATTATTTTCCACTTTTC  
AGGATGAATCAAGCCTATACTTTCTCTTAGAGTATGCCCCAATGGGGACTTTCTTTCTTTAATGAAAA  
AATACGGTTTCAATTAGACGAAACCTGCGCACGATATTATGCTGCGCAAATAATAGATGCCATAGACTACT  
TACATTTCAAACGGTATTATTTCATAGAGATATAAAACCAGAAAATATTCTTTTAGATGGAGAAATGAAGA  
TCAAACGACTGATTTTGGTACTGCGAAGTTACTGAATCTTACAAATAATAGCGTTTCGAAACCAGAA  
ACGATTTATCAACAAGGTCGAAATCTTTCGTTGGAAGTGCAGAATACGTATCTCCAGAACTTTTAAATG

130/251

ACAGTTTTACAGACTATCGTTGCGATATTTGGGCCTTCGGATGTATACTTTTCCAGATGATTGCCGGAA  
AACCACCATTCAAAGCTACCAATGAATACTTGACTTTCCAAAAGGTAATGAAAGTTCAGTACGCCTTTA  
CACCAGGTTTCCCACTTATTATCAGAGATTTGGTTAAGAAAATCTTAGTAAAAAACTTAGACCGAAGAT  
TGACGATAAGCCAAATTAAGGAACATCATTTTTTCAAAGATTTGAATTTTAAAGACGGCTCTGTTTGGT  
CAAAAACGCCTCCAGAGATCAAACCATATAAAATCAACGCCAAATCCATGCAGGCAATGCCAAGCGGAA  
GCGATAGAAAACCTGGTGAAGAAATCAGTCAACACACTTGGCAAATCGCATCTAGTGACTCAAAGGTCAG  
CTTCAAGTCCCTCTGTTGAGGAACTACTCATTCAACCCTATACAATAACAATACTCACGCTTCTACTG  
AAAGTGAAATATCAATAAAGAAGAGACCCACTGATGAAAGAACAGCGCAGATACTTGAAAATGCAAGAA  
AGGGTATAACAATAGGAAAAATCAACCAGGCAAGAGAACACCAAGTGGTGCAGCTTCTGCTGCCCTAG  
CAGCTTCTGCTGCTTTAACCAGAAAAACCATGCAAAGCTATCCAACCTTCTAGTTCGAAAAGTAGCAGGT  
CAAGCTCTCCTGCGACAACATCAAGACCAGGAACCTATAAGCGTACTTCTTCTACAGAAAAGTAAACCAT  
TTGCCAAATCTCCACCTTTGTCAGCATCAGTTTTATCGTCAAAAGTCCCAATGCCTCCATACACACCTC  
CAATGTCGCCCCCTATGACACCATATGATACATATCAAATGACACCTCCCTATACGACAAAACAGCAGG  
ATTATTCTGATACCGCAATTGCCGCACCTAAGCCTTGTATTAGTAAGCAAAATGTTAAAAATAGCACAG  
ATTCTCCCTTGATGAACAAGCAAGATATTCAATTGGTCCTTTTACCTGAAAAACATCAACGAACATGTAC  
TAAGGACGGAAAAAATGGATTTTGGTTACCACAAATTACGATATCTTAGAGAAGAAAATGCTTAAACTAA  
ATGGTTCAATTGTTAGATCCTCAACTGTTTGGTAAGCCTAGACATACTTTTTTATCCCAAGTAGTAGGA  
GTGGGGGAGAGGTTACAGGTTTTCGAAATGATCCAACCTATGACTGCTTATTCCAAAACAGAAGATACGT  
ACTATTCGAAAAATATTATCGATTTGCAGCTCTTGGAAGATGATTATCGAATTGAAGGAGGTGACTTAT  
CGGAGTTGCTTACTAACAGAAGCGGAGAAGGTTACAAATGCAATCAAAACAGCTCACCAATGAAAGACG  
ATGATAAATCCGAATCTAACAATAAAGGAAGCTCTGTTTTTCTGGCAAGATTAAAAAATTATTTTACC  
CTACCTCAGCAGCTGAAACGCTCTCTTCTCTGATGAAAAAACCAAGTACTATAAACGAACCATGTAA  
TGACATCATTTGGAAGGTTTCTAGTATTTGCCAAGAGGAGGCAGCCAAATCCAGTTACAAATTTAAAGT  
ATGAAGTAGAATATGACATAAATTTGCGTCAACAGGGTACCAAAATAAAGAATAATCATTCCTTTGG  
AAATGGGAACATATATAGTTGTGATTGACACACCTTACAAGTCATTTCTTTTGAGCACTGATAAAA  
AAACCACGAGCAAATTTGTTTACTGTTCTCAAAAAAATCTTAATTTCGAATACAAATAAAATAGAGAAAG  
AACTGTTGCAAAGAAACCAAAAGGTAATTGAAAGAAGAACATCATCATCCGGAAGAGCCATACCTAAAG  
ATCTTCCAACCTTCCAAGTCTCCTTCGCCAAAACCCAGGACGCATAGCCAATCTCCATCAATTTCAAAGC  
ACAATTCGTTTTCTGAATCGATTAATAGCGCTAAGAGCAACAGATCAAGCAGAATTTTGAACCTTTA  
TCAATGCCAAGGAACAAAATTCAAAAAAACACGCTGCTCCAGTACCGTTAACCAGTAAATTAGTTAACG  
GATTGCCAAAAGACAAGTTACCGTGGGATTAGGTCTAAACACAGGAACAAATTTCAAAAACTCATCTG  
CAAAATCGAAGAGGTCGTAA

YOL100W 1081aa public: 1..1081 (SEQ ID NO 714)

MYFDKDNSMSRPLLPSDEQKLNINLLTKKEKFSHLDPHYDAKATPQRSTSNRNVGDLLLEKRTAKPMI  
QKALTNTDNFIEMYHNQQRKNLDDDTIKEVMINDENGKTVASTNDGRYDNDYDNDINDQKTLDNIAGS  
PHMEKNRNRKVIEHDSSSQPIAKESSKAQKNIIKKGIKDFKFGSVIGDGAYSTVMLATSIDTKKRYAA  
KVLNKEYLIRQKKVYVSIKLTALQKLNNSPSVVRLFTFQDESSLYFLLEYAPNGDFLSLMKKYGS LD  
ETCARYYAAQIIDAYLHNSNGIIHRDIKPENILLDGEMKIKLTDFTAKLLNPTNNSVSKPEYDLSTR  
SKSFVGTAEYVSPPELLNDSFTDYRCDIWAFCILFQMIAGKPPFKATNEYLTFFQKVMKVQYAFTPGFPL  
IIRDLVKKILVKNLDRRLTISQIKEHHFFKDLNFKDGSVWSKTPPEIKPYKINAKSMQAMPSSGSDRKL  
KKSVENTLGKSHLVTQRSASSPSVEETTHSTLYNNNTHASTESEISIKKRPTDERTAQILENARKGINNR  
KNQPGKRTPSGAASAALAASAALTKKTMQSYPTSSSKSSRSSSPATTSRPGTYKRTSSSTESKPFKSP  
LSASVLSSKVPMPYPYTPMSPMPYDQYQMTPPYTTKQDYSDTAIAAPKPCISKQNVKNSTDSPLMN  
KQDIQWSFYLNINEHVLRTKLDFTVNTYDILEKKMLKLNGSLLDLPQLFGKPRHTFLSQVARSGGEVT  
GFRNDPTMTAYSKTEDTYYSKNIIDLQLEDDYRIEGGDLSELLTNRSGEGYKCNQNSSPMKDDDKSES  
NNKSSVFSGKIKKLFHPTSAAETLSSSDEKTKYKRTIVMTSFGRLVFARROPNPVNTLKYELETD  
INLRQOGTKIKELIIPLEMGTNHIVVIQTPYKSFLLSTDKKTTSKLFTVLKKILNSNTNKKIEKELLQRN  
QKVIERRTSSSGRAIPKDLPTSKSPSPKPRTHSQSPSISKHNSFSESINSAKSNRSSRIFETFINAKEQ  
NSKKHAAPVPLTSKLVNGLPKRQVTVGLGLNTGTNFKNSSAKSKRS

YOR302W 578bp CDS:501..578 public:1..578 (SEQ ID NO 715)

GTGTATGATGTAATCCATCACCCCCCTATAAAACACCTGTGCACCGCATATTTCCATAGCGCGTGACG  
CTAAGTACAAGAAACAGCGAGGGGCCGTTAAGTGCAGGCTTTACCGAGGGCGCCGGCTGGCGCTTCCCG  
TGGAAGGGTGTGTTGACTCATCATCGCATCGCATACCTCATGATGAGTAAATAGTTGCGATTTCACTTA  
TCACCTCTCGCGGAAAAAAAAGCGGATGACATGATATATAAGGCTCTCTCGTAAGACACTTAACTATCC

131/251

AACGTTCATTAGATTATTCGGTCAATTTCTTTTTTCATGCCCCCTCCTTTTTCTTTTCTTTTCTTGACTC  
GTCGTTTCTTTTTCTTTTTTTTTTTTTTTTTTTTTCTTCAGAACTATAACACATAGATACACTCGAACAT  
CTAATTGTTTAAATACTGCAAAGAATACAAGGTAATCGACTCTTCTACATACCCTTTTTGCAGATTTGA  
AATAAAAAAACATTATATGTTTAGCTTATCGAACTCTCAATACACCTGCCAAGACTACATATCTGACC  
ACATCTGGAAAACCTAGCTCCCACTAA

YOR302W 25aa public: 1..25 (SEQ ID NO 716)  
MFSLSNSQYTCQDYISDHIWKTSSH



132/251

**Figure 2****Candida spp. h mologues**

YBL002W\_homolog 393bp public: 1..393 (SEQ ID NO 397)  
ATGGCCCCAAAGCAGAAAAGAAACCAGCTTCCAAAGCTCCAGCTGAAAAGAAACCAGCTGCTAAGAAA  
ACCGCTTCCACCGATGGTGTCTAAAAAGAGAAACCAAAGCTAGAAAAGAAACTTATTCCTCATATATATAT  
AAAGTTTTTGAAACAAACACATCCAGACACTGGTATCTCCCAAAGGCCATGTCAAATTATGAATTCGTTT  
GTTAACGATATTTTCGAAAGAATTGCCACCGAAGCCTCCAAATTAGCTGCTTACAATAAAAAATCCACA  
ATTTCCGCTAGAGAAATCCAACTGCTGTTAGATTAATTTTGCCAGGTGAATTGGCCAAACATGCCGTT  
TCCGAAGGTACCAGAGCCGTCACAAAATACTCATCTGCTTCTAGTTAG

YBL002W\_homolog 130aa (SEQ ID NO 398)  
MAPKAEKKPASKAPAEKKPAAKKTASTDGAKKRTKARKETYSSYIYKVLKQTHPDTGISQKAMSIMNSF  
VNDIFERATEASKLAAYNKKSTISAREIQTAURLILPGELAKHAVSEGTRAVTKYSSASS

YBL064C\_homolog 732bp public: 1..732 (SEQ ID NO 399)  
ATGAGAGACAAAAACAAACAAAAAATCTTTTTTTTCGCCACGCACACTACCATGTGCGCAA  
CAACCACATTTACGTCTCGGATCTACCGCACCTGATTTCAAAGCTGATACAACCTAACGGGCCTATTCTGT  
TTTCACGAATACATTGGTGATAGCTGGGCTATCTTGTCTCACATCCCGCTGCCACACCAAGTGTGTGT  
AGCACCGAGCTTTCTGCGTTTCGCACGACTCGAACCGGAGTTTACGAAGAGAGGGGTGAAAT'TGCTTGCA  
ATTTACGCCGACCCTGTTGAAGCAAATTCGACTGGATTGATGATATGGAAGATTTTAGCGGATCCAGG  
GTCAAATTTCCAAATTATCGCAGACCCTGAGAGAAAAGTTGCTACCTTGTACGACATGATCGATCACCAA  
GATGCCACCAATCTCGATGACAAAGGGCTTCAATTGACAATTCGTGCAGTGT'TATCATTTGATCCAAGT  
AAGAAAATCAGATTGATCATGACCTACCCTGCCTCGACCGGTAGAAACACCGCTGAAGTATTGAGAGTA  
CTCGACTCATTTACAGCTTGTGTTGATAAAACAAAAGGTTATCACTCCAATCAATTGGGTTCCAGGTGACGAT  
GTTCTTGTCCATATGGGTGTCCAGATGATGAGGCAAGAGTTTGT'TTCTTAAATATAGGGCTATAAAG  
CCATATATTAGATTGACTCCGTTGGAAAAGGAAGACAAGTAA

YBL064C\_homolog 243aa (SEQ ID NO 400)  
MRDKKQTKKKKSFFFATHTTMSQQPHLRIGSTAPDFKADTTNGPIISFHEYIGDSWAILFSHPAHTSVC  
STELSAFARLEPEFTKRGVKLLAISADPVEANSWIDDMEDFSGSRVKFPPIIADPERKVATLYDMIDHQ  
DATNLDDKGLQLTIRAVFIIDPSKKIRLIMTYPASTGRNTAEVLRVLDLQLVLDKQKVITPINWVPGDD  
VLVHMGVDPDEARVLFPKYRAIKPYIRLTPLEKEDK

YBR149W\_homolog 981bp public: 1..981 (SEQ ID NO 401)  
ATGAAATTAGCCACTGAAATTGATTTCAAACCTCAACAAATGGTAAAACCATTCCCTGCCTTAGGACTAGGT  
ACTGTTGCCCTCAAAGATCCTAAAGATGTTAAGGATCAAGTAATCACTGCTGTTAAAGCAGGATATCGT  
CATATTGATACTGCTTGGTTTTATGGTACTGAAAAATATATTGGTGAAGCATTACAAGAATTATTTGCT  
GAAGGAATTATTTAAAGAGAAGATTTATTTATCACGACAAAATTTTGGCCATCATATTGGGCTAATCCA  
GAAAAATCTTTAGATGAATCTTTAAAGATTGCAACTTGATTATGTTGATTTATTTTACAACATTGG  
CCAATTTGTTTACATGGTGATGAAAATGGATTACCGAAAAATACCTAAGGATGAGAATGGTGAATTGATT  
TATGATGATGATCCAAACCCCAATGGTACTAAATATATCGACGTTTATCATAAATTAGAGGATATTTTA  
GAAACAACCACCAAAGTTAGATCAATTGGTGT'TTCTAATTTATTCAAATTCCAAACCTTCGTCAATTATTA  
CCTAAAGTTAAAAAACATATTCCTGTTTGTAAATCAAATTGAATATCATCCACAATTACCTCAACAAGAT  
TTAGTTGATTATTTGACTAAAAATAATATATTGATTTCTTGTATTTCACCAGTTGGTAGTTATGGAGCT  
CCAGTATTGAAAATCCCATTAGTTAAGCAATTGGCAGAAAAATATCAAGTCACAGAGAATGAAATTGCT  
GATGCTTATAATATTTTGAATGGTAGAGTTACATTACCAAGATCTTCTAATCTTGAAAGAATTAAACC  
ATTATTAGATTACCACATTTGACTAAAGAAGAATTGGATGAATTGTATCAAGTTGGAGTTAAAGATCCA  
CAAAGATATATTTGTGATCCTTGGGGGTATGGTATAGGATTCCGTTGGTGGAAAGGCGATACTTTAAGT  
AAAGAATTTGATTAA

YBR149W\_homolog 326aa (SEQ ID NO 402)  
MKLATEIDFKLNGKTIPALGLGTVASKDPKDVKDQVITAVKAGYRHIDTAWFYGTEKYIGEALQELFA  
EGIIKREDLFITTKFWPSYWANPEKSLDES LKDLQLDYVDLFLQHWPICLHGDENGLPKIPKDENGELI  
YDDDPPTNGTKYIDVYHKLEDILETTTKVRSIGVSNYSIPKLRLQLLPKVKKHIPPVCNQIEYHPQLPQDD  
LVDYCTKNNILISCYSPVGSYGAPVLKIPLVKQLAEKYQVTENEIADAYNINLNGRVTLPRSSNLERIKT  
IIRLPHLTKEELDELYQVGKDPQRYICDPWGYGIGFRWWKGD TLSKEFD

YBR289W\_homolog 1389bp public: 1..1389 (SEQ ID NO 403)  
ATGAAACCAATGCAAAACGTTAAGGAGTGGTCAGAAAAATTGAAACAGGAAGGTAAAGATGTACCTCTT  
GATTTGAAAGTGTATGAAGATTTGATTAGAAAGGATAAGGAATTTGTGGGTAAATTGAATAAACAGTTG  
CATGACAACAAATTTATTATGGAAAATATTAACAGAGATATCAAGTCTTATAATCAAATCAAACAATTG

133/251

AGGATGAATTCTATTGCGTTGTCCAACAAAGGACAGTATAATAACAGTATTTGGGGGGAAGGATATCAA  
GGTTATGGCAATGGAATAACAACTCCAGTACAAAGTTATTTATCCCAACAGGGATTTAACTGATAGA  
ATCATCAATGAAAGAGTGATGAAAAACAAAAATAAACCAAAACATTATGTACCCATTTCGATTAGAGTTT  
GACCAAGAAAGGGATCAATTTAAATTGAGAGACACATTTCTTTGGGATTTGAATGAAGAGATTATAAAA  
GTGGAAGATTTCACTGCTCAATTGTTAGAGGATTATAAATTTATCTCCAAAGTTCATTATGAAACAATT  
TTGTCATCTATTTAAAGAGCAGATTGCTGACTATCTGCAGAAACCTAGCAAAACAAATGGGTGAATTGAGA  
ATTCCAATTAAGATCGATATCACCATTAACAATACACAATTAAGTACCAATTTGAATGGGATATATG  
AATAGCCAGGAAGGCGATGCAGAAGAATTTTCATCTTACATGTGCGACGAATTGTGTCTACCGGGAGAG  
TTTTGCACTGCCATCGCGCATAGCATAAGAGAACAAATCGCAGATGTACTATAAAGCATTGAATATGGTA  
GGGTACGGTTTTCGACGGTTCACCAGTACACGAAGATGAGATTAGAAATCATTTATTGCCACCTTTAAGA  
TTAGTATCATCGGACTCTGGAATCGTGGATGATTTTTTCTCAATTTAAGAAACCCATCAAGTTTGCCA  
GACTTTTACCTACGTTAGGTAAATTGTCCCAATTGGAAGTTGAAAGATTGGACAAGGAAATGGAGAGA  
GAAAGTAGAAGGAAAAGAAGACACAATTACAATGAAGATCAGCAACAGGGTCTGGTCGAGGCTTCAGT  
TCGAGAAGAATTGCAGCTCATGCTGGTAGGGGAAACACCATTCCCGACTTGTGAGACATACCCAAGACA  
TTTAGGACGCCTGCCCCCTCATCCATATTGCCAGGTGCTGTTGATATGGGTGTACCTGAGGTGTATGAA  
TATAATGAAGTTTAAATCAATAGAAGTCAAGTTAGGAATCCAGATTATAGACCGCCAACACCTATTCGT  
GTTGAAATGAAGTGTGATTATAACCATGATCCAATTGAAGGTACTTTTATGGTTACAATCAAATTA  
CCCGTATAA

YBR289W\_homolog 462aa (SEQ ID NO 404)

MKPMQNVKEWSEKLKQEGKDVPLDLKVYEDLIRKDEKFGVGLNKLHDKNFIMENINRDIKSYNQIKQL  
RMNSIALSNKGQYNNNSIWGEYQGYNGITNSSTKLFIPNRDLTDRIINERVMKNKNPKHYVPIRLEF  
DQERDQFKLRDTFLWDLNEEIIKVEDFTAQLLEDYKFISKVHYETILSSIKEQIADYSQKPSKTMGELR  
IPIKIDITINNTQLTDQFEWDILNSQEGDAEEFSSYMCDELCLPGEFCTAIAHSIREQSOMYYKALNMV  
GYGFDGSPVHEDEIRNHLLPPLRLVSSDSGIVDDFSILRNPSLPDFSPTLGKLSQLEVERLDKEMER  
ESRRKRRHNYNEDQQQSGRGFTSRRIAHAHAGRGNTIPDLSDIPKTFRTAPSSILPGAVDMGVPEVYE  
YNEVLINRTQVRNPDPYRPTPIRVENELVDYNHDPIDEGTFMVTIKLPV

YCR004C\_homolog 597bp public: 1..597 (SEQ ID NO 405)

ATGGCACAAGGAAAAGTAGCAATTATCATTTATTCATTATATCATCATGTTTATGATTTAGCCTTAGCT  
GAAAAGCTGGAATTGAAGCTGCTGGAGGTGTTGCTGATATTTATCAAGTTGCCGAAACATTATCTGAT  
GATGTTTTAGCTAAATGCATGCACCAGCAAAACCAGATATTCGAATTGCAACTCATGAACTTTAACT  
CAATATGATGCATTTTTATTTGGTATTCCAACCAGATTTGGTAATTTCCCTGCTCAAATTAAGCTTTT  
TGGGATAGAACCAGGTGGTTTATGGGCTAAAAATGCTTTAAGAGGGAAATATGCTGGTGTTTTCGTTTCT  
ACTGGTACTCCAGGTGGTGGTCAAGAAACTACCATTATTAATAGTTTGGAGTACTTTGGCTCATCATGGG  
ATTATTTATGTTCCATTTGGGTATGGATATCCTGGTATGACTGATTTAGAAGAAGTTTATGGTGGATCT  
CCTTGGGGGGCTGGTACTTTTGCTTCAGGTAATGGGTCAAGAAAAGTTACTGATTTAGAAAAAGCTATT  
GCTAAACAACAAGGTGAAGATTTCTTTAAACTGTCTTCAAATGA

YCR004C\_homolog 198aa (SEQ ID NO 406)

MAQKQVAVIIIIYSLYHHVYDLALAEKAGIEAAGGVADIIQVAETLSDDVLAKMHAPAKPDIPIATHETLT  
QYDAFLFGIIPTRFGNFPQIKAFWDRTGGLWAKNALRGKYAGVVFSTGTPGGGQETIIINSLSTLAHHG  
IIYVPFGYGYPGMTDLEEVHGGSPWGAGTFASNGSRKVTDLEKAIKQQGEDFFKTVFK

YCR013C\_homolog 450bp public: 1..450 (SEQ ID NO 407)

ATGATAACAATGTTACCATTTTCAGCAGATTTGACAGCAGCATCCAATAAGGATTTAGTACCGTTGGCG  
AATTTTTCAAATTCGAAAACACCTGGTGGACCGTTCCAAACAATGGTCTTAGCTTTGGCAACAGCTTGT  
TGGAAACAATTCGACAGATTTTGGACCACAGTCCAAACCCATCCAGTTGTCTGGAATACCTTCAGCATCA  
GTAGCAGAAGAAGTTTTGGCATCTTTGTGCAATTTATCAGCAGTGACAAAATCAACTGGCAAGATCAAT  
TCAACATTGTTTTTCTTAGCTTTTTCAACCAAGTGTTCAACGTTTTTAGCACCGGCTTCATCGAAAAGA  
GAATCACCAATTGGCATTTTGTTCAGATTTTCTTGAAAGTGAAGGCCATACCACCACCAACAATCAAC  
ATATCAACCTTGTCCAACAAGTTGTCAATCAATTGA

YCR013C\_homolog 149aa (SEQ ID NO 408)

MITMLPFSADLTAASNKDLVPLANFSNSKTPGGPFQTMVLALATACWNNSTDFGPQSKPIQLSGIPSAS  
VAEEVLASLSNLAVTKSTGKINSTLFFLAFSTKCTFLAPASSKRESPIGILFKIFLKVKAIPPPTIN  
ISTLSNKLIN

YDL147W\_homolog 840bp public: 1..840 (SEQ ID NO 409)

ATGGATAGGAGTTGGGTAGTAGGTTGTGCCATAAAGGGTGGTTGTTTAGTTAGTTATGGCACATGTTGT  
GGTAGTTTGATTTTTTTTTTGTGGTCCACACGACTGGCCAAACATTTATCAAAAAATCGAGTTCAACTTT  
TTTTTTTTTCCAGTTCGCCACCACCACTACTTTTACCACCCTAACAACATGTCAAGAGAAGATCCA  
ATTAAGGCTGAAAAGACTTTTTCTGCTACTTTAGATGAACAATTCCTTATTGATTGAAAAGATCTCTGAC

134/251

TACAAGCAAGCATTAGATAAGTATCTTGTCTTGGAGAAACAACTCGTCAGTCTTCCGATTTGGCTTCA  
TCAAAAAGAGTTCTCAACAAGATTGTTACTGCATTGGTTGATAATAACGATTGGGAGTATTTGAATGAC  
TTGATAACTATCTTGTCAAAGAAACATGGTCAGTTAAAGTCGTCAATTCAGCATTATCAAAGATGTG  
ATTGATAATTTGGATAAATTTGGATGAAAACAACAAGCAACAATTAGAGTTGAAGATGAAATTTGATTGAA  
ACTATTAGAACAGTCACAGACAAAAAGATTTTGTGTAAGTTGAAAGAGCCATTGTTTCAAGACAGTTG  
GCCAAAATTTATTTGAACAAATTGAATGATTTGGATAAGGCAGTGGAAATCTTGTGTGATCTACAAGTA  
GAAACGTATTCGTTAATGCCATTCAAGTGACAAGATTGAGTATATCTTAGAACAAATTCAGTTGACTTTA  
CAAAAGGGGGACTATGGCCCAAGCCAAGATTTTGTAGTCGAAAGATTTTATTAAATCGTTGAAGAAGCTT  
TGCCAAAGCTGA

YDL147W\_homolog 279aa (SEQ ID NO 410)

MDRSWVVGCAIKGGCLVSYGTCCGSLIFFCGPHDWPNIYQKIEFNFFSSPPPTTFTTTNNMSREDP  
IKAEKDFSATLDEQFPLIEKISDYKQALDKYLVLEKQTRQSSDLASSKRVLNKIVTALVDNNDWEYLND  
LITILSKKHGQLKSSIQAFIKDVIDNLDKLDENNKQQLKMKLIETIRTVTDKKIFVEVERAIVSRQL  
AKIYLNKLNLDLKA VEILCDLQVETYSMPFSDKIEYILEQIQLTLQKGDYGPSQDFESKDFIKIVEEL  
CQS

YDR253C\_homolog 1752bp public: 1..1752 (SEQ ID NO 411)

ATGCAAAATACTAACCCTAATAATAGTAATAGTAGTAAGAATAATAGTGATAATCATCATCAACAACAA  
CAACGACAACGACAACAACAAGTTGATCAATATCAATCTATTACATTACCACCATTACAATATCAATCT  
AATACTCACGAATCGATAGTATTACCTTCGCAACAACCTAAAAGAGGTCGATCTGAACATTTTAATTCA  
CAATTCACGTAATATAAATTCAGACAGTGTTATTACCAAGTTCTCGTGATAATAATAACACCACA  
AATATACCTTATACCTATAAATTTACCAAGTAGTACCAATTCCTAACAATCCAATTACTTCTAGTAGCAAT  
TCAAGAATGTTTTTACCTTAATCTGTGAGTCCATTATATCCCGTGGTCACCACACCATTACAGCATTA  
TCACCACCAACACAACACCATCAACAACAACAGCAACAATTACATAAAAAATTCAAAACATCAAATTCA  
GGTTCCAATACTCCGATTACTGGTGGTGGGAATTGGATCTCCTAGTACTACTAGTTATTTAGCTAATTCT  
GCTAATATCAGTTATAC TAGAAGTCAACCATTAAGAAGATAACAACCAACATCTTCCACAAC TAAGGAT  
AATAATAACACGATAATTGAAAATGAAGACCAGAAGTTTTCGATTAGCAAAAGAAGCATTAGTAGCT  
ACTGCCAAGGGAGTTAAGACGAATCATTCCTAATAATATGGTAAATTTGGTAATAATACTTCTAAGATT  
GATATTAAATAATCATAATAAGAACAACAACAACAAAAGTGATGGTAATGAAACCATACTTGATTCTACA  
ATTGCAGATTTATTAGAAGATTACAATATGCTAGTGCTCCTCATGGTAATCCCATTGGCCAAATAAGT  
GGACTTCAAAC TAATTTCTAAAGGATTACTTGAAGTACAAGATGAATACCTCTAATTTCCCTGATTTACAA  
AACAATAATTTTTCAAAGTTAATAATGGTGATAATAATAATAC TAGTAATAGCAAGTTTAGTAATAAT  
TATCATCATCCATCAGGTAATGAACCAGGATGGAATTTTCTTGTGATGAAGCATCAACGAAAACAACA  
TCAAACAATACAGATCAACAGGAACAACAGGAACAGGAATAGGAGCAACAACCAATATAATATCAGAA  
TCAGAATCGGAATTAAAAGTGAACGAGAATCAAGTATTGCCAATATAATCAATCCCTCAACAACAACA  
ACTTCCACAACAATAATAAGAATAACAATAACACTTCATCATCTACTAAAAC TAGAAAATATTCTCAA  
GATCCAACAAGAAAATTTCTTGTGATAAATGTCCCATGTCATTTCTGTCGATCATCAGATTTAAACGT  
CATGAAAACAACATTTAATCTATCCACCTAATATTTGTCAATTTTGTGGTAAAGGTTTGTCTAGAAAA  
GATGCTTTTAAAAGACATATTGGGACTTTAATCATGTAAGAAGAAATGCTGATAAGAATTTATATATTGAA  
AATTTAAATTTTAAATAATTTCAAGTCAAGATGATGATGAAGAGGAGGAGGATGAAGAAGAAGAA  
GAAGGATTGGAAACAGGATAGATTGTATAAGAAGAGGAGGAAGAGTAATAATAATCAATCAATATAA  
GAAGAAGGATTTGAACATAATGATGACGATGATGATGATGAAGAGGATGAAGTGAACGAGAATTT  
CCAATTTATGGATATCAACAGAATTGA

YDR253C\_homolog 583aa (SEQ ID NO 412)

MQNTNRNNSNSSKNNSDNHHQQQRQRQQQVDQYQSITLPLQYQSNTHESIVLPSQQPKRGRSEHFNS  
QFQRNINSRPVLLPSSRDNNNTINIPILPSSSTNSNNPITSSSNSRMFSPNPVSPLYPVVTPSSAL  
SPPTQHHQQQQQLHKKFKTSNSGNTPTITGGGIGSPSTTSYLSANSANISYTRSQPLKDNNTSSTTKD  
NNNTI IENEDQKFFRLAKEALVATAKGVKTNHNSNNGKFGNNTSKIDINNHNKNNNNKSDGNETILDST  
IADLLRRLQYASAPHGNPIGQISGLQTNKGLLEVQDEYSNFPDLQNNNFFKVNNNGDNNNTSNSKFSNN  
YHHPSGNEPGWNFLLEASTKTTSMNTRSTGTGTGIGATTNIISESESELKVKRESSIANIINPSTTT  
TSTTTNKNNNTSSSTKTRKYSQDPTRKFPCKDCPMSFRSSDLKRHEKQHLTI PPNICQFCGKGFKARK  
DALKRHIGTTLTKRNADKKLYIENLNYLNNSSQDDDDDEEEDEEEEGLEQDRLYKKRRKSNNNNQIIK  
EEGFENDDDDDDDEEDEVKREFPTYGYQQN

YDR276C\_homolog 516bp public: 1..516 (SEQ ID NO 413)

ATGTGTTTATGTCTTTCGGATTTATTTCTTATTATTTCTTTCAGTATTATTTCCACCATTACCTGTTTGG  
ATTAGAAGAGGATGTTGTTTCATGTGATTCAATTAATTAATATGCTTATGTATTAGGATATTTCCCA  
GGGTTAATTCATTTCATGGTATATAATAGCTAAATATTCTTCTTATTATTATCAACAACAACAACA  
CGTAAAGATACCATTTATTATGTTTATCGAAGTGATTTAGAAAATCAAACACCAAGAAGAGATGGCAGA  
GATGGGAGAGATGAATGTCATCATGACCACCACCACCACCATCATCATCACACCAGGCAGAAATCA  
CAAAGTGCGGGATTAATAGTTTCTAATAATCATAATAATAATAATAACTATGGATCTGTGGTTGAA

135/251

GGTTCATCATCATCGAATTTGACTCCTGTGGCTCCTATTCCTGTTGAAAATGGAGCTCCACCACCAGCT  
TATACTGAGATTGATAATAAAACACAACATTAA

YDR276C\_homolog 171aa (SEQ ID NO 414)

MCLCLSDLFLIILSVLPPLPVWIRRGCCSCDSLINIALCMLGYFPGLIHSWYIIAKYSSYYYQQQQQQ  
RKDTIYYVYRSLENQTPRRDGRDGRDECHDHHHHHHHHNQAESQSAGLIVSNNHHNNNNNNYGSVVE  
GSSSSNLTVPVAPIPVENGAPPPAYTEIDNKTQH

YEL039C\_homolog 333bp public: 1..333 (SEQ ID NO 415)

ATGCCAGCTCCATTTGAAAAAGGTTTCAGAAAAGAAAGGTGCCACTTTATTTAAACTAGATGTTTACAA  
TGTCACACCGTTGAAAAAGGTGGTCCACACAAAGTTGGTCCAAATTTGCATGGTGTTCGGTAGAAAA  
TCCGGTTTAGCTGAAGGTTATTCTTATACTGATGCTAACAAGAAGAAAGGTGTTGAATGGACTGAACAA  
ACCATGAGTGATTATTTGGAAAATCCAAAGAAATATATTCCAGGTACTAAAATGGCTTTTGGTGGTTTA  
AAGAAACCAAAGGACAGAAACGATTTAGTTACTTATTTGAAGAAAGCTACTTCTTAA

YEL039C\_homolog 110aa (SEQ ID NO 416)

MPAPFEKKGSEKKGATLFKTRCLQCHTVEKGGPHKVGPNLHGVFGRKSGLAEGYSYTDANKKKGVVEWTEQ  
TMSDYLENPKKYIPGTMFAFGGLKKPKDRNDLVTYLKKATS

YER112W\_homolog 321bp public: 1..321 (SEQ ID NO 417)

ATGTCAGCAGGTATTCCAGTAAGACTTCTAAATGAAGCACAAGGTCATATAATCAATAGAATTGATA  
AATGGAGATACATACCGTGGGAAGCTATTAGAAAATGAAGATAATATGAATTTATCCTTATACGAGGCA  
ACTATAACACAAGGCAAATCGGGGAAAGTAAGTCATATGGACCAAGTGTATATAAGAGGGTCAATGATT  
AGATTTATATCTGTGCCTGATATTTTAAAGAATGCTCCTATGTTTTTATGAAACCTGGAGATAAACCA  
AAACCTCCAATAAGGGGCCCTCCACCAAAAAGAAAGAGAGTATGA

YER112W\_homolog 106aa (SEQ ID NO 418)

MSAGIPVRLLEAQQGHIIISIELINGDTYRGKLLNEDNMNLSLYEATITQKSGKVSMDQVFIRGSMI  
RFISVPDILKNAPMFFMKPGDKPKPPIRGPPPKRKRV

YFR010W\_homolog 1239bp public: 1..1239 (SEQ ID NO 419)

ATGGTTTTAGGCACTCCAGACAAGAATTTGCCTTCAAAGCCAGTTGAAAAACAAGTTTTCTCGAAGAT  
TTGAATAAAAAATCAATTGGTTAAAGTTAGTAATGAACCTAGTGGGTTGACCAATTTAGGGAACACTTGT  
TACTTGAACCTAAGTTTACAAACAATATTCCATATTGATGATGTGAATAACAGGTTGAAAGATTACACT  
TTTGGTGGAGCCAATCAAGCCAATAGTGCCTTTGTGTTGTCATTGAAAAGTATGTTCCAGCAAATGTCTG  
AAAAACAAGAAGTTATAACTCCTTCTACATTTCTTTCTCTTTTTCAGAAGATCTTATCCTCAATTTGCT  
GAACAACAAAATGGTATTTATAACAACAAGACGCCGAAGAAGCATTTTCCCAAATTTGAGCTCTTTG  
AGAAGCGAATTGAAAATAGATGATGTGTTCAAATTAACACCAAGACTCAATGCTTGGCTATT  
CCAGAAGATGTACAGAAGGTTTGAAGAAGCATATAAATGAATTGTCATATCGGCGTCAAGACCAAT  
TTTTTGAGAGATGGATTGTTGGCTGGATTAAAGAAGAACGATTGAAAAACATAATCAACTTTGAATGCT  
GATACTGAGTATGAAACAACCAAGACCATAACTAGATTACCAAATACTTGACAGTACATTTTATTAGA  
TTTTTCTGGAAACGAGACATCAATAAGAAATCCAAGATTTTGAGAAAGGTTCAATTTCCCATTTGAATTA  
GATTTAGCAGAAATGTTGGATGTATCAATAAAGGCAGATAAAGTTTCCAATAGAGATACAATTAGAAAA  
GTTGAAAAAGATAATTTGGATATGATAAGAGATTTCAAAAAGACCAAAAATGACACCAGTTTAACACCA  
TTGGAACAACAAGAGGAGATGAGATGAAAATAACATCAATCAAGAGTAAGTTTAAAGACGACTTGAAT  
AGCGCTTTGCCCCACGTTGATTTTAACACCACCACAGAAAACCTTCTAGTGTGTATGAATTAAACGCA  
GTCATTACTCATGCTGGATCATCTGCCGATGGTGGTCATTATAAAGCATACGTCAAGGATCCAACAGAC  
TTGGATGGCGAGAGATGGTGGTTATTTAACGATGATAAGGTGAGCTCCGTAAACAAAGAAAAGATCGAA  
ACTTTAGCTGGCGGTGGTGAAAGCGACTCAGCTTTATTATTGATTTACAAAGGCTTAGGGCTTTAG

YFR010W\_homolog 412aa (SEQ ID NO 420)

MVLGTPDKNLPSKPVEKQVFLEDLKNQLVKVSNESGLTNLGNTCYLNSSLQTIHFIDDVNNRLKDYT  
FGGANQANSFVLSLKSMFQQMSKKQEVITPSTFLSLFRSYPQFAEQQNGIYKQDAAEEAFSILSSL  
RSELKIDDFKITFNTKTQCLAI PEDVTEGFEEAYKLNCHIGVKTNFLRDGLLAGLKETIEKHNSTLNA  
DTEYETTKTITRLPKYLTVHFIRFFWKRDINKSKILRKVQFPFELDLAEMLDVSIKADKVSNRDITRK  
VEKDNLDMIRDFKTKNDTSLTPLEQQEEDMKITSIKSKFKDDLNSALPNVDFNTTENPSSVYELNA  
VITHAGSSADGGHYKAYVKDPTDL DGERWWLFNDKVVSVNKEKIETLAGGGESDSALLLIYKGLGL

YFR052W\_homolog 834bp public: 1..834 (SEQ ID NO 421)

ATGTCCTTTACAAAACTCACTGCAGAAATATACTCACTATTTGGAAAAGGAGATTATCAAGGTTGCCAA  
CAATTACTTGCTCCGATTAACTAGAATTAGTCAAACATGATTTGTTGGTTCCTTTACCATCCAACACC

136/251

ACCGATAAAAACCAAATTAATGATTTGAGAATTGCCCAAAGAATTTTGAAATTGGAGCATTATCGTCA  
TTATTAACCAACAACACTATTCGGTTTTGAGAATTATTTTGCTCAGTTGAGACCATTTTACTCTAACCC  
AAATTACATAATTTACAAAAGTCCATATCAATACCGATATAACAAAATCATTTCATTATACTTGT  
TACTTGTGTGAGTCAGGGTTTTGATTTCAAATTCATGTTGAAGTAGAAGTGATTTATAATTCATCACA  
TATGATGCCCAACAAGACAAGTATTTACAATTTCCAATAAATTTAGAAAGCAATTTAATGGAAGGTAAT  
TACATAAAAATCTGGAAGTTATTTAAAAGAAGAGAAAAACTTACCATGTCAAGAATACACCCATT  
GATACTTTTGATAAATGCTTTACGTTTTGAAATTGCCAAATCTTTGGAGAAAACCTACGATTTCGATT  
ATTTCTAATTGCAAGAATTTATTATATTTACCACAAGAATTGTCCGATGCTAACTTTGAGAAAAC  
AAGGAACTTATCAAGTTGATAATTGGAATTCGAGGATGGAGTTATATATTTCACTAAGAATGAAAT  
GAAACCAATGTTGATAACCAATCGGTTATAAGAATTTATTAGGGTACGCTGAACAAATCGAATCCATC  
GTATAA

YFR052W\_homolog 277aa (SEQ ID NO 422)

MSLQKLTAEIYSLFGKGDYQGCQQLLAPIKLELVKHDLLVPLPSNTTDKNQINDLRIRIAQRILEIGALSS  
LLTNNYSGFENYFAQLRPFYSNPKLHNLQKVHINTDITKIIISLYLLYLLSQGLISKFHVELEVIYNSSQ  
YDAQQDKYLQFPINLESNLMEGNYIKIWKLLKEEKNLPCQEYTHFVDTLINALRFEIAKSLEKTYDSIP  
ISNCKNLLYLPQELSDANFEKTLKETVQVDNWKFDGVIYFTKNENETNVDNQSVIKNLLGYAEQIESI  
V

YGL080W\_homolog 354bp public: 1..354 (SEQ ID NO 423)

ATGTCATCATTTTAAAAAATTCAGTATCAAAATTTGGGATTCCTATAGCTGCTATTTTAGATTGAAAAAAGATCCT  
CATTTTTGGGGTCCAGTATCAAAATTTGGGATTCCTATAGCTGCTATTTTAGATTGAAAAAAGATCCT  
GATTTAATTAGTGGACCAATGACTGGTTCATTAATACCTTTATCTTTAGTGTATGAGGTATTCAATG  
GCAGTTACTCCTCAAAATTTATTTATTTGGGTGTCAATTTGTTAATGAATTGGCACAATTGAGTCAA  
GGATTTAGATGGGTAAACATCACTATGATACTTCTTCAAATGATGGTGAAGATACCAAAAAGATAACT  
CAAAATTGA

YGL080W\_homolog 117aa (SEQ ID NO 424)

MSSFKKFTDFLFSKQSLRYVCTTHFWGPVSNFGIPIAAILDLKKDPDLISGPMTGSLILYSLVFMRYSM  
AVTPQNYLLFGCHFVNELAQLSQGFWRVVKHHYDTSSNDGEDTKKITQN

YGR070W\_homolog 4146bp public: 1..4146 (SEQ ID NO 425)

ATGTCGAGTAATAGTTCTTGGTCTAACAACGATTCTTACCAACTGAGGAACAATCCTAATAATGGTAAT  
AACCATAACCCACATTTAATGTCAACAACACTCACAATCTGTAAATATTCCTTCTCATTTGTTGCCT  
CAAGCATTTATAGAACAACAACAACCACCACAACCACAACAATATCCGCAAGACGGCCAA  
GCTCATAACAAAAACCACCAATCAATAATCGTTTCATCAATCACAACCACCACAACCTGCGCCATCAA  
TACATCCCATCCAAACAAGAACAATGCAACAACCTTACCCAACTGCCGAACAATAATCAACACTTT  
CCTCCACCACAGGAAAGATCATATAGTTTTTCATCGACTATGGATCCTGGCTCACCTAGCAAAATGACG  
CCACCTAATTTTTTCAAAAGGAACCAATCATTTTTCTGGCTACCAACAACCACCACCACAACAACAG  
TATCCGCAGTCACCCCATATAAGGCATATAACCAACAACCCACACTCACCAGGTGGACTTCAACAGCCA  
TACATTGCGCAAAGACAAAACATGCCACCTGGATATATTAACCAGAATCCATATTCTCAGCAAAATAGA  
TCAGTATCATCTTTGACTCAAGATAGGACAGGACACAGTACAACACCTTCCTTATCCTGTCAACAAT  
GATGATCCTGGATATCAACTACAACCCTGGCAATTCATACACACCCACCACAACAACAACAACA  
CAACAGCCTCCACTCCAGACACGTAGACAACCTCGTAAGGCCCTTCGAGCAACTTGCCCCAATTCAA  
ACTGATCAAGTTTACTATAGCCCTGATGCTAGAAGAATTGTTTCCACACCTACACACCAGCAGAATTTT  
CCCCTCCCATACCACCAGAAGCTAGAACAAAATCACTTACTTCGGCATCATTTAAACACCAGAAACAA  
CCACTGCAACCTCTGCAACCATATTTCCAACAATCTCTGAACTGCCAGGTAAAGACAGCAACGCTCGT  
AATTCCTCCAGCAGTTCCCTTCATCATACATTTCTTAACCTCAAAATCGCGATCATTTACATCTATC  
AGTAAATTGTCGTCCTTATCAACTAAGAAATTCGGTTCTCTTCATCCGTCAATACCAACAATAATGAT  
CGTTATCAATCCAGTGGAATATTAGAAACAATCACAATCATAACCACACCAACCAAACTAGCCACAAC  
ATTCAATTATGCTAAACCATCAGTATATCCGCAATTTTATCTGAAGTGGCCAAATTTGTTTAAAGAGGCG  
ATTATTTTGACGATCAACACCAAGGATGGTTTGAATACCATGATACCTTTACCGGGAAAATGGCAGTT  
GATATATTATGTCGCATTATTGGAACAAATGATCGTAACCTGGCCTTGTTATTGGGAAGATCATTTAGAC  
GCTCAGAAGTTTTTCCATGATGTTTACTTACAATCATAGATTAAGGGATTCCGGTACATGAAATTTATGCC  
TTTAAACAATGTTTATAATGATGTTGATTTTTTCAACGAAGAAAATGGAGGAGCTGGTCTGGTTAGCAAT  
GGGGAATAAGTGCATTAAATTTCAAACATGGGTCTGTTCTTGATAGCAGCACACAGTTACAGAATGCT  
TTGAATGACCATATATCCGATTATCATACCTCACAAGCAGTGGATCATTAATAAAATTGCTAGTAGT  
GCCACTGGTAATGGTTTCAGTAGGTGTTGCTGGTAAGGAGTTGAGTGCAAGTCAACAAACAGGTGTTAAT  
GGAGTTTTCATATTTTGACAGAATGTTATTCGCCCATGTAGCAGAAATAGTCTTTGTTACAGTATT  
GCCTGTCCAAGAAGATTAGAGCAACAAGCTAGATTAATTTGAAACCTCAAGGTGGTTGCAACGTGCT  
GTTTCAAATTTATCATTGATGATCAGGAAGAAACCGAACTTTATGGCACAAGACTGTACCTCAATCA  
GTTTTAGATAAATTAGACAAGCATGAAAAGACTCGACAAGAATTGATTTATGAATTTGTTTATACTGAA  
CGTGAATACGTCAGGATTTGGAATTTATGACTGATTTCTACATTATGCCGTTACGAAATCCTGCCAAT

137/251

AATATTATTCCTGATTACCAAAGAGAAACATTTATTCAAACCTGTGTTTGGGGGAGTGCCTGATTGTGTTG  
AGATTGGCCAAGAGACTCAGTGAAGCATTAAC TCGAAGACAACAACAACAAAAGCCCGTTATTGAGACC  
ATTGGTGATGATTTTTTAGATTATGTTGGTGATTTTGAACCTTTTGTGACATATTCTGGAAATAAAGTG  
TTTGCTACTTTTGAACATGAAAGACAACAAGTTAATATGAAATATGCTAGATTCTTAGATGCGATT  
GAAAAGAAACCAGAATCGAGAAGACAAGATTTATCATCTTTTAAATTAAAGGGGTTCAAAGACCAGCA  
AGATAACAGTTATTGTTATCGGGTATTTTGAACATACCAAGCCAGAGTCACCCGACTACAAGTATTTG  
ACGAAAGCAAAAGAAGAGATTGAGAAATTATTGGTGAAATCAATATCCAACTGGGGAATGTACTGAT  
CGACACAAAGTCATGGTTTTCATAGGTTATTGGGCAAAACAACTTTGGAAAATAGGTTTAAATTCAAA  
TTATCCTACAATAATCGTATTATCTATCAAGTGACTTTGAATAGAAAGAGGGATAACGAAAAAATTGAT  
TTATACTTGTGTTGAACATGCGTTGTTATTAGTGAAACACAAGATTCAAAACAAGCGTGAACAACATAAA  
GTATTTGAAAAACCAATGTATTTACCATTGTTATTTGTCAATAGTGGTATGGAGATCCCACTAATAGA  
ACAATCATGCCTCATAGATACCATGGATCCTTGGTATCTGATACTAGTATAAGACCTCAAAGAGCGAGAA  
TCTAATTATATTGGTAATACTTTGAATTCCTCATCAACACCTAAATTCCAATTGAATTTTTTTGGGTTA  
GGTAGTAATCAAGTTCACGCCTCATTATTGCTGATGACTTGACTATTGAGAACCAAGTGTGCTGCAA  
ATATCGGCCCCAACAGAAGAAATTAATTGATGCTAATGACATTTTTTCATTGTGTAAATTTGAAACGAGA  
AGATTCACTGGGAATAATAAAATCAATTGTGCTGTTCTTGTATGGTGGGAAGAAATTTGTGTATGGT  
ACTGATTACAGGGGTATGGGTTAGTACTGTTCTGTTCAATTAGTGCCACATCTAATGAAAAAATCTGTAGT  
GATCCCACTATGGTCATTTCCAAAACCTTATGTCACCTCAAATTGAAGTGATTGTTGAATACTCCAAGTTG  
TTAGTATTGAGTGACAAATCATTATATGAATTTGATTTATCTTGTACCGATTCTTTGGATCATGTGAAG  
AATACCAAACCTGGGGAATTTGCTTTTGAGTCATGTGTCTATTTTCAAAGTTGGTGTGTTGTATGGGAAA  
TTGCTAGTGATTGGTGCTAGAACAGGTAGTCTGCATTCAATTTGTATATTTGAGCCTGTTAATCCATTT  
GATAAATCGAATAAGAATAAGAACAAGAGATTAGAAATTCAAGAAATTAATTTTCAGTTCTGATCCAAAT  
TCCATCTCATTTTGAAGACTAACTTTGTATTTGGGTGTGCTAAAGGTTTGAATTTTATCTTCTCAA  
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GTGACACCATTAGCAATTCATCGATTAGGACGTGATTTCTTATTGTGTTATTCTGAATTTGTATTTTGT  
ATCAATCGAAATGGATGGAGAACAATCATGATTGGGGGATATTTTGGGAAGGTAATCCACAAAATGTT  
GCGATTTTCTTCCCTTACTTGTATCATTTGAACCTGGATTTGTTGAAATTAGAGATTTGCATACAACT  
AATTTATTAAGAGCTTTAACGGGAGAGAATATTAGATTTTGCATTGCAACGAACATGAAGCTATGTTT  
GCTTGTGAAGAAAATGGATATGATATTATTATTTCCATTGATTCTTGAATTTGAAACCAAGTCTCCA  
ACATAA

YGR070W\_homolog 1381aa (SEQ ID NO 426)

MSSNSSWSNDSYQSRNPNMNGMNHNPMLMSQQHSQSVNIPSHLLPQAFIEQQQQPPQPPQPPQYPODGO  
AHNKNPPIINRFHQSQPPQSRHQYIPSKQEOMQOPYPTAEQNNQHFPFPQERSYSFSSMTDPGSPSKMT  
PPNFSQRNQSFSGYQQPPPPQQQYQPSPHKAYNQTHTHQGGLOQPYIAQRQNMPPGYINQNPYSQNR  
SVSSLTQDRTGAPVQHLPPVNMDDPGYQLQPSAIQSHHPQQQQQQPPPLQTRRLRKAPSSNLPPIQ  
TDQVYVSPDARRIVSTPTHQNFPTPIPEARTKSLTSASLKHQKQPSQPSQPYFQQIISESPGKDSNAR  
NSSSSSLHHTFSLTSKRSRFTSISKLSLSTKKFGSSSSVMTNKLDRYQSSGTIRNNHNNHNNHTNQTSHN  
IHYAKPSVYPAILSEVAKLFKEAIIILTINTKDGLEYHDTFTGKMAVDILCRIIRTNDRNLALLLGRSLD  
AQKFHFDVTYNHLRDSVHEIYAFNNVYNDVDFNEENGAGSVSNGENSALNSKHGSFLDSSTQLQNA  
LNDHISDYHTSQSSGSLTKIASSATGNGSVGVAGKELASQQTGVNGVFTILTETCYSPTCSRNSLCYSI  
ACPRRLLEQQARLNLKPQGGLOQRAVSKLSLHDQEETETLWHKTVPQSVLDKLDKHEKTRQELIYEFVYTE  
RDYVKDLEFMTDFYIMPLRNPANNIIPDYQRETFIQTVFGGVPDLLRLAKRLSEALTRRQQQKQKPIET  
IGDVFLDYVGDFEFVYTSNKNVFATFEHERQQQVMKYARFLDAIEKKPESRRQDLSSFLIKGVQRP  
RYQLLSGILKHTKPESPDYKYLTKAKEIEKLLVKINIQTGECTDRHKVMVLHRLLGKQTLNRFNFK  
LSYNNRIIYQVTLNRKRDNEKIDLYLFEHALLVKHKIQNKREQHKVFEKPMYLPLLFVNSGMEIPTNR  
TIMPHRYHGSVSDTSIRPQRAESNYIGNTLNSSSTPKFQLNFFGLGSNQVHASLFADDLTIQNVLSQ  
ISAQKKLIDANDIFSLCKFETRRTGMNKNINCAVPCYGGKKLLYGTDSGVVWSTVRSISATSNEKICS  
DPTMVISKTYVTQIEVIVEYSKLLVLSDKSLYEFDLSDTSLDHVKNTKSGKLLLSHVSSFVKVGCDGK  
LLVIGARTGSSHSICIFEPVNPFDKSNKNKNRLEIQEINFSSDPISISFLKTKLCIGCAKGFELSSQ  
TGTKESILDEADPSLDFATQRESVTPLAIHRLGRDFFLLCYSEFVFLINRWRTNHDWGIWFEGNPNQV  
AIFFPYLLSFEPGFVEIRDLHTTNLLRALTGENIRFLHSNEHEAMFACEENGYDIIISIDFLNLKPKSP  
T

YGR132C\_homolog 966bp public: 1..966 (SEQ ID NO 427)

ATGCTCATTATTGACACCAAAATAATTTCTTCACCTTTTTTTCTTCTTTCTTTCTTCAAGACAAGC  
ACAGTTCTTCTCCCTCTGCTACTGCTAAACGTCCTCAATCAAACACTATGTCACAACGAATTGCAGATTTT  
GTTTCTTAAATAGCCTTGCCAGCTGGTATCACCATTGGCACAATCAGCCTTGATGATGTTCTCT  
GGGGGTAAGCGTGCAGTTATATTTGACCGTTTAAAGGGGTCAAACAGGGAGTTATTGGCGAAGGTACC  
CACTTTTTTGGTGCCATGGTTACAAAAGGCAGTGATATTTGATGTTAGAGTTGAACCACGAGTAATTA  
ACCACTACAGGATCTAAGGATTTACAGAATGTTTCATTGACATTGAGGGTGTGAGTAGACCCGAAGTA  
AGAAAATTGCCTACTATTTACCAAACCTTTGGGGTTGGATTACGGGGAAAGGGTGTGCTGCCATTGGT  
AATGAAATTTGAAATCGATTGTGGCACAATTTGATGCTGCTGAATTGATCACCCAGAGAGAGGTTGTT

TC TCGCCAGAATAAGACAAGAGTTGTCAAGAAGAGCCGCAGAGTTCAATATAGAATTGGAAGATGTGTCTG  
ATTACACATATGACATTTGGTAGAGAGTTCAACAAAGCCGTGAAAAAGAAACAAATTGCACAACAAGAT  
GCAGAAAGATCAAAAGTTCCCTTGTGGAGAGAGCAGAACAGGAAAAAGAGGCTGCGATTATCAGAGCTGAA  
GGGGAGGCCGAATCAGCAGACGTTGTTTCCAAGGCGTTGGCCAAAGCTGGGGATGGGTTATTGATGATC  
AGAAGATTGGAGGCATCAAAGCATATGCATCAACATTGGCCCACTACCAAAATATCACTTTATTACCT  
AATGGTGGCGCTGGCGCGCAGGATAGCGACGGGTCCAAAAAATCATTTATTGGTGAATATTGGCCGCTTAA

MLIIDTKIISSPFFSSFSFFKTTSTVSSPSLSLNQVSNMTMSQRIADFVSKIALPAGITIALAQSALYDVP  
GGKRAVIFDRLKGVKQGVGIGETHFLVPWLQKAVIFDVRVEPRVITTTTGSKDLQNVSLTLRVLRSPEV  
RKLPTIYQTLGLDYGERVLPAIGNEILKSIQAQFDAEELITQREVVSARIRQELSRRAAEFNIELEDVS  
ITHMTFGREFTKAVEKKQIAQDAERSKFLVERAEQEKKAAIRAEAGEASADVVSKALAKAGDGLLMI  
RRLAESKDIASTLANSPNITYTLPPNGGAGGSDSGSKNSLLLNIGR

ATGTTCAAGAAGATACGATTCAAGAACCACATATTTTTCACCAGAAGGTAGATTATACCAAGTGGAAATAT  
GCTCAAGAAGCCATATCCAATGCTGGTACAGCCATAGGGATATTATCTCCTGAAGGTGTCGTTTTCAGCG  
TGTGAAAAGAAAGTCACCTCCAAGTTATTGGACGATGATGGATCAGCTGAAAAAATTATACATTATCAAC  
GATCAAAATGATTTCGCGCTGTTGCTGGTATGACTGCCGATGCATCAATTCTTGTGAATAATGCAAGAAATT  
CAAGCCCCAACGATTTTGAAGTTGTACGACGAAGAGATTCCTTGTGAAATGTTGATCAATCGTGGTTTGT  
GATGTCAAAACAGGTTTATACCCAACATGGTGGGTTTGAGACCAATTTGGTGTATTAGTTTTCCTTTATGTCGGG  
TATGATGACAGATATCAATTCCAATTGTTTACATCGAATCCTTCTGGTAATTACAGTGGTTTGAAGGCCA  
ACTAGTATTGGTGTCTAACAATTCGCTGCTCAAACTTTATTGAAGAAAGATTACAAGGACGATTTGACT  
TTAAAAAGATGCATGCGAATTGGCTATCAAGGTTTATCAAAAACTATGGATGCTTCAAACATAAATAGT  
GAAAAATTAGAATTTCGCTACCTTAAGTTTGGGCAAGACAAACAAAGTGTGCATAAAATTTGGAACGAT  
AAAGATATTGACATCCTTAATTTAAGGCTTCGGGGTTTTGAACGAAAAAATAGCCGATGATGAATAG

MSRRYDSRTTIFSP EGRLYQVEYAQE AISNAGTAIGILSPEGVVLACEKKVTSKLLDDDDGSAEKLYI IN  
DQMICAVAGMTADASILVNNARIQAQQYLKLYDEEIPCEMLINRVCDVKQGYTQHGGRLRPFQVSVFLYAG  
YDDRYQFQLFTSNPSGNYSWKATSIGANNSSAAQTLLKKDYKDDLTLKDACE LAIKVLSKTM DASNINS  
EKLEFATLSLGKDNKVLHKIWNDDKDIDILIKASGVLNEKNSDDE

ATGACATCTCAAAAACAAACCACCGCCTTAAAGAAAGATATTTTAGAACTTATTGGTAATACCTCCATTATGTCAAAATTGAACAAAATTCCACAATCGTTGGGAATTAAAGCCAAGGTCTATGCCAAAGTTGAATTATTC AATGCCGGGAGGATCAATTAAAGATAGAAATTGCCAAAAATATGGTATTGGAAAGCCGAAAAACAAGGTAAA ATCAAAACCAAGGCTATACCTTTGATTGAACCAACCTCAGGTAATACCTGGTATTGGTTTGGCTTTGGTTGGG GCCGTTTCGTTGGATACAGAACCATTACCTTACCAGAAAAAATGTCAAACGAAAAAGTTTCTGTTTTG AAGCCCTTAGGTGCTGAAATCATTAGAACTCCAACCTGAAGCTGCATGGGACTCTCCAGAATCTCATATT GGTGTTGCTAAAAAATTGGAAAAAGAAATACCAAACCTCTATTATTTTGGACCAATATGGTAACCCAGCC AACCCAGATGCTCATTTATTATGGTACTGGTTATGAAATTTTGGGAACAAACTGAAGGTAAAAATTACTCAC TTGGTTGCTGGTGTCTGATCTGGTGGTACCATCAGTATGGTATTTCCAAATACTTGAAAGAAAAAAATTC TAAATTCATGTTACTGGTGTGCTGACCCAAAAGGTTCTATTTTACGTGAACCAAGTAATCTTTAAATAATTC ACCGAAGGTTACTTTGGTTGAAGGTATTGGTTATGATTTTTATTCCAGATGTGTTGAACAGAAAAATATGTT GATGATTGGATCAAAACAGATGATGCTGAATCTTTTAAATTGGCTAGAAGAATTATTAGAGAAGAAGGT ATTTTGGTTGGTGGTTCTTCTGGTTCTGCCCTTACAAGCTGCTTTACAAGTAGCTAAAGACTTGACTGAA GACGATACCTGTCGTTGTTGTTTTCCAGATTCATCAGATCTTACTTGTCTAAATTTGCCGATGACGAA TGGTTAATCTCCAATGGATTCTGAAGTTGAAGATTACCCGGGTGCTAAACAGGCTGACGAATCTTGAAT GGTAAAGACTATCAAGGATTTGGTTGCTGGCAAAGCTCCAGTTGCTACGTGCATTTTACTCTGACACAGTT GCCAAGACTTTTTGATTTATTGCAATCCAATGGGTTTGATCAATTGCCAGTTTTTGAATAACTCTGGAAGA TTAGTTGGTTTGATCACCTTTATCCAAGATATTGAAATCTTTATCCACTAAAAAGATTCAAACGACCAAT TCAATCAGTTTCGATCATCATTTGATTTTCAAGAAAGTTGGCTGATTTTGAAAAATCTTTACCATCACTAAA AAATCAGGATTCACTAAGAGAAGTTATGAACCAATCAAGTTGGACACCCCATTAGCTGCTTTGAATAAA TTCCTTGAACCAATTCAAATGCTTATAATCACAGATGATGAATTGAACCAAGTTCAAATTGTTACTAAG GTCGAATTTGCTTTTCGTATTTTGAACATAAAACCGCTAGTTTTTAA

MTSTNKPALKEDILELIGNTPLVKLNKIPQSLGIKAKVYAKVELFNAGGSIKDRIAKNMVLEAEKQGK  
IKPGYTLIEPTSGNTGIGLALVGAVRGYRTIITLPEKMSNEKVSVLKALGAEIIRTPTEAAWDS  
PESHI  
GVAKKLEKEIPNSIILDQYGNPANPDAAHYHYGTGYEIEWEQTEGKI<sup>1</sup>THLVAGAGTGGTITGISKYLKEKNS  
KIHTVGDPKGSILAEPESLNNSTEGYLV<sup>2</sup>EGIGYDFIPDLNKRKYVDWDWIKTDDAESFKLARRIIREEG  
ILVGGSSGSLQAALQVAKDLTDDTTVVVVFPDSIRSYLSKFADEWLI<sup>3</sup>SNGFEVSDSPGANKADEFLN



139/251

GKTIKDLVAGKAPVVTVTLSDTVAKTFDILLQSNQFDQLPVLNNSGRLVGLITLSKILKSLSTKKIQTNN  
SISSIIIDFRKLADFEKSFITTKKSGFTKRSYEPKLDTPALALNKFETNSNAIITDDELKPVQIVTK  
VDLLSYLTKNASF

YHR138C\_homolog 384bp public: 1..384(SEQ ID NO 433)

ATGAATCAAAATAAGAAATTAAGTGGTTTAAATATTATTAGCGATTATATCAATCATTACTTTATTCAAC  
TTTAAACAATTTCCCAAATAACTGCCATCAGATCATTGTCTCCCCCTGCCCTCTTCCACCGCTACTAAT  
ACTAATACTAAATCAACAATGTCAGATTCCAAAGGTTACATTATCACTTTGAAAGATACTTGTGCTGAT  
TCCGAAGCTAGTTCAATTAAATCAAAGATTACTGAATTGGGAGGTAAAATCACTAATGAATTTAGTTTA  
ATCAAAGGATTTTCTGCTCAATTGCCAATATCCATGCTGAAGCTTTACCTAAAGATTTTGTGCTGGTATT  
GCCAATATTGAAGAAGATGGTGAAGTTCGTACACAATAA

YHR138C\_homolog 127aa(SEQ ID NO 434)

MNQNKLTGLILLAIISIITLNFNFKTISQITAIRSFVSPASSTATNTNTKSTMSDSKGYIITLKDTCAD  
SEASSIKSKITELGGKITNEFSLIKGFSQQLPTIHAEALPKDFAGIANIEEDGEVTRQ

YHR179W\_homolog 1212bp public: 1..1212(SEQ ID NO 435)

ATGACAATCGATAACGAAGGCATTGTCAATTAAACCAATTGGGTTCAACAAAATTATTCCAACCAATAAAA  
CTTGGTTTAAACACTTTATCACAAAGAATAGCATTTCACCATCCACACGTTATAGAGCAACCAAAGAT  
AATATCCCTACCGATTACAAATTAGAGTATTATTCTCAACGATCAGAAATATCCTGGAACTTTAAATCATT  
ACTGAAGCAACTTATACATCACGTCAGGTGGATTAGTACCATATGTTCTCGGGATTATATAATGATGCT  
CAAACTAAAAGTTGGAAGAAAATTAATGATGCGATTTCATGCCAATGGAAGTTTCAGTTTCAGTTCAATTG  
TGGTATTTAGGTAGAGTTGCTAATCCTAAAAATTTGAAAGATGCTGGATTACCATTGTGTTGGAGCCTCA  
TCAGTTTATTGGAAATGAAGAAAGTGAAAAATTTGGCCAAAGAAAGCTGGAAATGAATTGAGGAATTGACA  
GAAGAAGAGATCGATCACATTGTTGAAGTTGAATATCCGAATGCTGCTAAACGTGCCATTGAAGCAGGA  
TTTGATTATATCGAAGTGCATTACGCTCATGGTTACTTGTAGATCAATTTTAAATCTTGCCTCTAAT  
AAAAGAAGCTGATAAATATGGTTGTGGTAGTATTGAAAAATCGTGTCTCGTTTATTATTAGAATTATTGAT  
AAATTGATTGATATAGTTGGAGCTGAAAGATTAGCTATCCGTTTATCACCATGGGCCACGTTCCAAAAT  
GTTGACGTCGAAGGAGAAGAAATTCATAGTTATATCATTGATCAATTACAAGAAAGGGCAAATCTGGT  
AATGAATTTAGCGTATATTTCTCTTGTGTAACCAAGCTGTTCAAGCAAGTTGGGATATTGCTAAAGAGAAT  
CAAGTTGGCTCAAATGAATTTATTTTGAACATTGGAAGGGGAAAGTAATTAGAGCAGGTACTTATGCT  
CATGAATTAATAAAAATTAATGAAGATATTAATAATGATAGAACTTTAATTGCCTTTTCAAGATTTTTC  
ATTTCTAATCCTGATTTTAGTGAAAAATTTACATGATGGGATTTCTTTGACTCCTTATGAAAGAGCAACA  
TTTTATAATCATGATAATTTTGGATATAATACTTGGATTAAATATGGAGAAAAATAAAGTTTTCATGAA  
CAAGAAGAAAGGAAAAAATTGGGTAAACCTTTAGCTTAG

YHR179W\_homolog 403aa(SEQ ID NO 436)

MTIDNEGIVIKPLGSTKLFQPIKLGFNLTLSQRIAFAPSTRYRATKDNIPTDLQLEYYSQRSEYPGTLII  
TEATYTSRQGLVPYVPGIYNDAQTKSWKKINDAIHANGSFSSVQLWYLGRVANPKNLKDALPFGVGS  
SVYWNEESEKLEAGNELRELTEEEIDHIVEVEYPNAAKRAIEAGFDYIEVHSAHGYYLLDQFLNLASN  
KRTDKYCGSLIENRRLRLRIIDKLIDIVGAELAIRLSWPATFQNVVDVEGEEIHYSYIIDQLQERANSF  
NELAYISLVEPRVQASWDIAKENQVGSNEFILKHGKGVIRAGTYAHELNKINEDINNDRTLIAFSRFF  
ISNPDLVKKLHDGILSLTPYERATFYNHDFGYNWIKYGENKVFNEQEERKKLGKPLA

YIL074C\_homolog 1392bp public: 1..1392(SEQ ID NO 437)

ATGTCATCTCCTCAACAAATGTCAACTCATTCCAACAAGCCTTGAATTTATCAGGATCTCCAATGCT  
GTTTCTACATCACCAACTCAATCATTCTTGAGTCAATATGTTCCAAGCAAGCCAGCTAAAGCTTTGAAA  
CCTTTCAAAACTGGTGATATCAAAATTTTATTATTGGGAAATGTTAACCAAACTGCCATAAATATTTTC  
AAAAACCAAGGTTACCAAGTTGAATTTTATAAATCATCATTACCCGAAGATGAATTATTAGAGAAAATC  
AAAGATGTTTCATGCCATTGGTATTAGATCAAAGACTAAATTAACAGAAAAAATCCTTAAAGCTGCTAAA  
AACTTGGTGGTTATTGGTTGTTCTGTATTGGTACCAATCAAGTTGATTTGGAATTTGCTGCCAAATCA  
GGTATCGCTGTTTCAACTCTCCATTTTCAAATTCATGATCAGTTGCTGAATTAGTCATTGCTGAAATC  
ATTACTTTGGGTAGACAATTGGGTGATCGTTCAATCGAATTGCACACTGGTACTTTGGAATAAAGCTCAGT  
GCCAAATGTTGGGAAATCAGAGGTAAAATTTGGGTATTGTAGGTATTGGTCACATTGGTTCCCAATTA  
TCTGTCTTGGCTGAAGCTATGGGTATGAATGTTATCTATTATGATGTCATGACCATTATGCTTTAGGT  
AACTCGAAACAAGTTGAAAGTTTGGACGAATTGTTGAAAAAAGCCGATTTCTGTTACTTTGCACGTCCCA  
GCTACTCCAGAAACCAAGAATTTGTTGAGTGTCTCCACAATTTGCCGCTATGAAAGATGGTGTCTTACGTT  
ATAAATGCTTCTAGAGGTACTGTTGTTGATATCCAGCTTTGGTTCAAGCCATGAAAGCCGGAATAAT  
GCTGGTGGCGCTTTAGATGTTTACCCTCATGAACGACGAAAGAAATGGTGAAGGTTTATTTCAGTGATAGT  
TTGAATGAATGGGCCAGTGAATTTGTGTTTCATTGAGAAATGTGATTTTGACTCCACACATTGGTGGTTCT  
ACCGAAGAAGCCCAATCTGCTATTGGTATTGAAGTTGGTAATTCATTGACCAAATACATCAACGAAGGT  
GCCTCTCAAGGTGCTGTTAACTTTCCAGAAAGTTTCATTGAGACCATTAGATTTGGATCAACAAAATGTT



140/251

GTCAGAGTATTATATATCCATCAAAACGTTCTGGTGTGTTGAAAACGTGCAACAATATCTTATCCAAT  
CATAACATTGAGAAACAATTCTCCGATTCTCAAGGTGATATTGCTTACTTAATGGCCGATATTTCTGAT  
GTTGATATCAGCGATATACAGTCATTATATGAACAATTAGAACAAACTCCATATAAAATTGCTACTCGT  
TTGTTGTATTAA

YIL074C\_homolog 463aa (SEQ ID NO 438)

MSSPQQIVNSFQQALNLSGSPNAVSTSPQSFLSQYVPSKPAKALKPFKTGDILKILLLENVNQTAINIF  
KNQGYQVEFYKSSLPEDELLEKIKDVHAIGIRSKTKLTEKILKAAKNLVVIGCFICGTNQVDLEFAAKS  
GIAVFNSPFSNSRSVAELVIAEIIITLARQLGDRSIELHTGTWNKVSAKWEIRGKTLGIVGYGHIGSQL  
SVLAEAMGMNVIIYDVMTIMSLGNSKQVESLDELLKKADFVTLHVPATPETKNLLSAPQFAAMKDGAYV  
INASRGTVVDIPALVQAMKAGKIAGAALDVYPHEPAKNGEGLFSDSLNEWASELCSLRNVILTPHIGGS  
TEEAQSAIGIEVGNLSLTKYINEGASQGAVNFPEVSLRPLDLDDQNVVRVLYIHQNVPGVLKTVNNILSN  
HNIEKQFSDSQGDIAYLMADISDVIDSDIQSLYEQLEQTPYKIATRLLY

YIR037W\_homolog 486bp public: 1..486 (SEQ ID NO 439)

ATGTCCTCAATTTTACGAATTAGCTCCAAAAGACGCCAAAGGTGAACCATATCCATTTGAACAATTGAAA  
GGGAAAAGTTGTCTTATCGTCAATGTTGCTTCCAAATGTGGATTCACTCCTCAATACAAGGTTTAGAA  
GAATTGAATAAGAAATTTGCTGATCAACCAGTACAAATCTTGGGTTTCCCATGTAATCAATTTGGCCAC  
CAAGAACCAGGTAGTAACGAAGAAATTTGGATCATTCTGTTTATTGAACACGGTGTACATTCCCAGTC  
TTGGATAAAATTTGAAGTCAATGGTGACAATACCGATCCAGTTTATAAATATTTGAAATCACAAAAGAGT  
GGTGTTTTGGGATTGACCAGAATTAATGGAATTTTGAAAAATTTCTTGATTGACCAAAATGGTAAAGTT  
ATTGAAAGATTCAAGTTCATTGACTAGTCCAGAAAGTATCGGTACCAAGATTGAAGAATTGTTGAAGAA  
TAA

YIR037W\_homolog 161aa (SEQ ID NO 440)

MSQFYELAPKDAKGEYPFPEQLKGVVLIVNVASKCGFTTPQYKGLEELNKKFADQPVQILGFPCNQFGH  
QEPGSNEEIGSFCSLNYGVTFPVLDKIEVNGDNTDPVYKYLKSQKSGVLGLTRIKWNFEKFLIDQNGKV  
IERFSSLTSPESIGTKIEELLKK

YJR096W\_homolog 849bp public: 1..849 (SEQ ID NO 441)

ATGTCATATCGATTAAATCAAACCTCAATTCGGTCATACCATTCATCAATTGGATTAGGATGTTATGAT  
ATCCCAAGAAATAAAACGGTTTCGGTAGTTTATGAAGCTTGTAAGTTGGATATCGTCATTTTGATACT  
GCAGTGTTATATGGAACGAAGAAGATCATTGAAGGTATAAGTAAATCTTACGAGAGAACCCCAAT  
ATACCACGATCTGAGTTTTTTACACCACAAAGCTTTGGAATAATCAATTGGGTACTTCAAGCACTAAA  
CAAGCCATTTCAACAATGATGGCTCAAGTTGGTGATAAATTAGAATATATTGATTTATTATTGATTCAT  
TCTCCATTACCAGGTAAGACCAAACGTTTAGAAAGCTGGAAAGTTTTCGAGGATGCTGTGGAAAAAGGA  
TGGATTAAAAACATTGGGGTTTCTAATTATGGTAAACATCATATTGAAGAATTGTTGACCAATGCAACG  
ATCCCTCCAGCTGTCAATCAAATTTGAAATTAGTCCTTGGTGTATGAGACAGGATTTAGCTACTTGGTGT  
TTAAGTAAAGGTATCAATGTTGAGGCATATGCACCATTAACCCATGGTAACAAATTACAAGTCAACAAT  
ACTGAATTTCAAGAAATTATGCAAAAGTATAAATCAATCAGCTGCTCAAATATTGATTAAATGGTCAATTA  
CAAAAAGGTTATATACCATTACCAAAAAACAAAACCTCCATCTCGATTAAAGGAAATCTTTCTGTTGAT  
GATTTTGAATTGACTAATGAAGAAATTAAGGCTATTGATCAACCTGATGCTTATGAACCAACAGATTGG  
GAATGTACTGATGCTCCATAG

YJR096W\_homolog 282aa (SEQ ID NO 442)

MSYRLIKLNSGHTIPSIGLGCYDIPRNKTVSVVYEACKVGYRHFDTAVLYGNEEVIEGISKFLRENPN  
IPRSEFFYTTKLWNNQLGTSSTKQAISTMMAQVGDKLEYIDLILLHSPLPGKTKRLESWKVLQDAVEKG  
WIKNIGVSNYKHHIEELLTNATIPPAVNQIEISPWCMRQDLATWCLSKGINVEAYAPLTHGNKLQVNN  
TEFQEIMQKYNKSAQILIKWSLQGYIPLPKTKTPSRLKENLSVDDFELTNEEIKAIQPDAYEPTDW  
ECTDAP

YKL196C\_homolog 603bp public: 1..603 (SEQ ID NO 443)

ATGAAGATTTATTACATTGGTATTTTAAGATCAAGTGGAGACAAGGCTTTAGAGTTAACTTCAGCCAGA  
GATTTATCACAGTTTTCCTTTTTCGAAAGAAATGGGGTATCCCAATTCATGACTTTTTCGCAGAAACC  
GTATCCCAAAGAACTCAACCTGGACAGAGACAAAGTGTTGAAGAAGGTAATTATATTGGTCATACTTAT  
ACCAGATCAGAAGGAATTTCTGGTATCATTATAACGGACAAAGATTACCCTGTAAGACCAGCATATACA  
TTAATAAATAAAATCTTGAAGAATATTTATCATTCATCTAAATCTGATTGGGAAAAACATTGATAAA  
GCAAATGAAACTTTACAATATGGACAATTAGAAGCATATTTGAAAAAATATCAAGATCCCACTCAAGCT  
GATTCAATCATGAAAGTTCAACAAGAATTAGATGATACTAAGGTTGTTTTACACAAAACATTTGAAGGG  
GTTTTACAAAGAGGAGAGAAATTAGATTCATTGGTTGACAAATCAGAAGCATTGTCAAGTTCTTCAAGA  
ATGTTTTTATAACAAGCAAAGAAAACCAATTCTTGTGTGTGATTATGTGA

141/251

YKL196C\_homolog 200aa(SEQ ID NO 444)

MKIYYIGILRSSGDKALELTSARDLSQFSFFERNVGSQFMTFFAETVSQRTQPGQRQSVEEGNYIGHTY  
TRSEGISGIIITDKDYPVRPAYTLINKILEEYLSLHPKSDWENIDKANETLQYGQLEAYLKKYQDPTQA  
DSIMKVQQELDDTKVVLHKTIEGLVLRGEKLDLSVDKSEALSSSSSRMFYKQAKKTNSSCCVIM

YKR076W\_homolog 771bp public: 1..771(SEQ ID NO 445)

ATGGATGACAAAGGGTGGAGATTTCCTACAAAGGAAGAATTGAAGACATTAACAACTGAAGACGACATT  
TCATTAGGTACACCTGACCATAACTATGATTTTTTCCCGTCTTAGAGAATTGTACTTTAAGGCTGAACCA  
GAATACGAGGGAAGATTACAGTTCCAGTATTGTGGGACAAAAAGAAGGTACAATCGTAAACAATGAA  
TCTGCTGAAATCATCAGAATGTTGAATACTGAATTCAATAGTATTTTGCCAAGTGAATATGCCGAAGTT  
GATCTTGTTCCTCAAAAGACTTAGAATCTCAGATTGATGAATTGAACAGCTGGATTACGATAATATTAAC  
AATGGTGTATTATAAAGCTGGATTTCATCCAAAGCAAGAGGTGTACGCCAAAGAATGTCAAAATGTGTTT  
GATCATTTTGGACAAAGTGGGAAGCCATTTTGGAGAAAAACCACAATGGGTCCAAGAAGGGAGAATTTTGT  
TTGGGCAACCAATTGACTGAAGCAGATATCAGATTGTACACAACAATTATTAGATTGTATCTGTCTAC  
GTTCAACACTTTAAGTGTAAATATTGGTACAATCAGAACTCACTATCCATACATCCACAATTGGCTCAGA  
TTATTGTATTGGAAGATTCTTGGTTTCCAAGAACTACCAATTTTCGAGCACATCAAGTACCACTACACC  
AAATCTCATATCAAGATTAATCCATACGGTATAACACCATTGGGTCCAGTACCAATATTTTACCATTG  
GAAGAAAAGTAA

YKR076W\_homolog 256aa(SEQ ID NO 446)

MDDKGWRFPTEELKTLKTEDDISLGPDPHNYDFSRLRELYFKAEPYEGRFVTVPLWDDKKEGTIVNNE  
SAEIRMLNTEFNLSILPSEYAEVDLVPKDLSEQIDELNSWIYDNINNGVYKAGFASKQEVYAKECQNVF  
DHLDKVEAILEKNHNGSKKGEFLLGNQLTEADIRLYTTIIRFDPVYVQHFKCNIGTIRTHYPYIHNWLR  
LLYWKIPGFQETTNFEHIKYHYTKSHIKINPYGITPLGPVNPILPLEEK

YKR092C\_homolog 1287bp public: 1..1287(SEQ ID NO 447)

ATGGGTGAGTGTGGCTGGGGAGAGGGAATATTTAGCAGCCAGAGGAAAAAGAGACCAAGATTCGTTTTT  
GGGCTCATCTCTCTCTCTCTCTCTCTTACTCACACAAAAGAAGAGCTACGATTAAAGTTTGGCCAAATGGG  
TTGGAAAAAAATTTTTTTTTTAAATTTCTTTTTTACCTCTTAAAGAGTCAATTATTACAACACTACTACCA  
ATAGCAAAGATGAGTTCCAATACTCAAGATTAGTTTTAGCTTATATTAATGATTATGTTTCCAGAAAT  
GAAGAAATTGTCAAAGTTGAAGAAGGCATTATCGAAATTTCTTAGCAGGCAAAGAATTACCAAAAGTTTCT  
AAACAGTTGGAATCCATTATTGATGAAGTGGAAAATCAAGAAAAGAAAAGCAAACCAAGAAACTCATCA  
TCTGATAGTGAAGACTCTTCATCTGAGAGTGAAAGCTCCACTTCGGACAGCGAAAGCTCCTCCTCAGAT  
AGCGACAGCTCTTCCCTCAGACAGTGAAAGTTCTTCCCTCAGACAGTGAAAGTTCTTCATCAGACAGTGAA  
GACAGCGATGACGAGGAAGACAAGGAAGACAAGGAAGCAGAAAAGATAACAAAGACAGCGAAGACAGC  
GAAAACGAAAAAGTGGAAAGAAGACAACAAAGACACCAGCTCTGATTCAAGTTCCAGTTCCGACTCAAAA  
TCTGATTTCAGACTCAGACTCAAGCTCCAGCTCTGATTCAAGTTCTGACTCTGATTCAAGTTCTGATTCC  
GACTCCAGCTCCAGCTCTGATTCCGACTCCAGCTCCAGCTCTGATTCCGATTTCAGACTCAGATTCTGAT  
AGTGACAGTGACGACAATTCCCTCAGAAAGTAGTTCTGAAGACGAAGAATCATCTAGTGATTTCAGAAATCC  
AAAGAGGAACAAAAACAACCAGAAGACAAGAAAAGAAAGCACACAGATGATATCAAAGAAGAAAAACCA  
GTTAAAAAGTTCAAAAACGAGTCAGAAATCATCAGCATCATCTTCTACTGATTCAATTTCTGCAACTCCA  
GAACCAGAAATTAAGCCAGGCCAAAAGAAAACATTTTTCTAGAATAGATAGAAGTAAGATTGTTGAA  
AATTCAGTATTACAAGACAATACTTACAAGGGAGCTGCAGGAACCTGGGGAGAAAAGGCTAGTGAAAAA  
TTATTACAAGTCAGAGGTAAAGATTTACAAAGAATAAAAAATAAATGAAGAGAGGAAGTTATAAAGGA  
GGTAGTATCACTTTAGCTAGTGGGTCCCTATAAATTTCGAAGATTAG

YKR092C\_homolog 428aa(SEQ ID NO 448)

MGECGWGEGIFSSQRKKRPRFVFLISLSLSYSHKRRATIKVCPNGLEKNFFNFHLLKSQQLQLLP  
IAKMSSNTQDLVLAYINDYVSRNEELSKLKKALSKFLAGKELPKVSKQLESIIIDEVENQEKKSKPRNSS  
SDSEDSSSESESSTSDSESSSSSDSDSSSSSDSESSSSSDSESSSSSDSESDDEEDKEDKEAEKDNKDS  
ENEKVEEDNKDTSDDSSSSSDSKSDSDSDSSSSSDSSSDSDSSSDSDSSSSSDSDSSSSSDSDSDSD  
SDSDDNSSSESSSEDEESSSDSESKEEQKQPEDKKRKHDDDIKEEKPVKKFKNESSASSSTDSIPATP  
EPELKPQQRKHFSRIDRSKVNFEVSVLQDNTYKGAAGTWGEKASEKLLQVRGKDFTKNKNMKRGSYK  
GSITLASGSYKFED

YLR043C\_homolog 312bp public: 1..312(SEQ ID NO 449)

ATGGTTTCACGTTGTCACTGAAGTTAACGAATTCCAAACCTTTTAAAGGAAAAACAACCTTAGTTATTGTT  
GACTTTTTTGGCACTTGGTGTGGTCCATGTAAAATGATGTCTCATTATTAGAAAAATTCAAAATGAA  
TATTTCTAATATTAATTTTTGAAAATTGATGTTGATCAATTTGGGTTCTTTAGCACAGAATATAATGTT  
AGTTCTATGCCAACTTTGATTTTATTCAAAATGGTGAAGAAGTCAATCGTGTCAATTTGGTGCTAACCCA  
GCTGCTATTAAACAAGCTTTGGCTTCTCTTGCTTAA

142/251

YLR043C\_homolog 103aa (SEQ ID NO 450)

MVHVVEVNEFQTLLKENNLVIVDFVFATWCGPCKMIAPLLEKFQNEYSNIKFLKIDVDQLGSLAQEYNV  
SSMPTLILFKNGEEVNRVIGANPAAIKQALASLA

YMR273C\_homolog 4938bp public: 1..4938 (SEQ ID NO 451)

ATGTCACCTGCCTAACACGTCATTCATAGCGATTCAAATTTTGAATCAGCTGTACAAGATCTTGAACAA  
GAGAAGAAAATGGTGGCAGCCTTAAAGAGACTATCTATAGGTCATATGATGCAATATGATCCCGACTTG  
CCACCAGGCAGTATGGATGATATTGATCCCTTTGCAACAATAACAACAACAGCAATACCGCTAGTAAC  
AATAACCACTATAATGGTCATACCAGAGATCACACCAGCAACAACAACAATACACACAATCATTCTCCC  
AACTCAAATTTGAACCACCATCGTGGTCAAAGTCCTTATGATGAAGATTTAATTCCACAGAATATCCAC  
AGATCACACTCAACTCGATCAGATCAAAATCACATTCAACTTCTCCTTCTACTTTCGCCTCAACACAAG  
CAACAACAACAACAACCGCAACCTTTCCACATGAACACAGACTCCTCCATATAACAATACCA  
AGCCAGTCAAGAGACGTAGTTTTTACGACAATCCAGCGTGTGACGTGAGAAAGTCACGATATTTTT  
TTCGATGCCGAGGATGAAGTTTATGATAGTTTATCCCTTTGTGTGGGTACCAGCTAACTCTCATCT  
CAAGTGAATCCTGAATCGTTCAAGAGTTTAAATCAAACCTCAAGTGAAGAGATATTGGAAGAAAGCTA  
TCTCGAAAGTCAACTATTTCAAGAAAGTCAACTTTATCACGCAGCTCCTCAACCAGTACCAAAGAGACA  
TTAGCCCCAGAACAGAAATAAGTCCAGAATGGAATGTGATGTGTACCTCCTTCTCCAGTAAGAAAA  
TCTTCCTTGGCTTAACCAATGATGGTCAACAATAAAGAGACGTTTCTCGAAAATCGTCGTCTCGGTT  
TCTTCAACTTCTCCACAAAAGATCCAGCTAAGAGAGAATCTTGGTACTTCAACAACCTCAAAAAGTAC  
CTGAATCCATCATTTGCGAGAGCTAACTTCAGAATTGGAGCAGTTGTCAAAAATGGCGGGGATGGACAAG  
AATGACGCAGTAACTTTGGCAAGAATTTGTGGGCACAATCATTGGGGTATACAGATGTGAAAAATTA  
GCATTTGACGAATTAGATAGTTCAACAACAACCGCTACTGCAACAACACCCAATTCAGTGGGTTCTCCA  
GGAAGTTATGACTCTGCAACCCACCTCGCACCACGACCTTGCATTTACAACAACGATTACAACATCAA  
TTTCAACAAGCTCAAATCAAGGCAGAAAGGGAGGCAGAAAGATCGACAAGACATCAACAAGCGAACA  
CAGTGGCCAGTATCGAATGACGATAGTCAACAATCTGTGTCACAGTTGACAGCAAGTGAGGGAGGTTCT  
ACTGCTAATGCTTTTACCAGTGCTGGGAGTGGTGTGCTGACTTTGCCTTGAAACGAAGTAGAAGAAGTAT  
TACCGGAAAAAGGAAACAGATTCGAAACAAAAGACTTCGAATAATTCGCCTCCTACAAGAAAGTACAAT  
GTCCGGAATTTCCAGTTGTTATTTAACTACAAGAAACAGTAGATTCTCCTTCGCTGTACCTTCACCT  
TCACCATCTACATCTCAAAGCATGATGGGTACAGGGTGAAACACAAGAAATCTCAAAGGCCATTGGAA  
CAGCATTTGGCTAACCAATGATGGATGGTTAGATATGTACATAACCCGTATCCCACTGCTTCAACC  
ACTATTGATTTTCACTCGTATGGGTGCTAAGAAATCAGCCAGACAATCACTTAGTCCAGAGAATGCAATG  
GATGGCAGATCTCGAACAAGCCCGAAAACAAGACTCATCGTGGCTATCTGCATCAAGAAAGGTCTCAT  
CCTTATCATCAACAACCACAGCCTCAAGTGCAACCTCAAACCCGCCAACAACCTTCCACCAGCACAACA  
GCTCATAGACAATCGACGAGACAAACCCACAATCATCCGAGCACAGGAGTTGAAAAGCATCACCGACAG  
GATAACAAGCGTGTAATGCTGTGAGCTTCTAATACAGACATAAATGATTTTATGGCTCAACTGAATCAA  
TTTCAAGCTAATGGAACAAGAAACCATCGATATGACAACCTCCATAAAAAGGATAAGACTGCATTTTGG  
CCAAATGAAGACCACCAACGTAAGTCCCATTTCGACAAGAAATTCAAATGTAAGAAATTTGTCTTCTCG  
TCTCAACAGCATTTACATCAACCGTATCTGACAACCTTCTGTGCGCCCAAGTCACGTCAACTACATCAA  
AATTTAGACAAGTTGAGATCCGAGATCAATGAATTTAAGGAAAGCTTGAATAAATCGGAATTACCTGGT  
GAGGAATCAAAAAGAGAACACAGACTGCGTCACGACCAGCACCACCAACAACGACAACGACCAGCACCA  
TCACAGCACCAACTTGAGCCTCGCAATTACAACCAATGACCGTCACCAAGACAACAGCATGAACAT  
GTACAACCCCAACAAGTCCAGCCCTTACAGTCAGATAGTATGATTTTATGATCAGTTATCAAGATTTAAGC  
GTTGAAGATCAATTTGGGTATTGAACAGGAAGCATTGAGAGAATTAGGCAAGGAAAAGGGCATTTCAT  
GAGATTGATATAGATGATGCATTTGATGAAAATTTAAANNTCTGCCTATCAATGAACGACATGGCTCT  
CAATTCACACTTGATCATGACATTTTGGACAGCTTTAATTTGGTAGATAATCAGTTGGTTGGATCTGCA  
GATGAAGGAATTGATAATTTGAAGGGTAAGAATGAAATACCCGTTGGGCGACAACAACCACAACAACA  
CGTCAACAACCAAGAGCTGCTTCGCCACCATCTCACAGCAGTACTTGGGGCATGATGAATTGCACTTG  
CAACAAGGTAAAGATACAAATAAAAAAGTTGGTCCCTCGTTTAAAGTATTGATACATTGCAGAACAAGCCT  
ATTCACCTTGAGGAACTGCAACTGGATTTGGAATGAATGCGTTACCTTCCCCTACGTTGCATTTAGAT  
GAATCTCAAATAGCACCTCTGGACATCTGAGAAAGGCAAGCAATTCGCAAGCTACGACGATTACTAT  
AATATAGCCGACAAATCATCTACTGCGGGTACCCCCAAAACAAGAAAGGAGACCAAGTTAAAACGAAA  
TTATTTCAATAAAGACCTAATTTGGAGATTATAGACTCTGATAACTATAAGGAAAAAATGGGCATTGAG  
ACATCTAACAATAAAAAATGAAAAAGAGAAATCTTTTGGTTTGGTTAGTACAACATCATCTGTGGGA  
GCAAATGATACATCTGAAAATGAAGGGCCCAAGAAATGAAAAAGAAAAAGTCGTGGGGCTGGTTGCCG  
GAGCGTTCTGCCAGTGCCTCGTCTGCAGATATCAACAATTTGCCCGCTTTGCCCTTTGATAAACTACCT  
ACAAGATCATTTCTCAAATCCCGAAACGTCAACTGACCAACACCAGAAACATGATCTTGAGAACGGTTCA  
GATCTTGAACGTGAATTGGAACACGAACCTGAACCTTGAACCTTGAATTTGAGTTGGAGCTGGATCTTGA  
TACGAGCAACAAGAAAGCACCAGATGCTTCAATGGTAAATGATTCAAGCTTTGCAAGTTGATTCTATC  
TCTATGAAGTCGACAGACAAGGAAACGTGCTTTCCAAATTTTCAAGAAAAAGGCAAGGTACCAGGT  
TCAAGCTCACAGTCAGTATTTTCAATTTGAATCAAAAAGTTTCAAGGGCCAGCGTCGATGAATCGGAC  
AACGACGCGAAACTGATCAAAAAGAGGGCAACAATAGCAGCAGGTTATTTCAAGAAAGAAATCAAGGGCC  
AAATTTGTCAGAACAGAGAATTCAGTGAATAAGGAAAGCTTCGACCTTTGAATTTAGTGTCAAACGAA  
TCGACAGACGATCGAGGAGAAAGAGAATTTGCGACAAAGTAATGGCACTCGTAAGGCAGAAAGAGTTGAG

143/251

AGTCAAGAGCAACAGGAGGAACAGTTCCCTGTAACCTCGTCGCCGATACATCAATTCAACATTGAACAT  
CTCAAAGACGACTTTGTCACTCTTGGGGAGAAGGACGATGTTTTAGATTCTGGTACTGATGACTTGGTT  
GAAGATGTAAGATCTCGTAACATTCAGAGCACAATAGTTATTGTTGATGAGGATGAAACTCCTATTCAA  
AATAACAATGATAACAAAGATTTGGGGATGCTAAAAGTTGACGAATTGTCCAAAAAGAAATCAATTAGC  
AGGAAAAAACGGAACAATATGCAAAAGAAGAACCTTTCTACTGAACTTACTGATACAAACAAAGAGGTA  
GTAGAGGAGGTTCTTGCAACTGAGCAAAGTGTCAAACCAAGCCAAGGGGAAGATCTTTTGTCTAAGAAT  
GAAGATAAAGAGAAATTAGATATCCAAGAAAAGTTGAAGAAATCAATAAAACGTACATCAAGGGCCAAC  
CAGCCTATTGAGTTTACTGATTACGCCTTTGGGTTCCCTTGGCCACCACCATCTCAATCAACTTTAGTG  
ATGCTTGACTACAGATTTCCAGTTCATGTTGAGCGTGCCATTTATAGATTGTACACACTGAACTTGCT  
AACCTTAAGCGTTCACTAAGAGAGCAAGTTTGTGTTGTCGAATTTTATGTATGCCTACCTCAACTTAGTT  
GATCATACATTACATTTAGAGCAACAAAATATGAGCAGTGAGGATGGCGATCAGATGGAACGTGACGAC  
GACGAAGAAGAAGAAATGACTGACACTGATGAGAAAGACATGATTTTTGGAGAGAGTAATATTGCCGAT  
GACGATGATCTTTATTCCTGAAGAAGCAAATGGTGATTTCGATTGGGATTAACCTTAGATATGGATGGTTTA  
CATAGGAAACAGCATCATCAATCTGGAATCGAAGTATAG

YMR273C\_homolog 1645aa (SEQ ID NO 452)

MSSPNTSFHSDSNFESAVQDLEQEKMMVAALKRLSIGHMMQYDPLPPGSMDDIDPFANNNNNNSNTASN  
NNHYNGHTRDHTSNNNNTHNHSNPKLNHHRGQSPYDEDLIPQNIHRSHSTRSRKSHSTSPSTSPQHK  
QQQQQPQPPFPHEPQTPPYNKSPSPVKRRSFYDNSSVLTSESHDIFFDAEDEVYSSSPLLWVPANSH  
QVNPESFKSLIKTQVEEILERKLSRKSTISRKSTLSRSSSTSTKETLAPEPEISPESECDVSPSPVRK  
SSLSSSSQQNQNEVDVRKSSSSVSSTSPQKDPAKRESWYFNNSKRYSNPSLRELSELEQLSKMAGMDK  
NDAVTLARTLSAQSLGYTDVEKLAFFDELSSQTTATATTPNSSGSPGSYDSANPPRTTTLHLQQLQHQ  
FQQAQIKAEREAERSTRHQSEQQWPVSNDSSHKSSSQLTASEGGSTANAFTSAGSGADFALKRSRRTD  
YRKKETDSKQKTSNNSPPTRKYNVRNSQLLFNYKKPVDSPSSSPSPSTSQSMMGHRVKHKKSKQKPLE  
AALANPMDGSDMSHNPYPTASTTIDFSRMGAKKSARQSLSPENAMDGRSRTKPKENKTHRGYSHQERSH  
PYHQQPQPVQVQPTRQQLPPAQQAHRQSTRQTHNHPSTGVEKHHRQDNKRVMSASNTDINDFMAQSNQ  
FQTNGTRNHRYNLHKKDKTAFLPNEDHQRKSHSTRNSNVRNLSSSSQQLHQPYSTTSVAPKSRQLHQ  
NLDKLRSEINEFKESLNKSELPGEEKREHRSRHDQHHQQRQRPAPSQHQLPRNYNHNDRHQRQHEH  
VQPPQVQPLQSDTSFDISYQDLSDVEDQLGIEQEALRELGEKKGHSHEIDIDDAFDENLKKSPINERHGS  
QFTLDHDLDSFNLVDNLVGSADGIDNLKGKNEIPVGRQQPQQRQQPRAASPSSQQYLGHDELHL  
QQGKDTNKKVGPRLSIDTLQNKPIHPEETATGFGMNALPSPTLHLDSEQNSTPGHSRKASNSASYYDDY  
NIADKSSTAGTPKTKKETKVKTKLFNKDPNLEIIDSDNYKEKMGIIETSNNKKLKKKSFGLLSTTSVG  
ANDTSENEGPKKLKKKSWGLRERSASASSADINNLPLPLDKLPTRSFSPNETSTDQHQKHDLENGS  
DLERELEHEPELELELESDFDYEQQRKHQDASMVNDSSFAVDSISMKSTDKENVLSKFFKKKAKVPG  
SSSQSVFVSFESKSGASVDYESDNDAKSIKKKGNSSRLFKKKSRAKLSEQENSVNKEKLRLNLVSNE  
SQTIEEKENLRQSNGRKAERVESQEQEEQFPVTSSPIHQFNIEHLKDDFVTLGEKDDVLDSDGTDLDV  
EDVRSRNIQSTIVIDEDETPIQNNNDNKDLGMLKVDLSKKKSI SRKKRNNMQKKNLSTELTDNTKEV  
VEEVLA TEQSVKPSQGEDLLSKNEDKEKLDIQEKLKKSIRKTSRANQPIEFTDSAFGFPLPPPSQSTLV  
MLDYRFVHVHVERAIYRLSHLKLANKRSLREQVLLSNFMYAYLNLVDHTLHLEQQNMSSSEDGDQMERDD  
DEEEEMTDTDEKDMIFGESNIADDDDLIPEEANGDSIGINLMDMGLHRKQHHQSGIEV

YNL112W\_homolog 1332bp public: 1..1332 (SEQ ID NO 453)

ATGTCATACAATAACGGAGGATATAATAATAGAAACGGAGGTAGTTACGGTGAGGCTACGGCGGTGGT  
GGTAGCAGAGGTGGAAGAGATGGCTACAGTGGTGGTGGCAGAGGCGGTGGCTACGGTGGTGGTGATAGA  
GATCAAGGTGGATACAGAGGTGGAAGATTCACTGGTGGTGGCCGTGGTGGTGGTAGATTTAATGATGCT  
CCAAGACAAGAATTAAC TGCTCCACAATGGGATTTAGAACAATTGCCAAAATTTGAAAAAATTTCTAT  
TCAGAACATCCAGATGTTGCTGCCAGATCTGATAGAGACATTGAACAATTTAGAAAAGAAAATGAAATG  
ACAGTTAAAGGTCATGATATCCCTCATCCAATCACTTTTGTGATGAAGCTGGTTTCCAGATTATGTT  
TTACAAGAAGTCAAAGATCAAGGTTTCCCTAAACCAACTCCTATTCAAGTGTCAAGGTTGGCCTATGGCT  
TTGAGTGGTAGGGATATGATTGGTATTGCCGCCACTGGTTCGGTAAAACCTTTATCTTATTGTTTACCA  
TCTATTGTCCATATTAATGCTCAACCACAATTACAATATGGTGATGGTCCAATTGTTTTGGTTTTAGCA  
CCAACAAGAGAATTGGCAGTGCAAATTCAACTGAATGTTCCAAATTTGGTAAATCATCAAGAATTAGA  
AACACTTGTGTTTTATGGTGGTGCACCAAAAGGTCCTCAAATTAGAGATTTAGCCAGAGGGGTTGAAATT  
TGTATTGCCACTCCAGGAGATTAAATTGATATTGTTGGAAGCTGGTAAACTAATTTGAAAAGAGTCACT  
TATTTGGTTTTAGATGAAGCTGATAGAATGTTAGATATGGGTTTTGAACCACAATTAAGAAAATTTGTT  
GATCAAATTAGACCTGATCGTCAAACCTTTGATGTGGTCTGCTACTTGGCCAAAAGAAGTGCAACAATTG  
ACTAGAGATTATTTGAACGATCCTATTCAAGTCACCATTGGTTCATTGGAATTGGCTGCTTCTCATACT  
ATTACTCAATTGGTTGAAGTCATTGATGAATTTTCCAAGAGAGATAGATTAGTAAAACATTTGGAATCC  
GCTTTAAATGAAAAGATAACAAAATATTGGTTTTTGTCTTCTACTAAAAGAACCTTGTGATGAAATCACC  
ACTATTTTAAGATCAGATGGTTGGCCAGCATATGCCATTCAAGTGGTGATAAAGAGCAAAATGAAAGAGAT  
TGGGTTTTAGATGAATTCAGAAAGGGTAAAACCTTCTATTATGGTTGCAACTGACGTTGCTGCTAGAGGT  
ATTGGTATGTATAATTTTTAA

144/251

YNL112W\_homolog 443aa (SEQ ID NO 454)  
MSYNNGGYNNRNGGSYGGGYGGGSRGGRDGYSGGGRGGGYGGGDRDQGGYRGGRFSGGGRGGGRFNDA  
PRQELTAPQWDLEQLPKFEKNFYSEHPDVAARSDRDIEQFRKENEMTVKGHDIPHPITTFDEAGFPDYV  
LQEVKDQGF PKPTPIQCQGWPMALSGRDMIGIAATGSGKTL SYCLPSIVHINAQPQLQYGDGPVILVLA  
PTRELAVQIQTECSKFGKSSRI RNTCVYGGAPKGPQIRDLARGVEIC IATPGRLIDMLEAGKTNLKRVT  
YLVLDEADRMLDMGFEPQIRKIVDQIRPDRQTL MWSATWPKEVQQLTRDYLDNDPIQVTIGSLELAASHT  
ITQLVEVIDEFSKRDRLVKHLESALNEKDNKILVFASTKRTCDEITTYLRSDGWPALAIHGDKEQNERD  
WVLDEFKRGKTSIMVATDVAARGIGMYNF

YOL151W\_homolog 1032bp public: 1..1032 (SEQ ID NO 455)  
ATGTCAACACCAATTACTGTTATTGTTTCTGGAGCCACAGGATTTATTGCTCAACACGTTGTTAAACAA  
TTATTAGCTAAAACTATCAAGTCATTGGTACAGTTAGATCAACAGCCAAAGGTGATCATTATTAAAA  
TTATTTCAACAATCCACAAAACCTTATCTTATGAAATTGTTGAAGATGTTGGAAGCTAAAGGTGCGTTTGT  
AAAGTATTACAAAAACATGGAGAAGCAAAAGTGTTCTTACATTTAGCTTCACCATTCCATTTTAAATGTG  
ACTGATGTTGAAAAAGAATTGTTATTGCCTGCTGTTGATGGTACTAAAAATGTATTACAAGCAATTTAT  
AATTTTGGTAACAATATTGAAAAAGTGGTTATCACTTCATCTTATGCTGCCATTAGTACCGCTTCTAAA  
GAAGCTGATAAAAAATGCAATTATTACAGAAAAGGATTGGAATGAAATCAGTTGGCAAGATGCTTTACTT  
AATCCAGTTAATGGATATCGTGGATCCAAAAAATTTGCTGAAAAAGCTGCTTGGGATTTTATAAAATCT  
AATGATAAATGTTAAATTTTCATTGTCGACAATTAATCCATCATTGTATTGTTGGTCCACAATCATTGGT  
TCAGAAATTAACAAAGTTTAAACACTTCTAGTGAAATCATTAAATCTATTTTGAAATTGAAACCAAT  
GATTC AATTCCTGCGTCAAAGGAGGTTGGGTTGATGTAAGAGATGTTGCCAAAGCTCATATCATTGCC  
TTTGAAATGAGGATGCCAAAAATCAAAGAATATTGTTGAATTCAGGTAGATTTACATCTCAATCACTT  
GTTGATATTATTAATGATAAATTTCCAGATTTGAAAGGGAAAATACCAGTTGATGAACAGGTTTCAGAT  
AAATCTGTTATTGCTGAAAGTTTGGCTACTATTGATGATACCAAATCTCGTGAATTATTAGGATTTGAA  
TATTATAACCTTGAACAATCAGTTTATGATACTGTTGAACAAATTGTTAATGCTCATAAGTTGTAA

YOL151W\_homolog 343aa (SEQ ID NO 456)  
MSTPITVIVSGATGFIAQHVVKQLLAKNYQVIGTVRSTAKGDHLLKLFNPNQNLSEIIVEDVGTKGAFD  
KVLQKHGEAKVFLHLASPFHFNVTDVEKELLPAVDGTKNVLQAIYNFGNNIEKVVITSSYAAISTASK  
EADKNAIITEKDWNEISWQDALLNPVNGYRGSKKFAEKAAWDFIKSNDNVKFSLSTINPSFVFGPQSFG  
SEIKQSLNTSSEIINSILKLPND SIPASKG GWDVDRDVAKAHIIAFENEDAKNQRI LLNSGRFTSQSL  
VDIINDKFPDLKGKIPVDEPGSDKS VIAESLATIDDTKSRELLGFEYNNLEQSVYDTVEQIVNAHKL

YOR286W\_homolog 546bp public: 1..546 (SEQ ID NO 457)  
ATGTTTGCATTTAAAAATCTACTACTTCAATTCTCAAACAGTGGTCGCCCCAACATCATCTCGTTAT  
TTATCCACCGTCACATTAAGATCAATCCCAAGAACATTCCATAATGCCACTAAAGTTTCATTATTCAAT  
GGATTAAGAACTACACCAAGATTTTATAGTGTATTGACTGAATCTCCAGAGGCAAAAGTATATAAATAT  
GCCGATGTTAAGGATGTGGCCGTACACCCTGAAAACACCCTGATTCTGTTTTAGTGGATGTTAGAGAA  
CCAATGAATTTGGAGATGGTCATATACCAGGAGCTTTGAATATTCCATTTAAAAGTAGTCCCGGCGCA  
TTGGATTTGT CAGAAGAAGATTTCCAAGAACATTTTGGATTTCTTAAACCAAGTACTGATAAAGAATTG  
ATTTTCTATTGCTCTTGGAGGTGTTAGATCTACTGCAGCTGAAGAATTGGCCAATACTTTTGGTTATAAG  
AAAAGAGGAAATTATCTTGGAAAGTTGGGAAGATTGGGTAAAACATGAAAATAAAAAGAACTAA

YOR286W\_homolog 181aa (SEQ ID NO 458)  
MFAFKKSTTSILKTVVAPTSSRYLSTVTLRSIPRTFHNATKVSLFNGLRTPRFYSVLTESPEAKVYKY  
ADV KDVAVHPENHPDSVLVDVREPTEFGDGHIPGALNIPFKSSPGALDLSEEDFQEHFGFPKPKSTDKEL  
IFYCLGGVRSTAAEELANTFGYKKRGNYLGSWEDVWKHENKKN

YPL078C\_homolog 702bp public: 1..702 (SEQ ID NO 459)  
ATGTCCATGATCAACAGAATTGCATTGAGAAGTGCTCGCCAGCCATGGGAATGGCTTTCCGTCCAGCC  
CCAATTGGTTTGAGATACTTGTCTGCTCCAGCTGACCCAAAACAAAAGGCCAATTCATCATTGATGCA  
TTACCAGGTAACAACCTATTATCTAAGACTGGTGTTTTGGCTACTTCAGCCGCTGCTGCCATCTATGGT  
ATTTCCAATGGATTATTTATTATACACGATGAAACCAATTTTGTCTTGCTACTTTTGCAAGTTTCACAGCT  
TTGGTTCGCCAAATTCGTTGCTCCTTTATACACTGAATGGGCGGATGGTGAAATCAAAAAAGTCAACGAT  
ATATTGAATCAATCTAGAACTAACCATATCGAAGCCGTTAACAAGAGAATTGAAACCGTTTCAGAAATTA  
AAAAACGTTGTTGCAACCACTGAAGATTTGTTTGCTTTATCTAAAGAAACCGCTCAATTCGAAGCTGAT  
TCATTTGAATTAACAACAAAATTTGGCTGTTTCTCAGGAAGCTAAATCTGTTTTGGACTCTTGGGTTAGA  
TTTGAACAACAACAAGACAATTGGAACAAGAACAATTGGCCAAAGAAGTCATTGATAAAGTTGACAAA  
GAAATTGCTAATCCAAAATTC AAGACAAGTATTGGCTGAATCTCTTAACGAAATCGAAAAATTTGTTT  
GCTAAAACTAG

145/251

YPL078C\_homolog 233aa (SEQ ID NO 460)

MSMINRIALRSARPAMGMAFRPAPIGRLRLYSAPADPKQKANSIIDALPGNNLLSKTGVLATSAIIYGI  
ISNGLFIIHDETILLVTFASFALVAKFVAPLYTEWADGEIKKVNILNQSRTNHI EAVNKRIETVSEL  
KNVVATTEDLFALSKETAQFEADSFELKQKLAVSHEAKSVLDSWVRFEQQQRQLEQEQLAKEVIDKVKD  
EIANPKFQDKVLAESLNEIEKLFKN

YPL085W\_homolog 2490bp public: 1..2490 (SEQ ID NO 461)

ATGTTGTCCTTAAAGTTGAAACATGCATTGACTTTAGCTGATTATGGATTGATCAATGAATCACAGAGA  
TATATTGATCATATTAATTCTAGTATCAAGACATTGGGTAACAAATCACCTTTTGTACGCCTAATTTG  
CTTCATGAGTTTCAGAAATTTGATTATGAGAATCACTGAAGTTGGATCTGGAGATGATCAAAACAACCTGG  
TTTTCCGGTAAGATTAGTCGAGTCAATCTTGATAAGATCTGGGGACAAATTGATAAAATTTATTGTTGGT  
GGAGATGAAC TGAAAAATGGTAACAATAACGATGGTAAATGGAACTGGCAATGGAACTGGTAGTGTGTTTC  
AATAAAATTTAGCCCTTCCGTGTCGAGAAATGCATCAAGTGTGAATTTACACAATTATGTACAACTTCA  
ATGATTAGGCAACCATCACATTTACCATATCAACCACAACAACACCGCAACCGCAACAGCAATTATTG  
GATCAAGTTTACATTGAAAGAAAACCTACAACCTGGATTCACTCCGCAACCAACCACTTAGTTGGTCAT  
CCATCAACGACATCAGTTAATAAAATATTTCTCCAAGTATTAAATCGAGTCCTCGTCAAGCACAACCTGAAT  
AAGTTTGAAAAATATGCCCCAAGCAACAATTCATCTCATATAATCTTAGTCTTGTGTAAGAAAGGTC  
GCTGTTTACTAGTGCTGATGGTCCTGAATACCCCTCACCACCAACCAACAGAGATCAATGCGTCAACA  
GTTCCCGTGCCACTTCCACCACCAACCAACCGGTAAGCATGCCACAACATGTATCTAGGTCTCCACGT  
AGCCATCAACTGCACCAACCAACCAACATTTACCACCACTGCATTCACATCATGTTCAACAACCATCTAGA  
GATCGGTCAACCATTAGCGACACGAATCTACCCTTATAGCAATAGTGTGGCGGACAAATTTCTACTACG  
TCAGTGGGTTCTATTTCTTAGTCAAATACCACCTTGGTCGACAGACTCATGGGAAACAACCTTTCTATTTCA  
AGTGTAAATTTCTGGAGATAGTATTGACAGCAGTTGGTTTAGGAGAACAAAGAGAAATGTTTTACCCCATCA  
ACCGGACAAACAGGGAAAAACAGCTACAAGTGAAGTGAATAGAAATGAGGAAGGTTATGGATTGTTGGGGT  
CACTATCATCATGATCAACCTGAACTATAACGGAATCTCCAGAAATTAAGAGGCTTACAACAACCAACAG  
TCCAGTGAAGCAGAAATTAGTAAAGACATTTCAAATGATGTAGCATTTGGATAGTGCTAAGATACCAGAA  
GCTTCACAGGAACCAAGAAAGAAACGGACGAATCAGGTAATGTGGCAGCTGCTCCACCACCTCTACCT  
GCTCCAGTTGCACCTCCTAGAAAAACAAATCTTCTAGATCTAATCCATATGCTCCATCTACAGATATT  
GGTGTAGTACTAGTAATGCACCATCAGCAATAGGACAAACACCTAGTGGGAAACCAAGTGTGAGAAATCA  
GGATCAAGAACTAACAGATATGGACCAACCAACCAAGGAGTTGGTAATAACAACCAACCTATTGATGTTTCG  
CCACCTTCTGCTACTAATAATACCTGGTAATGAAGATTCCATTAGTATGTTTCTCTATGGTGCTTATCAA  
AATGAGTCTAGTCTCCACTCAAGCAACCGTCACAATTTGATCAGACTGCAGTTGCATCTGCCCTGCT  
CCACATCCATTACAACCACAATTTGGCGGTTCCAGAAAGAGTTCCAACTAAAAATGTCGCCAATATTGAT  
GATAGTTTTGATGAAAAATAGTTTTCAGCAGCTGATACATTAACAACCTTACAATAATAATATGGTAAATAAA  
CCATATGGACTGTCAACCAATGGGACCAACTGTTGCAACTAATGGACCTGGATCAGTTACTCTGACACCT  
TTGATTTTAAATCAAGGTTCTGCAAAATATGAAATTTATCAAAATCTCAGTACTATTAGTGTCACTGGAAC  
GGAGCCGGAACCTGTTACTGGGACTGGTGGAGCATTCGATGGATTTCCTATACCAGGATCACCTGATGAA  
ACTACTCGACCAAAATTTCTATATTTGGTGGTCTACTAGAGGATTATTTCTTCAAGATTATCAGAAATCA  
CAAAGTGTATTATATCAACAATATGCAATTGCTGATGATACAGTTGGTGATTATATTCCTATTATGGAA  
GAAGATGATGAAGATGATGAAGATGAACAAGCTAAGCAACAGAAACAAAAAGAAAAAGAGGCACAAGAA  
CAAGAATTGAAGAGAAAGCAGGAACAACAACAACAAAGCTGCAGCAAGAAATAACAACAATAGTGGC  
GGTGGTGGTGGCAAAATCTTTAGCTTATTCGGTGGTGGTGGTAATAATAAGAAACAAGATAATGATGCT  
AAAGTTTATAAAGCTCATTTAGGACAAAGAATACTTTTGTATGATGAAAAATTGAAACGTTGGATA  
GATTAA

YPL085W\_homolog 829aa (SEQ ID NO 462)

MLSLKHLKHALTLADYGLINESQRYIDHINSSIKTLGNKSPFVTPNLLHEFQNLIMRITEVSGDDQNNW  
FSGKISRVLNLDKIWGQIDKFIVGGDESKNGNNDGNGTGNGSGSVFNKFPSPSVSRNASSVNLHNYVQPS  
MIRQPSHLPYQPQQQPQQQLLDQVHIERKPTTGFTPQPPLVGHPPSTTSVNKYSPSIKSSPRQAQSN  
KFEKYAPSNNSSHHNL SLVEERSAVTSADGPEYPHHQHQQSINASTVPVPLPPPTPPVSMPQHVSRSR  
SHQSHQPPPTLPPSHSHVQPPSRDRSPLATRIYPYSNSVGGQISTTSVGSIPSQIPLGRQTHGKQPSIS  
SHVSGDSIAAVGLGEQENVLPSTGQTGKTATSEVNRNEEGYGFGGHYHHDQPETITESPELRGLQPPQ  
SSEAEISKDINSNDVALDSAKIPEASQEPEEETDESGNVAAAPPLPAPVAPPRTKSSRSNPYAPSTDI  
GAISNAPSAIGQTPSGKPSVRKSGSRTNRYGPPPGVGNKQPTIDVSPPSATNNNGNEDSISMFSYGAYQ  
NESSPPLKQPSQFDQTAVASAPAPHLPQLAVPERVPTKNVANIDDSFDENSLAADTLTYNNNMVNK  
PYGSSPMGPTVATNGPGSVTSTPLILNQGSANMKLSNLSTISVTGTGAGTGTGTGGAFDGFPIPGSPDE  
TTRPNSIFGGHTRGLFSSRLSESQSVLYQQYAIADDTVGDIYIPIMEEDDEDEDEQAKQKQKEKEAQE  
QELKRKQEQQQQKAAAKNNNNSGGGGGKFFSLFGGGGNKKQDNDKAVYKAHLGQKNTFVYDEKLKRWI  
D

146/251

YPL190C\_homolog 396bp public: 1..396 (SEQ ID NO 463)  
ATGCCAAGTACAAAAAGATCATCTACTGAATACTCCCATAAAGACTCTAAAAAGAAAGTCAAACCTA  
GATTATGTAAATCTCAAACCATCACAAACGTTATATGTCAAAAATCTAAATACCAAATCAATAAGAAA  
ATTTTATTGCATAATTTGTACCTATTATTTCTGCATTTGGAGATATCATTTCTATAAATCTACAGAAT  
GGTTTTGCCTTTATAATATTTAGTAATTTAAATCTGGCTACATTGGCGTTGAGAAATTTGAAAAATCAA  
GATTTTTTTTGACAAACCACTTGTATTAAATTATGCTGTCAAGGAATCTAAAGCTATTTCTCAGGAGAAA  
CAAAAACCTACAAGATGAAAATGATGAAGAAGTGATGCCACTGTATGAATAA

YPL190C\_homolog 131aa (SEQ ID NO 464)  
MPSTKRSSSTEYSHKDSKKKVKLDYVNLKPSQTLVYVKNLNTKINKKILLHNLVLLFSAFGDIISINLQN  
GFAFIIFS NLNSATLALRNLKNQDFDKPLVLNYAVKESKAISQEKQLQDENDEEVMPSE

YBR112C\_homolog 3243bp public: 1..3243 (SEQ ID NO 465)  
ATGTATGCGACAGCCCATACAATTAACAACAACAACAACAACAACAACATCCACCACCACCTTTA  
AACGGTGGACTACATGCAAGTGGGGCTCCTCCAAATTCCCATGAAGCAGCAGCTATTGCTCAGCAACAA  
CAACAACAGCAGCAACACCACAATGGTCCTGGTATGATTGTTGCCGAGCTGCAGCTTCTGCTAACCAA  
CAAGCTGTCCAAGCCAGAGCCCAACAACAACAACAGCAGCAACAACAGCGATTACCTAGTTTACGCTGCT  
CTTAATGAAACTACAGTATCAACTTGGTTAGCCATTGGTTTCATTAGCCGAGAGTTTAGGTGACATTGAA  
CGTGCGCAGCTTCTTACAATTCCGCTTTGAGACATTCACCAAATAACCCAGATATTTTAGTCAAAATA  
GCAAATACATACCGTTTCAAAGATCAGTTTCTTAAGGCTGCTGAATTGTATGAACAAGCTCTTAATTTT  
CATGTTGAGAATGGTGAACTTGGGGATTATTGGGTCATTGTTACTTGTATGTTGGATAATTTGCAAAGA  
GCTTATGCTGCTTATCAACGTGCATTGTTTTACTTGGAAAACCTAACGTTCCAAAATTGTGGCAGCGA  
ATTGGTATTTTATATGACAGATATGGCTCATTAGAATATGCTGAAGAAGCCTTTGTGAGAGTTTGGAT  
TTGGATCCAAATTTGACAAGGCTAATGAAATTTATTTCCGTTTAGGGATCATTTATAAGCATCAAGGT  
AAACTACAACAGCATTAGAATGTTTCCAATACATTTTGAATAATCCACCACACCCATTAACCAACCA  
GATGTTTGGTTTCAAATTTGGTTCAGTGTATGAACAACAAGGATTGGAATGGTGTAAAGGATGCTTAT  
GAAAAAGTGTTACAGATTAATCCTCATCACGCTAAAGTTTTGCAACAATTGGGATGTCTTTATTCCCAA  
GCAGAATCAAATCCATCAACACCAGCTAATGGTGTGCACCACCACATAAGCCATTCCAACAAGATTTG  
ACCATTGCTTTAAATATTTGAAACAATCTTTGGAAGTTGATCAAAGTGATGCTCATTCATGGTACTAT  
TTGGGTAGAGTAGAAATGATTAGAGGTGATTTACTGCTGCTTATGAAGCTTTCCAACAAGCTGTCAAT  
CGAGATGCAAGAAACCCAACCTTTCTGGTGTTCATTTGGTGTGTTTGTACTATCAAATAAGCCAATATCGT  
GATGCATTGGATGCTTATACCAGAGCCATTAGATTAAATCCTTATATCAGTGAAGTATGGTATGATTTG  
GGGACTTTGTATGAGACTTGTAAATAATCAAATTAGTGATGCATTGGATGCATATAGACAAGCAGAAAGA  
TTGGATCCAAATAATCCTCATATAAAGGCAAGATTAGAACAATTGACAAAGTATCAACAAGAAGGTAAT  
ACTCACCCACCTCAACCACCGCCAAGTTCTCAACAACCTAGATTACCTCAAGGAATGGTTTTGGAAAGT  
ACTCAACAACAAGCAGCAACAACAACCACCACCTCCACAACAACAACAACAACAACACTTCAACACCAA  
CTGCAACTGCAACCTCAACCACAGCAACCACCTCAAACCCAATCAACAACCACTGTTACTTCAACCAAA  
TCTTCATTGCCTCCTCAACAATCCAACCATTAATCAACAAGCTGCAAGCCTTTAGTGAATCAACAA  
CAAAGTCCACCACCACCTCACTTGATGAACCTGGGACAACCGGGCAACAACCACAACAATTGCCACCA  
CATCTTCCACCACATACCCAGCAACCTTCTCAAATTCAGAAAAGCCTCCAACCTCAAGAACAACCACAT  
TATCAACCACCTCCACCTCCACAACATCAACAGCAATCGCAATCGCAACCGCAACCTCCACACCAACCT  
CAACACACTCAAAATCAACTGCCTCAATTAGTCAATTGGCACCACACCATTTAATCCTCCAGCTAAG  
CCACATGGTGCACCTCAACAAGAAGTGGTTTACCGGATTTATTACACAACCTCTGCTAATATCATATCA  
GCTCCATCACAAGTACCTCAACCACAACAACAATATCAACAACCACATATTGCACCTGTTAGACAAGAA  
CAAGTTAACCATGTTCCCTCAATTTATCTGGCTCCTAGACCAACTGAGACAACACTTCTCAAATCAAC  
AACCCAAATGAGTCAACCACAACAAGTTCACAACCTCAAAAAGGAGGAACCTAAACCAGAGGCTACT  
GTTTCTGCTCCAGTTCTTGAGGCTATTAAAGTTCAAGATCAAGTGACAATCCAGGAGTCAGCACCAGCA  
GCAGCAGCAGCAGTGTGAGCACCAGCTTCTGCTCCAGTTGGTGATATAAAAACAGATACTGTATCTACT  
ACTACACCTGCTACTTCAACCCTGCAGATGCTGTGCCAGTATCTGTGTCTCAAGTTGGTGAAGCACC  
AATGTTGTTCAAGAGAAGAAAGTTCCGGACACCGAGCAGATCGTTTCAAGTTGAAAAACCCGTGGAG  
TCACAACCAGAAGTTACACCAGCTCCAACACCAGCTCCAGCTCTTGCAACAGCACCACCTGAACCTGCA  
CCTACTGATAAGGACGTTGTAATGGCTCCAAGTAAAAGTGCAACACCTGTTTCTCAAAGTATTGTGGAA  
CAGAACACCAGAGTATCTGAAGCTACAAGGCCAGCAATCCAATGGTAAACATGATTAGAGACAAG  
AATGATGAAGAAAAAATTTTAAAGAGGCCAAGTGTGAAACGACTACTGAATCTGTACCAGTTAACCAA  
CCTGTTGAGAAAGAAAATGAAAAAGTTGAGGTACCACCGCCACTGGAACAACCAAGTTCAGAAAAGAGA  
GAAAAAGAAAGTCAACGGATCAATTAAGAAACCATTTGGAAAATGAAAGTAAGGTTGATATTCCTCAATTC  
TCATCAAATATCACAGCTCAAATGAAGAAGCAAAATCTGGAGAAGAACTAAAAAAGATACAACCAAG  
ACAAGTCCAGCAAAACAAGGGGAAGTTAAGGAAGTAATACCATCATCTACAGAACTGTATCAAAACCA  
GATGTTGAAAAAGACAATAAAGAGAAAGACAAGATGAAGATGAAGTGATGGCTGATGAAGATGACGTC  
AAAAAAGATGAAAATCCAGAACCTCCAATGAGAAAGATTGAAGAAGATGAAAATTATGATGATGAATAG



147/251

YBR112C\_homolog 1080aa (SEQ ID NO 466)  
MYATAHTIKQQQQQQQHPPPLNGGLHASGAPPNSHEAAAIAQQQQQQQHHNGPGMIVAAAAASANQ  
QAVQARAQQQQQQQRLPSSAALNETTVSTWLAIGSLAESLGDIERATASYNALRHSPNNPDILVKI  
ANTYRSKDQFLKAAELYEQALNFHVENGETWGLLGHCYLMLDNLQRAYAAYQRALFYLENPNVPKLWHG  
IGILYDRYGSLEYAEEAFVRVLDLDPNFDKANEIYFRLGIIYKHQKLOPALECFQYILNNPPHPLTQP  
DVWFQIGSVYEQQKDWNGAKDAYEKVLQINPHHAKVLQQLGCLYSQAESNPSTPANGAAPPHKPFQDDL  
TIALKYLKQSLEVDQSDAHSWYYLGRVEMIRGDFTAAYEAFQQAVERNDRNPFWCSIGVLYYQISQYR  
DALDAYTRAIRLNPYISEVWYDLGTLYETCENNQISDALDAYRQAERLDPNNPHIKARLEQLTKYQQEGN  
THPPQPPSSQPPRLPQGMVLESTQQQQQQQPPPPPPQQQQQLQHQSQSQPQPQPQTQSQPSLLQHQ  
SSLPPQIQPLHQAAKPLVNQQQSPPPHLMNLGQPGQQPQLPPLPHTQQPSQIQEKPTQECPH  
YQPPPPQHQQQSQSQPQPPHQPHQHTQNSPQLAQLPPHNSNPPAKPHGAPQQTGLPDLHNSANIIS  
APSQVPQPPQYQPHIAPVRQEQVNHVPSIYAPRPTETTLPOINNPNESTTTQVPQLKKEPKPEAT  
VSAPVPEAIKVQDQVTIQESAPAAAAAVSAPASAPVGDIKTDTVSTTTPATSTTADAVPVSQVGEAP  
NVVQEKKVPDTEQIVSQVEKPVESQPEVTPAPTAPALATAPTEPAPTDKDVVMAPSKSATPVPQSIVE  
QNTRVSEATKAPESNGKHDLEDKNDDEEKILKRPTVETTTESVPVNQPVKEKENEKVEVPPPSEQPSSEKR  
EKEVNGSIKKPLENESKVDIPQFSSNITAQNEEAKSGEETKKD'TTKTSPAKQGEVKEVIPSSTETVSKP  
DVEKDNKEKDKDEDEVMADDDVKDENPEPPMRKIEEDENYDDE

YDR145W\_homolog 1536bp public: 1..1536 (SEQ ID NO 467)  
ATGGAAAGGTTCAATCAAATTAGACAAAACTCACTGAAGTTCAAAGGAGGGTTTCAGTTGTTGGAACAA  
ACAAAGAAAACAGGAAATGTTACTCCAGAGCAAATTCACAGATTGATAAAGAAATAATTGAATGCAAG  
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CAACAACAGAGACAATTGCAACAGCGACAGCAACAACAGCAACAGCAACAGCAACAGAATAACAATCTA  
AAATCAGCTCAGAACCAGAACCAGAATCAAAACCAAAACCAAAACCAAAACCAAAACCAAAAC  
CAATACAAAGGAGTGCAATCTGCTGGACAAACACCTCAGCAACAGAGCTTTTCGCCACAGTTGCAGGCT  
GTACAACAACAACAATTTATGGGCAACCTGCAACAACAACAGCAGCAGCAACAACAACAACCTTAGAAAT  
GCGAATAAAAGTGCACCTTCAAGGTCAAGCTCCTTCACAGGCGCCAACTCCTTTACCTGTTCCGCCAACA  
CCTCAGAGTCAACCTACAGCACAAGCGGGTGTTCCTTCACAGGCAGCTACACCAGGATTTTCGAGCTTCT  
CAACCCACACCATCGCAAACTTCGAGAATCGGATCAGCTCTACAACAAGGGCACCAAGTCGACAGGCA  
TCTTCTACACCGCAATCTCAATTCCAACCACCATTAACCTGGAGAGTCGACATCCTTCTGCAACTACA  
TCAGAAAAGCCACTTCCCAACAACCTGGAAGCGGAACAGCGAAGAGTCTTAGTGTGCTGCTACTCCT  
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ACATTTAATAGTATCAATGATACGAGACCCAGTTTGACGGGAGGAGCTGCCAATCCTATGAGTATTTTA  
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AGTACCAGTGGACGAGTTTTTAAATAAACGAAATTTAGGTGATTTGATAAATACAATAGGTGTTGATGAA  
GGGGATGGTAAGACCAGTATTGATGGGAATGTGGAGGAATTTTGTGTTGGATTTGGCTGATGAATTTATT  
CATTCAGTGACAAGTTTTGCTTGTGCGTTAGCAAAACATAGAAAGGTGGATAGTATAGAGGCAAGAGAT  
GTTCAACTACATTTGGATAAGAATTGGAATATCAAGATTCCCTGGTTATGCAATGGATGAGATTCGAAAC  
ACAAGAAAAATACAACCTAGTAATAGTTATAGTCAGAAAGTACAAGGTGTCGAAGTTTCGAAAGCTGTG  
AATGATGATAATGCTTAA

YDR145W\_homolog 511aa (SEQ ID NO 468)  
MERFNQIRQKLTEVQRRVQLLEQTKKTGNTPEQIQQIDKEIIECKAKFQQYQKVGIYIRNQLVLQAKA  
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VQQQFMGNSQQQQQQQQQQLRNANKSALQGQAPSQAPTPLPVRPTPQSQPTAQAGVASQAATPGFRAS  
QPTPSQTSRTGSALQQRAPSRQASSTPQSQFQPLPSESRHPSATTSEKPLPQPGSGTAKSPSVAATP  
AQNNGTVTARSASPVATTTDSATTGRSGTPQQQSRSRSGSSLNLAGITRQSVPSLPISSSINVKQPTIT  
TFNSINDTRPSLTGGAANPMSILLDTPAITKLPTFDIEGDTGVIDSSTSGRVLNKRKLGLDLINTIGVDE  
GDGKTSIDGNVEEFLDLADEFIHSVTSFACRLAKHRKVDSIEARDVQLHLDKNWNKIPGYAMDEIRN  
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YDR154C\_homolog 333bp public: 1..333 (SEQ ID NO 469)  
ATGATGTCGTTCCAAAGACTGCTGAAAATTTTCAGAGCTTTATGTACTGGTGAAAAGGTTTTGGTTACA  
AAGGTTCTATTTTCCACAGAGTCATCCACAATTCATGCTTCAAGGTGGTGATTTACCAACTTTAACG  
GTACTGGTGGTAAAAGTATTTACGGTACCAATTTGCTGATGAAAACCTTTGTCAAGAGACATGACAGAC  
CAGGTTTGTGTTCTATGGCCAATGCTGGTCCAAACACCAATGGTTCCCAATTCCTTATTACCACCGTTC  
CATGCCCATGGTTGGATGGTAAACACGTTGTTTTCGGTGAAGTCACTGATGGTTTAG

YDR154C\_homolog 110aa (SEQ ID NO 470)  
MMSFQRSSKISELYSVKKVLVTKVLFSTESSHNSCFKVVISPTLTVSVVKVFTVPNLSMKTLSTRDMDT  
QVCCLWPMVSVQTPMVPNSSLPFHAHGMVNTLFSVKSSMV



148/251

YDR216W\_homolog 4257bp public: 1..4257 (SEQ ID NO 471)  
ATGATTTTACCAACTCACCAGAGTCAATACCTTAATTATTTTGTCAACCCAGTTTAAATGACTGAGTCC  
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GCGCCTACTCCCGCCTCGACTACCAAGAATTATAAGCACAAAAACAGAATACCAATACTGGAACATCC  
ATGTCGCCAAGTAATTTCAATAAATTCAACAAACAACATGCAGCAGCAGCAGCAGCAGCAACAACAACG  
TCAAAAAAGTCCAAAGACATCCCATTAGAGTTGACTGCATTTGGTACAACCCCTCTGGGAAACCACGT  
TTATTTTGTTCAGTCTGTACAAGAGCATTGCTAGGTTAGAACATCTACGTAGACATGAAAGATCA  
CACACAAAGGAAAAACCATTTAGTTGTGGTGTTCGTCAACGGAAGTTTAGTCGTCGAGATTTATTGCTA  
AGACATGCACAGAAATTACACGCTGGCTGTACTGATGCAATAACAAGATTAAGAAGAAAATCAATTAAG  
AAATCTCAGGATGGGGACGATGATGATGACGATGATGACGACGATGAAGAAATGGCAAATTTCTGAAGAC  
GAAAACGATCATGATGAATCGGGCAATGCAAGCACAAAGAATGGTAAAAAGGATAAAAAAGATCCACCA  
CCGGAGTTCAATTTAAATTTATTCAATCTGAAACAAAAGCCAACTAAAGCGAACACGACAAAAGTCAAAA  
GTGGCTAAATTATCAACAACGACATCAAGGAAAAATTCACCAATCCTACGAGAAAAAACTCCAGCTCT  
TTGCACAAAGCAGGTTCTTGATCAACGTCAAAAGGCTGCCGTTAATACAAAAATTTGTATCAAGTACCAAA  
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GCTCAATCGGGTGCCAACTATGCCATCAACATACCTGAGTTTAAATGATATATATCCACAATCTGATAAT  
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TCAGCAGATCATGTAACACCTCCAGTAAACGTAGTCAGCATGGGTCAATTTCTCATCAATCAACATTTT  
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TACATGATGCCAACGGTAACAATAAGCAATCAAGAAATCCAAATGGTGTGCTGCTCATCATCATCAT  
CAACAACAACAGCAGCACCAGCAGCACAATCATCAACATCAACCAATCAGTCTCTGCTCGGGTTATCG  
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TTCCCAATGGATTCTATATCAACAACCTTCAATGCAATGTCTTCGGGCCAATTCAAAACCTTTAAACCA  
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CAAAATAACAACAATACCAATGATAATCCGATTACCAAAATATCAATTATGACTTGAACCTTTCTTCAT  
ACTATTGATGATATAGGACAAGATGTTATTTCTAAATTTATGCCAGGAGGTTACTCGTTTTATGGAGAC  
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CAAAACAATCAATTTGCTCTTCACAACCAAGTCGTCAATCCTAGTGGTGCTTCACCACATTTAAACCAA  
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GAAATGCGATACAAAAATAATATAAACATGCAATCTCAAACGAGAATAGTATTTATCATTTATCGGTTG  
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CAATTGCAGAATCTTTGTAAATATGGATTCAATTGTTTGGTGCATGGTATATATGAAATCAAACAATAT  
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TATCAAGATTTAACTCAAAATTTATCATCGTCTTTTGGATGCTCACAGTACTGGGAATCCACTTAATTCA  
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GTTGAGGATTCCAACAGTAATAGTAGAAATCGAAGCAAAAATGATCCAACAAATGAAATCAATAACAAA  
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CGATTACTGATGATGAGTTGCGATATGATAAAGAAAACGATGTCATATTTGATAAACATATTA  
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TCCGTATTATCGATTTTTCGGTTTATGTTATGCGTAAAAATGATAATAATTCATCACCATTGCTAAT  
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GCCTTATCTATAAAATTAGAACAAGAATTCACAACTTGTATCTTTACAATGGGAATGTATTATCTTCA  
GATCATAATACAAATACAAATACCACCAATACTATTACTACTACTACTACTACAGACAATGGTACTAAA  
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GTTTTGAATTATATTTATGATTTAAATTTAAAGTTTGGGTATTTAAGAAATTTGGGTGATAGTTTATCA  
GAAATTAGAAAATATTTAATTGATAATGAATCTACTTTGAATGGTTAA

149/251

YDR216W\_homolog 1418aa (SEQ ID NO 472)  
MISPTHQSQYLYNFVNPVLMTESGDIIDSVTGTTTTTANMSNTTIDAPTPASTTKNYKHKKQNTNTGTSMSPSNSINSTNNNAAAAAATTTTSKSKSDIPELTAFGTTPSGKPRLFVCQVCTRAFARLEHLRRHERSHTEKEKPFSCGVCQRKFSRRDLLLRHAQKLHAGCTDAITRLRRKSIKKSQDGGDDDDDDDDDEEMANSEENDHDESGNASTKNGKKDKDPPPEFNLNLFNSKQKPTKANTTKSKVAKLSTTTSRKNSTNPTRKNSSSLHKQVLDQRQKAAVNTKIVSSTKIVSGTNSGVSIPTPSRRGASFSAQSGANYAINIPEFNDIYPQSDNVEFSTPQFLPSSLDNEMTWLNNIPNIPGLSDSVSAANLMRQNSITNSADHVTTPPVNVSQHGSFSHQSTFSATDMGQTRSESVNSLNTPFDDGSYMMPTVTISNQEIQNGVAHHHHHQQQQQHQHQNQHQPQNQSSSLGLSRNDMLSEDHYGYSFYDIPENILNFPMD SISTTSNAMSSGPIQNFKPLSPITQEIEHEITPRIDGRIGDFQNNNNNTDNP I HQNINYDLNFLHTIDDIGQDVISKFMPPGGYSFYGDNNVSATSSANDYNSPNNIVSPSQQNNQFALHNQSSHPGASPHLNQAMNMKRLHNYSSNKLFTNHIRHMINKALGKYPISGIMPTPTIPSNEKLEFYLSVFIQSFLAHLPIHPSKLN EYEIMAMTGNEDINNESARVCLPLLTATMGALLANNKNDAEHLYEASRRTIHIYLESRKTNSTNDKNYKNGKDKSSGNPLWLLQSLMLS VLYGLFSDNENNVYIVIRQLNALNSLVKTSIKNGKPIFFSNNGEDEELYNKLN SHDNGTSLFSNNLNDEMRYKNNINMQSQTRIVFIIYRLTNFLLMMYNVPLTF SINDINQLAVTSKDEETLWNFKNYQEFQEF SHKNNKTLD DYLNNKNEPIIFRELLT VIKFGISDSNISPEIEKKVTHQLQNLCKYGFNCLVHGIYEIKQYQEMKEVDTFKVL DYLTKFYPTNDGLGFNCFRLPANKDLEKIDYALLVDFTKISSIIDLKLKEQSWLKNYQDLTQNYHRLLD A HSTGNPLNSINDYDYLKLADCCISVLKILFKVEDSNSNSRNRSKNDPTNEINNKLNNNNNNNNNDMNNNSNGDQLISAFDPTDFGYLNDNNGYAKKEEFLRFTDDELRYDKENTMSYFDKHIKLDIFEEVEKSSNLIQAQMLFHAFSVLSIFSVMRKNDNNSSPFANTDLIFELNHRYSMVLRLLETLFLKRLRYQTSAGGGGGGVNNNNNNALS IKLEQEFTNLYLYNGNVLS SDHNTNTNTNTNTITTTTTTDTNGTKQNQHHSQDFGLEKTLYILKMGENVLNYIYDLNLKVCVFVKKLGDLSLSEIRKYLIDNESTLNG

YDR224C\_homolog 393bp public: 1..393 (SEQ ID NO 473)  
ATGGCCCCAAAAGCAGAAAAGAAACCAGCTTCCAAAGCTCCAGCTGAAAAGAAACCAGCTGCTAAGAAAACCGCTTCCACCGATGGTGCTAAAAAGAGAACCAAGCTAGAAAAGAAACTTATTCCTCATATATATATAAGTTTTTGAAACAAACACATCCAGACACTGGTATCTCCCAAAGGCCATGTCAATTATGAATTCGTTTTGTTAACGATATTTTCGAAAGAATTGCCACCGAAGCCTCCAAATTAGCTGCTTACAATAAAAAATCCACAATTTCCGCTAGAGAAATCCAAACTGCTGTTAGATTAAATTTTGCCAGGTGAATTGGCCAAACATGCCGTTCCGAAGGTACCAGAGCCGTCACAAAATACTCATCTGCTTCTAGTTAG

YDR224C\_homolog 130aa (SEQ ID NO 474)  
MAPKAEKKPASKAPAEKKPAAKKTASTDGAKKRTKARKETYSSYIYKVLKQTHPDTGISQKAMSIMNSFVNDIFERIEATEASKLAAYNKKSTISAREIQTA VRLILPGELAKHAVSEGTRAVTKYSSASS

YDR342C\_homolog 1653bp public: 1..1653 (SEQ ID NO 475)  
ATGTCATTAGATAATTCAACAGAAAACCGTGATTGGAAGAAAAGGAAGAAATTCCAAAGAACGAACATAACGAACAAGGCGAACAAAACGAGAACAATGAGCATATACCTACTTTGGAAGATAAACCATTTGAAGGAATATATTGGTATTAGTATTTTGTGTTTCCTTATTGCCCTTTGGTGGTTTCGTTTTCGGTTTCGATACTGGTACCATTCTCGGTTTCATTAAACATGACTGACTTTTTAGAAAGATTTGGTGGTACTAAAGCTGACGGTACTCTTTACTTTTCCAACGTTAGAACTGGTTTATTGATTGGTTTGTTC AATGTGGGTTGTGCCATTGGTGCAATTATCTTAAAGTCGGTGATATGTATGGTAGAAGATTGGTATCATGACTGATCATTTATTTATTTGTTGGTATTATTTGTTCAAAATGCTTCTCAACATGCTTGGTATCAAATCATGATTGGTAGAATTATCACTGGTCTTGCTGTTGGTATGTTATCAGTTTTGTGTCCATTATTTATCTCAGAGGTTTCTCCCAAACATTTAAGAGGTACATTAGTTTATTGTTTCCAATTGATGATTACCTTGGGTATTTTCTTGGGTTACTGTACCAGTTACGGTACTAAGAAATATTCTGACTCCAGACAATGGAGAATTCATTGGGTTTATGCTTTGCTTGGCCCTTGTTGCTTTGGTGGTATGGTAAGAAATGCCAGAATCTCCACGTTACCTTGTCGGTAAAGATAGATTGACGATGCTAAGATTTCACTTGCCAAAACTAACAAGGTTTCTCCAGAGGACCCGTGATTATACCGTGAACCTCAATTAATCCAAGCTGGTGTGAAAGAGAAAGATTGGCCGGTAAGGCATCTTGGGGTGCTTTATCACTGGTAAACCAAGAATCCTTGAAAGAGTTATTGTTGGAGGTATGTTGCAATCATTGCAACAATTGACTGGTGATAACTATTTCTTCTACTACAGTACCACCATTTTCAAGTCTGTGCGTTTTAAATGATTCTCTTGAAACATCTATTATCCTTGGTGTCACTCACTTTGCTTCCACTTTTGTGGTATTTATGCCATTGAAAGATTGGGTAGAAGACTCTGTTTATTAACCTGGTCCGTTGCCATGTCCATTGTTTCTTAATTTACTCATTGTTGGTACTCAACATCTTTACATTGATCAACAGGTTGGTCCAAACCAGAAAACAGATGGTAAACGATGATTTTTCATTACTGCACTTTATGTTTCTTCTTCTCGCTTCTACATGGGCTGGTGGTGTCTACTCCATTGTTTCTGAACTTTATCCATTAAAAGTCAGAAGTAAGGCTATGGGTTTTGCTAATGCATGTAAGTGGTTGTGGGGTTTCTGATTTCTTCTTCACTTCATTTATCACTGATGCTATCCACTTCTATTATGGTTTTGTGTTATGGGCTGTTTAGTGTTTTCCATTTTCTTTGTTTACTTTATGATTTACGAAACTAAAGGTCTTACTTTAGAGAAATTGATGAATTATACTCTACCAAGGTTGTTCCATGGAAATCAGCCGTTGGGTTCCACCTTCTGACGAAGAAATGGTTTCGTGCAAAAGGCTATACTGGTGATATCCACGCAGATGAAGAGCAAGTTTAA

150/251

YDR342C\_homolog 550aa (SEQ ID NO 476)  
MSLDNSTENRDLEEKEEIPKNEHNEQGEQNNNEHIPTLEDKPLKEYIGISILCFLIAFGGFVFGFDTG  
TISGFINMTDFLERFGGTKADGTLYFSNVRTGLLIGLFNVGCAIGALFLSKVGDYGRVVGIMTAMIIY  
IVGIIIVQIASQHWYQIMIGRIITGLAVGMLSVCPLFI SEVSPKHLRGTLVYCFQLMITLGI FLGYCT  
SYGTTKKYSDSRQWRIPGLGCFAWALCLLGGMVMPESPRLVVGKDRIDDAKISLAKTNKVSPEDPALYR  
ELQLIQAGVERERLAGKASWGALITGKPRILERVIVGMLQSLQQLTGDNFFYYSTTIFKSVGLNDSF  
ETSIILGVINFASTFVGIYAIERLGRRLCLLTGVSAMSI CFLIYSLIGTQHLYIDQPGGPTRKPDGNAM  
IFITALYVFFFASTWAGGVYSIVSELYPLKVRSKAMGFANACNWLWGFLISFFTSF ITDAIHFFYGFVF  
MGCLVFSIFFVYFMIYETKGLTLEEIDELYSTKVV PWKSAGWVPPSDEEMVRAKGYTGDIHADEEQV

YDR343C\_homolog 1641bp public: 1..1641 (SEQ ID NO 477)  
ATGTCTCAAGACAACGTCTCATCAACATCTACAGCTGAGGCTGTAAATAATGAAATCAAAGTCAAAGAT  
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ATCATTATGTGTTTCCCTTATTGCCTTTGGTGGTTTCGTTTTTGGTTCGATAC TGGTACTATTTCCGGT  
TTCATTAATATGTCTGACTTTTTAGAAAGATTCCGGTGGTACTAAAGCTGACGGTACTCTTTACTTTTCC  
AATGTCAGAACTGGTTTAATGATTGGTTTGTTC AACCGCTGGTTGTGCCATTGGTGCATTATTCTTGTCT  
AAAGTCGGTGATATGTATGGTAGAAGAGTTGGTATCATGACTGCTATGATTGTCTATATTGTTGGTATT  
ATTGTTCAAATTGCTTCTCAACATGCTTGGTATCAAGTCATGATTGGTAGAATTATCACTGGTCTTGCC  
GTTGGTATGTTATCAGTTTTATGTCTTTGTTGTTCAATTTCCGAGGTTTCTCCAAAACATTTGAGAGGTACT  
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TATTTCTTCTACTACAGTACCCTATTTTCAAGTCCGTTGGTATGAATGATTTCTTTCCAACTTCTATC  
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CTCTGTTTGTAACTGGTTCCGTTGCCATGTCTGTCTGTTCTTAATCTATTCCTTGGTGGTACTCAA  
CATCTTTATATTGACAAACCAGGTGGTGTCTAGTAGAAAACCAGATGGTGATGCCATGATCTTTATGACT  
TCACTTTATGTGTTCTTCTTTGCTTCTACATGGCTGGTGGTGTCTTACTCCATTATTTCTGAACCTTAT  
CCATTGAAAGTTAGAAGTAAGGCTATGGGTTTAGCTTATGCTTCCAATTGGACCTGGGGTTTCTTAATT  
TCTTTCTTTACTTCATTTATTTACTGATGCTATCCACTTCTACTACGGTTTCGTCCTTTATGGGATGTTTA  
GTTTTCTCCATTTTCTTTGTCTACTTTATGGTTTACGAACTAAAGGCTTACCTTGAAGAAGAAATTGAT  
GAATTGTACTCCACCAAGTCTTCCATGGAATCAGCTGGTTGGGTGCCACCTTCCGAAGAAGAAATG  
GCAACCTCTACGGGATATGCTGGTGATGCCAAACCAGAAGAGGAACACGTTTAA

YDR343C\_homolog 546aa (SEQ ID NO 478)  
MSQDNVSSTSTAEAVNNEIKVKDEFQRQEEQAHTSLEDKPV SAYIGIIIMCFLIAFGGFVFGFDTGTISG  
FINMSDFLERFGGTKADGTLYFSNVRTGLMIGLFNAGCAIGALFLSKVGDYGRVVGIMTAMIVYIVGI  
IVQIASQHWYQVMIGRIITGLAVGMLSVCPLFI SEVSPKHLRGTLVCCFQLMITLGI FLGYCTTYGT  
KSYSDSRQWRIPGLGCFAWALCLVAGMVMPESPRLVVGKDRIEDAKMSLAKTNKVSPEDPALYRELQL  
IQAGVERERLAGKASWGTLFNGKPRIFERVVGVMLQALQQLTGDNFFYYSTTIFKSVGMNDSFQTSI  
IIGVINFASTFVGIYAIERMGRRLCLLTGVSAMSVCF LIYSLVGTQHLYIDKPGGASRKPDGAMIFMT  
SLYVFFFASTWAGGVYSIISELYPLKVRSKAMGLANASNWTWGFLISFFTSF ITDAIHFFYGFVFMGCL  
VFSIFFVYFMVYETKGLTLEEIDELYSTKVL PWKSAGWVPPSEEMATSTGYAGDAKPEEEHV

YDR544C\_homolog 1700bp (SEQ ID NO 479)  
CTAAAGTCCAAAGTTGGTTCAATTTTGGCAGAAAAAAGAAGGAAAAATTCACTGGA  
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AGGAATTTCATCGGTGTTGTCTCGCAGTAAC TCAACTAGAAGATCTTTTATTGACCGCTTC  
CATAGAGATGAGTCTAGCACTGGCATTAGCAGACAACATGAGCAGCACCAGCAGCCTTTG  
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CCACAGGCCAAATCACTAGAGCCTGTATCAGAAGTACTAAAAGAAGTGTTCACCTATG  
CAAAACGGGTCCGAAAGGAAAGGTGAAAATCAGCAGTCGAGAGTTGATGTATCCTCTCAA  
ACCTTGTCAACAGTTACTCTACTCAGATGGATTTGGTGGTTCTGTAAACCATTAACA  
GAACCTGTTGATTCTCCAAATGTGATTAAATACAATGACTCGGACGACTCTTCTACAGAA  
GAACGTAGAGGCTCGTTACTTGAAAAACACAATTTAGAAGTACAACCTGTATCTTCCCCA  
TTCACTACTCAACCGCCAGCACC'TGTGCCACAAGAATCCAGATCTAGACAAAGCAGTGAT  
GGCATTCTACTCGTTTGAAGCGGGTGATGATTCCAACCCAATCTCGGCTACTCCAAGATCC  
GAGCAAAATGTGTTTGGACAGATGCCAGACCCAATTTGTCTCTCTGAAAAGACTCTTGCT  
CCACCACCACCACCTTCGAGAAAAGTTTTCACCATGAAGAACCAACTGTAAGGGATTC

151/251

GCTCTTTTCCACAATTTACCTGCTGCCTCCCATTCTGGAAGAGATTCCGGTAATGGCTCCA  
TTAGCAAGTCAAGACAGGGGTCAATTCGTTGTTGAAAAATGATTTCAAACACGAAAACTTG  
GCATCCACCCTCGGATTGAGCTCTTCTATTGCTGAAGTCATCAATGCCAGCTTTAAGGAT  
GGACAGTTGATTAAATCACAAGTAGTTGGTGAAGTGGCCTTCAATTATAATGGTAATGCT  
TCCGATCCACTTGTGGTCACTATTCTTAATAGTTTCGATAAAAGTACTCGTGAACAAGACT  
TTTATTGAGGATTTAGGTCAAAGCAAGTATAAAGTGAACCCAACTTCAATTACGTCTAAA  
ACTCTTGGTGGGTTGAAATATCTTTTGAAACCAACACAGGTACCAGTGATAATTCAACAA  
ATATGGAAATTTGAACCTCATCAGTCAAGTTTGATGGTTAGCATTCGTTCAACTACACCT  
TTGGTATTGGAAAATTTTGTGTCTCTGTAGCTTTGAATCAAGACATTGAAGCAACATCT  
GCTTCCTCAAAGCCTCAAGGTGCGTTTAATAAAGAGAAAAACAGAATAACATGGAGATAT  
CCACAGTCCCTCGCATTGAATGGTGTAGAGCGTTTGATAGCTAGATTTATGACTAATGGA  
TTGGGTTCCGAACATGAGTCTGGTGTGAGATTAAATTTCAAGTTAAGGATCCACAAGTC  
AAGTACTGTAGTATTTACAGTGAGAATGGCGAAGAGATTCTACGTTTAGAAATTTGGTT  
AGCGGTAGTTATAGTGGTCATCTTTAAGTTATCTGTTTGGAGATTAGTCTCTTGTGTAAT  
TGAAAAAATAAAGCTGA

YDR544C\_homolog 548aa (SEQ ID NO 480)

LKSKVGSIFGRKKKKEKFTGADSLAEDESLSVSLPPTTRNSSLRSNSSTRRSFIDRF  
HRDESSTGISRQHEQHQQPLSDPLPHAEPQPEIPQSPEAPQAKSLEPVSEVLKELFPPM  
QNGSERKGENQQSRVDVSSQTLSPVTPTHDGFSGSVKPLPEPVDSPNVIKYNDSDDSSTE  
ERRGSLLEKHNLEVPVSSPFTTQPPAPVPQESRSRQSSDGIYSFEAGDDSNPISATPRS  
EQNVFGQMPDPNLSPEKTLAPPPPSRKVLHHEEPTVRDSALFHNLPAAHSGRDSVMAP  
LASQDRGHSLLKNDPKHENLASTLGLSSSIAEVINASFKDGLIKSQVVGEVAFNYNGNA  
SDPLVVTIPNSFDKVLVNKTFIEDLGQSKYKVNPTITSKTLGGLKYLLKPTQVPVIIQQ  
IWKFEHPHQSSLMVSIRSTTPLVLENFVVSVALNQDIEATSASSKPQGAFAFNKEKNRITWRY  
PQSLALNGVERLIARFMTNGLGSEHESGVQIKFQVKDPQVKYCSIYSENGEEIPTFRNLV  
SGSYSGHL

YEL071W\_homolog 1584bp public: 1..1584 (SEQ ID NO 481)

ATGCAGAGGAGATTAGTACAGACTGCTTCGTATTTGATTAGACGAAACAACGTGGCATGTAGATTTCAGT  
CGTTATAATGGTTTGCCCGTTGCATCTTATTCTACAAAAACAGTACCTTTTACGGCAGATACCTTATTCC  
CAAAAAGTCCAACGTGATGCAAAATTCAGCAACTTGAATCTCAAGACATCGAATACTTTAAAAGTGTA  
TTACCTGAGAATTCATTATTACTGATGAAGACGACTTATTGTTTTCAACGAAGACTGGATGAGAAAG  
TATAGAGGTCAATCACAATTGGTTTTGAAACCGAAAACACCGAACAAGTCGCTTCTATCTTAAAGTAT  
TGTAATGATAACAAGCTAGCTGTTGTACCACAGGGTGGGAATACTGGGTTGGTAGGTGGATCTAATCCA  
ATTTTTGATGAAATCATCATTTCTTGTGCGCCATGAATAAAATCAGATCGTTTGATCCTGTCAGCGGT  
ATATTGAAAGTCGACGCTGGTGTATTTTGAAACAGCTGATCAGTATTTGGCTGAGCAGGGCTACATT  
TTCCCGCTCGACTTGGGAGCTAAAGGGTCTGTCTATGTTGGTGGCAATGTTGATGCTGCTGGTGGT  
TTGCGTTTGTACGATACGGTTCTTTCATGTTTCTGTTTATAGGTTTGAAGCTGTCTTGCCCCGCGGT  
ACAGTTTATAACTCTATGCATTCATTGCGTAAAGATAATACTGGTTATGATTTGAAGCAGTTGTTTATT  
GGATCTGAAGGTACTTTGGGTATTATAACTGGTGTTCGATTCTATGTCCATCAAGACCACAAGCGCAA  
AATGTGGCATTTTTAGCTGTATCGAGTTATGAGGCCGTTCAAAGGTTTTTGTCCAGGCTAGAAAGGAG  
TTGCAAGAAATTTATCGGCTTTTGAATTCATGGACAACACCTCACAAAAGTTGACTGCTAAGCATTTA  
GGTTTGGAGCACCTTATTGAAAGCGGTGACTTCCCATTCTATGTGTTAATTGAAACCTCTGGCTCCAAC  
AAAGAGCACGACGACGAAAAATTGGAACATTCTTGGGGAATGCAATGGAAGAAGGTTTAGTCGACGAT  
GGGATTATTGCACAAGATGAGGCTCAAATACAATCATTATGGTCATGGAGAGAATCCATCCCTGAAGCA  
ACCACTATTGGAGGCGGTGTTTACAAGTATGACGTTTCTATTCCATTGGCAGATCTTTACGGGTTAGTT  
GAGGACATCAATACCAGGTTAAATGATGCTGGAATCGCCAGCTTGGACGATGAATCGAAACTTGTGCTT  
GCTGCATTGGGTTATGGTCACATTGGAGATGGGAATTTACACTTGAACGTTTCTGTGAGAAAGTATTCT  
CCTGAAATTTGAAACTATCTTGGAGCCATTGTCTATGGAATGGATCGCAAAAAAATGGATCCATTTCG  
GCTGAACATGGGTTGGGATTCCAAAAGAAAACTACATTGGGTATTCCAAGAATGAGATTGAGGTCAAA  
TTAATCAAAGAAATCAAACAACATTACGATCCAAATGGAATCATGAACCCATATAAATACGTGTAA

YEL071W\_homolog 527aa (SEQ ID NO 482)

MQRRLVQTASYLIRRNNVACRFSSRYNGLPVASYSTKTVPFTADTYSQKVQRDAKFKQLESQDIEYFKSV  
LPENSIITDEDDLLFFNEDWMRKYRQSQLVLKPKTTEQVASILKYCNDNKLAVVPQGGNTGLVGGSNP  
IFDEIIISLSAMNKRISFDPVSGILKVDAGVILETADQYLAEQGYIFPLDLGAKGSCHVGGNVACNAGG  
LRLRLRYGSLHGSVLGLEAVLPDGTVYNSMHSRLRKDNTGYDLKQLFIGSEGLGIITGVSI LCPSPRQAQ

152/251

NVAFLAVSSYEAVQKVFVQARKELQEILSAFEFMDNTSQKLTAKHLGLEHPIESGDFPFYVLIETSGSN  
KEHDDEKLETFLGNAMEEGLVDDGIIAQDEAQISLWSWRESIPEATTIGGGVYKYDVSIPLADLYGLV  
EDINTRLNDAGIASLDDDESKLVLAALGYGHIGDGNLHNVSVRKYSPEIETILEPFVYEWIAKNGSIS  
AEHGLGFQKKNYIGYSKNEIEVKLIKEIKQHYDPNGIMNPYKYV

YER177W\_homolog 795bp public: 1..795 (SEQ ID NO 483)

ATGCCAGCCTCCCGTGAAGATTCCGTTTACCTTGCTAAATTAGCCGAACAAGCAGAACGTTATGAAGAA  
ATGGTTGAAAACATGAAAGCCGTTGCTTCCTCTGGCCAAGAATTGCTCTGTTGAAGAACGTAATTTATTA  
TCTGTTGCTTACAAGAATGTCATTGGTGCTCGTCGTGCTTCTTGGAGAATTGTTTCATCAATTGAACAA  
AAAGAAGAAGCCAAAGGAAATGAGAGCCAAGTTGCTTTGATCAGAGATTACCGTGCCAAGATTGAAGCT  
GAATTGTCTAAAATTTGTGAAGATATTCTCTCTGTGTTGAGCGACCATTTAATTACATCTGCCCAAAC  
GGTGAATCAAAAGTATTTTACTACAAGATGAAAGGTGATTACCACAGATACTTGGCTGAATTTGCTATC  
GCTGAAAAACGTAAGGAAGCTGCTGATTTATCATTAGAGGCTTATAAAGCTGCTTCTGACGTTGCTGTG  
ACCGAGTTGCCACCAACCCATCCAATCAGATTAGGTTTAGCATTGAACCTTCTCTGTTTTCTACTATGAA  
ATTTTGAACCTCCCAGATAGAGCTTGTCAATTTAGCTAAACAAGCTTTCGATGATGCTGTTGCTGATTTA  
GAAACCTTATCTGAAGATTCATACAAGGATTCAACTTTGATTATGCAATTATTGAGAGATAACTTGACT  
TTATGGACCGATTATCTGAAGCCCCAGCTGCCACTGAAGAACAACAACAATCCAGTCAAGCTCCAGCT  
GCTCAACCAACAGAAGGTAAGGCTGATCAAGAATAG

YER177W\_homolog 264aa (SEQ ID NO 484)

MPASREDSVYLAKLAEQAERYEEMVENMKAVASSGQELSVEERNLLSVAYKNVIGARRASWRIVSSIEQ  
KEEAKGNESQVALIRDYRAKIEAELSKICEDILSVLSDDLITSAQTGESKVFYKMKGDYHRYLAEFAL  
AEKRKEAADLSLEAYKAASDVAVTELPPTHPIRLGLALNFSVFYIEILNSPDRACHLAKQAFDDAVADL  
ETLSEDSYKSTLIMQLLRDNLTLWTDLSEAPAATEEQQQSSQAPAAQPTGKADQE

YGR192C\_homolog 1008bp public: 1..1008 (SEQ ID NO 485)

ATGGCTATTAAAAATTGGTATTAAACGGTTTCGGTAGAATCGGTAGATTAGTCTTAAGAGTTGCTTTGGGC  
AGAAAAGACATTGAAGTTGTCGCCGTCAACGATCCATTGCTCCAGACTATGCTGCTTACATGTTT  
AAATACGATTCTACTACGGTAGATACAAGGGTGAAGTCACTGCTTCTGGTGACGACTTGGTCATTGAT  
GGTCACAAGATTAAAGTTTCCCAAGAAAGAGACCCAGCTAACATTCCATGGGGTAAATCTGGTGTTGAC  
TACGTTATTGAATCCACCGGTGTTTTCACCAAACTCGAAGGTGCTCAAAAACACATTGATGCTGGTGCC  
AAAAAAGTTATCATCACTGCTCCATCTGCTGATGCCCCAATGTTTGTGTCGGTGTTAACGAAGACAAA  
TACACTCCAGACTTGAAGATTATCTCCAATGCTTCTTGTACCACCAACTGTTTGGCTCCATTAGCTAAA  
GTGCTCAACGATACTTTCGGTATTGAAGAAGGTTTGTATGACCACTGTCCACTCCATCACTGCTACCCAA  
AAGACCGTTGACGGTCCATCCCACAAGGACTGGAGAGGTGGTAGAACTGCTTCTGGTAACATTATCCCA  
TCTTCCACTGGTGCTGCTAAAGCCGTTGGTAAGGTTAAGTTTCCAGAATTGAACGGTAAATGACTGGTATG  
TCTTTGAGAGTCCCAACCACCGATGTTTCCGTTGTTGACTTGACTGTCAGATTGAAGAAAGCTGCTTCT  
TACGAAGAAATTGCTCAAGCTATCAAGAAAGCTTCTGAAGGTCCATTGAAAGGTGTTTTGGGCTACACT  
GAAGATGCTGTTGCTCCACCGATTCTTGGGTTCAGCTACTCATCTATCTTTGATGAAAAAGCCGGT  
ATCTTGTGTGTTCCCAACTTTCGTCAAAATTGATTTCTGTTGACGATAACGAATACGGTTACTCCACCAGA  
GTTGTTGACTTGTGTTGAACACGTTGCTAAAGCTTCTGCTTGA

YGR192C\_homolog 335 aa (SEQ ID NO 486)

MAIKIGINGFGRIGRLVLRVALGRKDIEVVAVNDPFIAPDYAAYMFKYDSTHGRYKGEVTASGDDLVID  
GHKIKVFQERDPANIPWGKSGVDYVIESTGVFTKLEGAQKHIDAGAKKVIITAPSADAPMFVVGVNEDK  
YTPDLKIIISNASTTNCLAPLAKVNDTFGIEEGLMTTVHSITATQKTVDPGSHKDWRRGRTASGNIIP  
SSTGAAKAVGKVIPELNGKLTGMSLRVPTTDVSVVDLTVRLKKAASYEEIAQAIKKASEGPLKGVLYGT  
EDAVVSTDFLGSSYSIFDEKAGILLSPTFVKLISWYDNEYGYSTRVVDLLEHVAKASA

YGR243W\_homolog 399bp public: 1..399 (SEQ ID NO 487)

ATGGCTTCAACAGTTCAACACGCATCCAAATTTCAACGTTTTTTAAATTCAGAGACCGGTCCTAGAACC  
GTGCATTTTTTGGGCTCCAGTGTTCAAATGGGCCTTAGTTGCTGCTGGACTTAATGACATACAACGTCCT  
GTTGAAAAATTGAGCGGAACCAACAGATAGCATTGTTTGGCACTGGTGCCATATGGACTAGATGGGCC  
GGGTTTGTATATAAAACCAAGGAACATGCTTTTGGCATCAGTGAATTTCTTTTGGGTGGAGTTGCTGGT  
TACCAATTGTTAAGAATTGTCAACTACAGAAGAGATTTGGGTGATTCCCCAATGCAAGTATTTAATTAT  
ATCTTGAACGGTGATGCAGCTGCTGTAAAAGAACCAGAACCAGCCAAGAATTAA

YGR243W\_homolog 132aa (SEQ ID NO 488)

MASTVQHASKFQRFLNSETGPRTVHFVAPVFKWALVAAGLNDIQRPVEKLSGTQQIALFATGAIWTRWA  
GFVIKPRNMLLASVNFLLGGVAGYQLLRIVNYRRDLGDSPMQVFNILNGDAAVKEPEPAKN

153/251

YHL021C\_homolog 1224bp public: 1..1224 (SEQ ID NO 489)  
ATGTTAAGACAACCATTACGCCAAATCCGTTTCCACTCGAAATTGGCACTTGAGGATACAACAGCAAA  
GAAGTGACAGTCACCATCAACGGCAGAACCTGTACATTCAACAACGTGTTTTTGAGAGACGCATGCCAA  
AGCCCAGACTCGGTAGACCCCATTTCTAGCCAAAACTATTCACTACAGCAGATGCAGCAACCGGCTTG  
CAAATTAACGCACCCCCAGTGGTAGAGGATTCTCTATTGAAAATCCAATGGAGCAACAATGGCAAACTC  
ACCAACTCAGTCTACCCCGTGTCTATTCTTAGAAAATACTCCACCAACAAACGACTCGGCAAAATCTTT  
GACAAAGATAGAAAAGTTATGGGACAAACAAGAACTCGAAAACAACCTTGCCTCCCTCAACATGGACTAC  
GACGACATTCTACCAACGACAACCTCTTTCTTCCAGACGTTGTACAACCTGAATAGGTACGGGTAAACA  
TTTGTCAACAACATCCCCACCCACAAATTTCTGACATGACAGAGGACAACGCCACGCAATGGCCAGTG  
TACAAGATCGCCGAAAAGTTTGGCTACATCAAGAAAACATTCTACGGGACATTATTTCGACGTCAAGAAC  
AAGAAGGAAAAAGCAACCAACATTGCCTACACCAACACGTTTTTGGCATTGCACATGGACTTGCTCTAC  
TACGAGTCACCCCGGGATTACAGTTGCTACACGCTATCCAGAATCTACGTTGGGCGGCGAAAACATC  
TTCTGTGACTCGTACCTTGCTGCTGAGCATGTCCGAAAACCGACCCAGGGCATAACGGCCTACACC  
CAGACCCCAATCACCTTCCACTACGACAACAACAACGAGTACTACTACTACAAGCGGCCGTTAATCGTT  
GAAGACCCCGAGGTTGGCGACGGGTTCCCGAAAATCGCGTCCATCAACTATGCCCCGCCATTCCAGGGC  
CCATTTCGAGGTTGACCCCCACCCAGACTTTATCCGCGGAATGCAGTTATTTCGAAACCTTCATCAACGAC  
CCGGCAAACCACTTTGAAATCAAAATGCCAGAAGGCACTTGTGTCAATTTTCGAAAACAGAAGAGCCCTT  
CACTCGAGAAACGCATTCTCCGACCTGAACAACGGCGACAGATGGTTAATGGGCACTTATGTTGACGGC  
GACAGTTTTAGATCAAAATTACGTATAGGCTATAGAAAAGTACATACCTAA

YHL021C\_homolog 407aa (SEQ ID NO 490)  
MLRQPLRQIRFHSKLALAGYNSKEVTVTINGRTCTFNNVFLRDACQSPDSVDPDISSQKLFTTADAATGL  
QINAPPVVEDSSLKIQWSNNGKLTNSVYPVSFLENYSTNKRLGKFFDKDRKLWDKQLENNFASLNMDY  
DDILTNDNSFFQTLNLYNRYGLTFVNNIPTQISDMTEDNATQWPVYKIAEKFGYIKKTFYGLFDVKN  
KKEKATNIAYTNTFLPLHMDLLYYESPGLQLLHAIQNSTLGGENIFCDSYLAAEHVTKTDPRAYTALT  
QTPITFHYDNNNEYYYYKRPLIVEDPEVG DGFPKIASINYPFQGPFEVDPHPDFIRGMQLFETFIND  
PANHF EIKMPEGTCVIFENRRALHSRNASDSNNGDRWLMGTYVDGDSFRSKLRIGYRKVHT

YHR162W\_homolog 354bp public: 1..354 (SEQ ID NO 491)  
ATGTCATCATTTTAAAAAATTCAGTATTTTATTTTCAAAACAATCCCTTAGATATGTCTGTACAAC  
CATTTTTGGGGTCCAGTATCAAATTTGGGATTCTATAGCTGCTATTTTAGATTGAAAAAAGATCCT  
GATTTAATTAGTGGACCAATGACTGGTTCATTAATACTTTATTCTTTAGTGTATGAGGTATTCAATG  
GCAGTTACTCCTCAAATTTATTATTGGGTGTCATTTTGTGAATGAATTGGCACAATTGAGTCAA  
GGATTTAGATGGGTAAACATCACTATGATACTTCTTCAAATGATGGTGAAGATACAAAAAGATAACT  
CAAAATTGA

YHR162W\_homolog 117aa (SEQ ID NO 492)  
MSSFKKFTDFLSKQSLRYVCTTHFWGPVSNFGIPIAAILDLKKDPDLISGPMTGSLILYSLVFMRYSM  
AVTPQNYLLFGCHFVNELAQLSQGF RVWKHYDTSSNDGEDTKKITQN

YLR109W\_homolog 531bp public: 1..531 (SEQ ID NO 493)  
ATGACTGACGGTAAATTCCCACTAACATTGAACCAAAATACATTCTTATTCTAAAGATCATGCAAGT  
TTAAGTCTTGTGCTAATCCAATACCATTGGATTAAATCTTTATTTCCAAATAATACTGTTGTTGTC  
ACTGCTGTGCCTGGTGCTTTTACCCCAACTTGACTGAACAACATATCCCTGATTATTTGAAACATTTG  
AAAGATTTCAAAGACAAGGGCGTCAAAAAAATCATTTGTTTTATCTGCCAATGATCCATTTGTAATGGCA  
GCTTGGGCTAAAGCTTTGGGTATAGTGAAGAAAATTATGTTATTTTGTCTACTGATCCTAATGCT  
TCTATTTCTAAAGAATTGGGTGATGGATTTGTTGCTGATTGACTCTGGCAGGTATGGGATTAAGATTA  
CAAAGATATGCTAGTATTGTTGTTAATGGAGAAATCACTTATTTGGAAACTGAAGATAGTTTGGGATTC  
CTGGAAATTTCTAGTGCTGAAACCATTTTAAAGAGAATCCACAATTAA

YLR109W\_homolog 176aa (SEQ ID NO 494)  
MTDGKFPTNIEPKYIPYSKDHASLTACANPIPLDLKSLFPNNTVVVTAVPGAFTPTCTEQHIPDYLKHL  
KDFKDKGVKKIIVLSANDPFVMAAWAKALGYTDEENYVIFATDPNASISKELGDGFVADLTSAGMGLRL  
QRYASIVNGEITYLETEDSLGFSEISSAETILKRIHN

YLR206W\_homolog 879bp public: 1..879 (SEQ ID NO 495)  
ATGAGAAAACAAAATAACAATTTATTGGATTGTAATGATGAAACACCACCACAACAACCTCAATATTAT  
TTAGCAACCGGATTCTATCAACAACAACCAATTTTATGGCCAGCAACCTCAATCGCAACAATCTCAA  
CAATATGATATGTTTGGGAACCCAATACAGAAATCCAATGGACACAGGATTATATAATCAACAGGCTAT  
TATCAACAACCACAACAGCAGCAACAACAGTTTCAACCAAAACAGTTTACTGGTTTTAACTATGGACAA  
CCACAACAACCACAAGCGCAACCAGAACCTTTACAACCATTGAAAACAGGATCCAATAATCCATTGCCC  
ATGCTCTTCTGGGTGACACAATACCAACAAGCCACCAACTCAATCCTTAAACAGTTTAGCTGAACAGCAA

154/251

CAACAGCAACAGCAGCAGCAACCACAATTTTTTACTCAGCCAACTACTGCTCCACTCAAACAACAAAAC  
ACATCATCATCAAGGTTTAAATGAACTCATGAGTTGAATGATTTATTAAGTCAAGGAACTGGATTAGAT  
ACATTCGGTAACACTGGAGATACTAGAATCCCACATCAACATACAAAGACACAAAATTTTATAAATTCA  
AGTGGAACTGGATATAAAACAACTGGTAATGAACCAATTAGATTAAGTTCTAATGCTACAGGTAATCCA  
TTTCTTAATACTGGTATTGGATATCAAGGTGCTACACAACAGCAAGTGCCACAACAGCAAGTGCCACAA  
ATCAATCCTGCTTATACTGGGTATGGATTGGTTACGCTCAACCTCAACAACACCAGCAATACCAACAA  
CAACAACAATCACGTAATGGTAATGATGGCCCAAGTTTAAATAGATATTTAA

YLR206W\_homolog 292aa (SEQ ID NO 496)

MRKQNNNLLDLNDETPPQQPQYYLATGFYQQQPQFYAQPPQSQQFQQYDMFGNPIQNPMDTGLYNQQAY  
YQQPQQQQQQFQPNQFTGFNYGQPQQPQAQPEPLQLKTSNNPFAMSSGSDNTNKPPTQSLNSLAEQQ  
QQQQQQQPQFFTPPTAPLKQONTSSSRFNETHELNDLLTQGTGLDTFGNTGDTRI PHQHTKTQNFINS  
SGTGYKQTGNEPIRLSSNATGNPFLNTGIGYQGATQQQVPPQQVPPQINPAYTGYGFGNAQPPQHQQQYQQ  
QQQSRNGNDGPSLIDI

YMR043W\_homolog 789bp public: 1..789 (SEQ ID NO 497)

ATGGCTATTAAAGAAGAAACAAATGAATTTAGTCAAGGTAATGAGGGGAATTCCTTCAACCAATAAC  
AACAATAACAGCAACAACAGCAACAACAATGCTGATGTTTCTGCACCAGTAGATGATGACGAT  
GATGACGATGGTACTTCTCAAGGTAAAACCTCAAAAGGAAAGAAAATTTGAGATCAAATTCATTCAA  
GAAAATCAAGACGTCATATTACTTTTTCGAAAAGAAAAGCTGGGATTATGAAGAAAGCTTATGAATTA  
TCAGTATTGACAGGTACTCAAGTGTTATTATTAGTTGTTTCAGAACTGGTTTGGTTTATACTTTTACC  
ACTCCTAAATTACAACCTTTGGTCACTAAATCTGAAGGGAAGAATTTGATTCAAGCATGTTTGAATGCT  
CCTGAAGAAGGATTGGGTGATGATCAAGAGAATCAAAGTGATGGAAATACAGGAGATTACCTGATCAA  
AGCCCTGCTCCAGCAACCAATCCAAATGTGATGGGTGCTGCAGGTCATGCTCATCATTCACAACAA  
CAACAGCAACAACAAGCTCAACAGCAAGCTCAGCAACAACAATGGCACCAATGCCTTCTCATGGTTTA  
CCTACACATTATTCCAATCCTCAAGGAGCTGGTAATCCTGGTGTACCTCCTCAACAACAAGGTCAACAT  
CAACCTGGTATTCCATTACAAGGTGGTTATAGTGATCAATACCTGTATTTTGGTAATATTCAAAATAAC  
AACATACCTAATCAACAGCAATATCAATGA

YMR043W\_homolog 262aa (SEQ ID NO 498)

MAIKEETNEFSQGNENSHSTNNNNNSMNSNSNNNADVSAVDDDDDDGTSQGKTQKERRKIEIKFIQ  
EKSRRHITFSKRKAGIMKKAYELSVLTGTQVLLLVVSETGLVYFTTTPKLQPLVTKSEGKNIQACLNA  
PEEGLGDDQENQSDGNTGDSPDQSPAPATNPVMGAAGHAHHIQQQQQQQQQAQQQAQQQMAPMP SHGL  
PTHYSNPQGAGNPGVPPQQQQQHQPPIPLQGGYSYDQYSYFGNIQNNNIPNQQQYQ

YMR256C\_homolog 330bp public: 1..330 (SEQ ID NO 499)

ATGAGAATGAAACAACCAGACGACCAAAAGTCTGAGAGAGAGAGAGAGAAAATATCGGCTCATTATT  
TTCAATTCACCTTTTAACTAGTTAATACTATTTACTTTCTTTCTTCTAATCCATCCACCATCCT  
ATCTATTCAATTATGAATCCACAAAGATTATTGAATTACAAAACATTATCAAAATACTCCTAAACCA  
TTATGGTTAAGAGGTAGACAATCGGCATTTTATGTTTATCCATTTTATGCTTTATTTGCTGTTAGTACT  
GCCATCCCATTATATTATAGTGTTAGAGCTGTTGCTGGTATAAAAGATGAATAA

YMR256C\_homolog 109aa (SEQ ID NO 500)

MRMKQPDQKSEREREKKYRLIIFNSLLILVNTIYFLSSNYP SHHPIYSIMNPQRIIE LQKHYQNTPKP  
LWLRGRQSAFLVYPFYALFAVSTAIPLYYSVRVAGIKDE

YOR267C\_homolog 2091bp public: 1..2091 (SEQ ID NO 501)

ATGCCAGATAAACATAAACTCAAACCTATTTGGAAAAAATAAACACGACAAAGATGACGAATTGTCTTGT  
TCAACGTCAAACCATTTCTCACGGAAGTACACGGAAGTTTTTAGGATTTTCATATTGGAAGACATGAATCG  
GGCGACTCGTTGACTTCTCCAGTTATGAGCAATTCATCCGAAAGTCATCATCACAGCCATCACCTTCAT  
CAAGCCAATTCAAGTGCAAACCATCGTAACCTTCTCCAGTTCATTCCAATACTGGTACTGCCACTACC  
ATTCCATCAATACAATCACCACAACCTCAAGCATCTGGATTACACCGCGGGGACTCCGATAAAAAATCA  
TCTGGCTCAGTTGTTGATTTGAAAAAATCTTCAAAACAAAGAAAACCTCAAATCCAAGAAAGGAAGGA  
CATAGTATTTTGGGACAATATAGCAATCAGTCCATTCAACCAACCAATGGCGAGGTTTCATTGCGCT  
GGTGCAGGGTCGGGGAACGGCAGTGCCTTGCAATCACGTGAACAATCATCTACGTATTAGCCACTTTA  
ATCAATCAAACATCTTCTCAACTTTTGTACAATGCTTCACATTCTGTCAATAGCAATCGAGATCCCTTC  
ACGGACGACAACCTCTCCATTGGTGAAGAAGTATGGTAAGATCGGGAAAGAGTTGGGCAGTGGAGCCGGT  
GGGTCCGTCAAATTAATCACCAGGCCAGTGACTCCAAGACGTTTGTGTTAAAGAATTTAGAGCGAAA  
AGATCTACTGAATCATTGAAGGATTACACTAGGAAATGTACTGCTGAGTATTGTATTGGTTCTACTTTG  
AGGCACCAACATCATTTAAACCATCGATATTATCCATGAAAACAATCGTTATTTTGAATTATGGAA  
TATGCACCTATAGATTTCTTTGCTGTTGTTATGAGTGGAGAGATGTCTCGAACGGAAATCAATTGTTGT  
TTAAAGCAAATTATTGAAGGTGTGGCATATTTACACAAATTAGGGTTGGCCCATCGTGATTTGAAATTG  
GATAATTGTGTTATAACGAATGAAGGGATTTTGAAGATTATCGATTTTGGTAGTGCTGTCATTTTCAAG



155/251

TATCCCTACGAACAGTTTGGTAACAACAATTCTATTACGCCGTGTCATGGTATTGTTGGATCTGATCCT  
TACTTGGCCCCGAGGTTTGAATCTCCTAATAGCTACAACCCACAACCTGTGGATTATGGTCTATT  
GCCATAATTTACTGTTGTATGACTTTGAAGAGATTTCCTTGGAAAATACCTAGTCAAGAAAAGGATAAC  
AGTTTCCGACTTTATTGCATGTATGATGATAATTTCCATGATTATTATTTAGTAACGAATGTCATAAA  
CTTTTGTGTGAACAGCGTAAACTAAAGAATACAATTGTTAGACTGAACAAAAGGAAAAAGCAGCTAGAA  
GAGGAAAAGGGCGACAAGCCTGAAGAAGACGAAGAAATGAAAGATGCCGATAGTGCACCACAGCAACAT  
CATCATTTCTCATGTATGTAGAGCTGGGAAAAAACTGGTGGATCTACGGTTGGCAAAGACAAGTCAAATGAA  
GCTGTTACCGTTTTAACAGATGAGCAAGCAGAAGAGATTATGGCACAATTAATAGATTGATAGAAAA  
CTACAAGAGTTTGAAGATAAAAAGAATCAACTTAAAGAGAAATATGAGGCTTTGCGAGATGCTGATCCT  
AGATATCAAAAACAGTTGGCACAATTCACGAAGAGGAAGAAAAGCAAAGACTAAAAGATGCCGAGCAC  
GGTGGCGATGAGAAAAAGAAATCACATCATAAACAGATTTCATGGTCCGTATAGATTGATGAGATTGTTG  
CCACATGCTGCTAGACCAGTCATATCAAGATTATTGGAGGTTGATCCAAAGAAAAGAGCAACTATGGAA  
GAAATTCCTAGAAGATGAATGGATTAAAGAAATTCATGCTGTACAGTTAAGCCAGTTTCAAATCAACA  
GATGCAACATTAGATTTTATTGAGGATGAGGACGAAGTATTGGTGAAAGGAGTACCTCCACACGAGCAT  
ACAATTGTGAAAGAAGGTTGA

YOR267C\_homolog 696aa (SEQ ID NO 502)

MPDKHKLKLFQKNKHKDDLSLSTSNHSHGSTRKFLGFHGRHESGDSLTSPPVMSNSSESHHHSHHPH  
QANSSANHRNPSPVHSNTGTATTIPSISQSPQASGLHRGSDSKSSGSVVDLKKFFKTKKTSNPRKEG  
HSILGQYSNQLHSPPPMAQVHSPGAGSGNGSALQSRQSSTSLATLINQTSSQLLYNASHSVNSNRDPF  
TDDNSPLVKYKIGKELGSGAGGSVKLITRPSDKTFVKEFRKRSTESLKDVTREKCTAEYCIGSTL  
RHPNIIKTIDIHENNRYFEIMEYAPIDFFAVVMSEMSRTEINCCCLKQIIEGVAYLHKLGLAHRDLKL  
DNCVITNEGILKIIDFGSAVIFKYPYEQFNNSIQPCHGIVGSDPYLAPEVLKSPNSYNPQPVDLWSI  
AIIYCCMTLKRFPWKIPSQEKDNSFRLYCMYDDNFHDYLSNECHKLLQLQRLKNTIVRSNKRKKQLE  
EEKGDKEEEDDEEMKDADSAPQQHHSHDVESGKTGGSTVGKDKSNEAVTVLTDEQAEIIMAQLNEIDRK  
LQEFEDKKNQLKEKYEALRDADPRYQQLAQIHEEEKQRLKDAEHGADEKKKSHHKQIHGPYRLMRL  
PHAARPVISRLLEVDPKKRATMEEILEDWIKIQCCTVVKPSKSTDTLDFI EDEDEVLVKGVPPHEH  
TIVKEG

YOR374W\_homolog 1500bp public: 1..1500 (SEQ ID NO 503)

ATGTTTAAAAAGGCCTTACCATTAGTCAGCAAGCTCACAAACACCAAAAGGTATCACTTATAACCAACCC  
CTTGGGTTATTTCATCAATAACGAATATGTTTACCCAAAAGCAACAAAAGACATTGAAAGTTATTTCTCCA  
TCCACTGAAGAAAAAATAACTGATGTTTACGAAGCTTTAGAAGAAGATATTGATATGCTGTGAAGCC  
GCACAAGCCGCATACCACAATGGTTGGGCTCAAGGGCCACCAGAACAAAGATCAAAAGTTTTGTTCAAA  
TTAGCCGACTTGATTGAAGAAAATGCCGAATTATTAGCTCAAATTGAACTTGGGACAACGGTAAATCC  
TTACAAAATGCCAGAGGTGATGTTGCCTTGACAGCTGCTTACTTCAGATCCTGTGGTGGTGGGCCGAC  
AAAATTTTGGGTTCCCAAATCAATACTGGTAACACTCATTCAACTACACTCAAAGAGTCCCATTAGTC  
TGTGGTCAAATTATTCCTTGAATTTCCCATTATTGATGGCTTCTTGGAAATTGGGACCAGTTCTTGCT  
ACTGGTTCTACCAGTGTGTTGAAGACTGCTGAATCCACCCATTATCTGCTTTTATATCTTTCCAAATG  
TTAGTCGAAGCCGGTATGCCAAAAGGTGTTATCAACATTGTTTCTGGTTTTGGTGCTACTGCTGGTGCT  
GCCATTGCTAAACATCCAAAGATTGAAAAAGTTGCTTTCACTGGTTCTACTGCCACCGGTAAAATTATC  
ATGAAATTGGCTGCTGAATCAAACCTGAAAAAGTTAACTTTGGAATTGGGTGGTAAATCTCCAAACATT  
GTTTTCAACGATGCTGATTGGACAAGACTATTCAAACTTGATTGTTTCTATCTTCTACAATTCTGGT  
GAAGTCTGTTGTGCTGGTCTCGTCTTTGATTCAATCCGGTGTTTACGACCAAGTTGTTGAAAAATTC  
AAAGAAGCTGCTGAAAGTGCAAGGTTGGTAACCCATTTCGACGAAGACACTTTTATGGGTGCCCAAGTT  
TCTGACGTCCAATTGTCCAAAATTTGAAATACGTTGAATCTGGTAAATCTCAAGGTGCTACTGTTGTT  
ACCGGTGGTGCTAGAGCTGATGGTAAAGGTTACTTTGTCAAACCAACTATTTTCGCTGATGTCAAGAAA  
GATATGGATATTGTGAGAGAAGAGATCTTTGGTCCAGTTGTCACTTTGATCAAATTTGATACTGTTGAC  
GAAGCCGTTGAATTGGCCAATGATTCCGATTATGGTTTGGCTGCTGGTATTCACTCTGCTGACGTTAAC  
AAATGTATTGATGTGGCCAACAGAGTTAAAGCCGGTACTGTTTGGGTCAACACTTATAACGATTTCAC  
CCAATGGTTCCATTCCGAGGATTCAGTGCTTCAGGTATCGGTAGAGAAATGGGTGAAGAAGTTTGCAT  
GAATACACTCAAGTCAGAGCTGTGAGAATGAAAATCAACCCACCAAACTAA

YOR374W\_homolog 499aa (SEQ ID NO 504)

MFKKALPLVSKLTPKGIYTNQPLGLFINNEYVHPKQKQTFEVIISPSTEEKITDVVEALEEDIDTAVEA  
AQAAHYHNGWAQGPPEQRSKVLFLADLIEENAELLAQIETWDNGKSLQNARGDVALTAAYFRSCGGWAD  
KILGSQINTGNTHFNVTQRVPLVCGQIIPWNFPLLMASWKLGPVLATGSTTVLKTAESTPLSALYLSQL  
LVEAGMPKGVINIVSGFGATAGAAIAKHPIEKVAFGTSTATGKIIMKLAESNLKKVLTLELGGKSPNI  
VFNDADLDKTIQNLIVSIFYNSGEVCCAGSRLLIQSGVYDQVVEKFKEAAESVKVGNPFDEDTFMGAQV  
SDVQLSKILKYVESGKSQGATVVTGGARADGKYFVKPTIFADVKKDMDIVREEIFGPVVTLIKFDITVD  
EAVELANDSDYGLAAGIHSADVNKCIDVANRVKAGTAVWNTYNDFFHMPVPFGGFSASGIGREMGEVLH  
EYTVQVRAVRMKNIPPN



156/251

YPL089C\_homolog 1836bp public: 1..1836(SEQ ID NO 505)

ATGGGTAGAAGAAAGATTGAAATAGAACCATTGACAGACGATAGAAATCGTACAGTGACTTTTGTGAAG  
CGTAAGGCAGGGTTATTTAAAAAGCTCATGAATTAGCTGTGCTCTGTCAAGTGGATTTAACGGTTATT  
ATCGTTGGCAATAATAATAAAGTATATGAATATTCTACTGTTGAGGCAATGAGATTTTAAATGCCTAT  
AATAAAACCATTAAGTCAGAAAACAAGTACATGAATCGAAGTCTCCAGAATATTATTCGAAATTTAGA  
AAGAAACGACATTTAAATGAACCACTTATGAATAAATCAGGGTCTGTAGTTGGCACTAATACACATTTG  
AACGATGAAGACTATGATCATAATGTTTCATGAAGCGGGCGATGAGGATTCGGAATATGAAAGCGATGAT  
AATTCCTCCACAACCTAAACGGCACAAAAGATCAGAGTCGGTTAAAAAGAGCAAAACCCCAAGTGTTT  
AATAGTACCCAACCTCCACCACCGCTCCACCACCTCATATATCTTTAAATAATGTTCCAACATTTACC  
AACCCCAAAATTACAAAAACAGATTGATGAGACAATAACACTTCGGCACCGCCCGCTACTGGGACA  
AAAAATGAACCAACGATGCAACGACCAGTATTGAGGGTACAAATACCGAATGATGCCAAGAGCAATACG  
AATAATTCCCATAGTGGTGTAAATAATAGTGATGGCAAGGACACGGCGAGAACAGTGACGGCAGTCGAC  
AATAGTGCAACCAACCAAAACACTCAATCGAGCAATACAACATCAGGTACAGGGACTGCTGATACCAAT  
TCATCGCAACTAAATTCAAATGGTAATAGTAATTTAGTGCCCGGGAATGTTCCAAATACCAGATTTTCG  
GGATATTCATCGTTTCGATCACCAGACTCACGAAAACCAACATTACCGTTACCTTTGCAAACCAATCA  
CAAACGTCATCTCCAGCTAGTGCTGTAGCACCAGGTTTACCATTGACAGGAGGAAGCAATGCATATTTT  
GCAGGAATGCAACAATCACCCGTGGGTGGTTTCGTATGTCAATTATCCAGCCCAAGTATATCAGCAGTAT  
CAACAGTTCCAAAATCAACTACAACATAAGAACAACAACAGCAACAGCAACAGCAACAGCAAAAAACAA  
CAATCTCAGCCCGCAGCCATCATCGCAACTGGTTGGAAATCAAAATGCACAATTGGAATCAGCAGCACGA  
TTCCGTTCTGGTTTACCGACAGGGACACAATTTAATAATGGTGAACAAACACCAATTTTCAGGATTGCCA  
TCACGATACGTTAATGATATGTTCCCTTCCCATCTCCATCAAACCTTTCTTGACCTCAAGATTGGCCA  
TCAGGTATAACACCAACTACTCATCTACCACAGTATTTTGTGAATATGCCATTGAGTGGAATTGGACTG  
CAACAAC'TGCAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACA  
CAACA  
CAACAGCAACTGCAAGTACCTGTTATCCCAATACAAACACAACATCACAACAATGGCTTCAACTACC  
AATCACAATCAGCTAATCTAATACCAGGGTTTTTACAAAACCCCAACACAAGCCACTGGAAATTCGGCA  
AATGCTTCCAAGCTGAGTGATGCTGGTGATGGTACTAATCCAACCACAGCAGGAAGTTCAAGTTCAGCA  
GATGTCAATAACACCAACAATGGACCTAATAAAAATACATAA

YPL089C\_homolog 611aa(SEQ ID NO 506)

MGRRKIEIEPLTDDRNRVTTFVVKRAGLFKKAHELAVLCQVDLTVIIVGNNNKVYEYSTVEANEIFNAY  
NKTIKVRKQVHESKSPEYYSKFRKKRHLNEPLMNKSGSVVGTNTHLNDEYDHNVEAGDEDSEYESDD  
NSPQPKRHKRSSESVKKEQNPKVFNSTQPPPPPPPHISLNNVPTFTNPQNYKKQIDETNNTSAPPATGT  
KNEPTMQRPVLRVQIPNDAKSNTNNSHSGVNSDGDRTARTVTAVDNSATNQNTQSSNTTSGTGADTN  
SSQLNSNGNSNLVPGNVPTNTRFSGYSSFRSPDSRKPTLPLPLQTKSQTSSPASAVAPGLPLTGGSNAYF  
AGMQLPTGTVSYVNYPAQVYQQYQQFQNLQLLEQQQQQQQQQQQQSQPQSSQVGNQNAQLESAAAR  
FRSGLPTGTQFNNGEQTPISGLPSRYVNDMFEQSPNSFLAPQDWPSGITPTTHLPQYFVNMPLSIGIS  
QQSQQQNAQQQSQVPVPIPIQTQTSQQMASTT  
NHKSANLIPGFLQNPTQATGNSANASKSSDAGDGTNPPTTAGSSSSADVNTNNGPNKNT

YAL003W\_homolog 693bp public: 1..693(SEQ ID NO 507)

ATGAGTGACAAAGAAGATTTAAATCTTATATCTGACAATAATAGAGTTATTTCAATGAGACAATTGATT  
TTACAATTACTGACTACAGGAATAAACAATAAATATAAACGATATACTAACATGTTTGATAGTACTACT  
GCCACTCAAGCTGATGTCACTGTCTACAAAGCTTTCCAAAAGGAATTCCCACAATTCACCAGATGGTTC  
AACCACATTGCTTCATTCAGTGAAGAATTCGAAGACTTGCCAGCCGGTAAAGCCCCAGCCGCTTCTGGT  
TCTGCTGCTGCCGCTGCTGAAGAAGAAGATGACGAAGATGTGCACTTGTTCGGTTCTGATGATGAAGTT  
GATGAAGAAGCTGAAAAATTGAAGCAACAAGATTAGCTGAATACGCTGCTAAGAAGGCTGCTAAAGGT  
CCAAAACAGCTGCCAAATCTATTGTCACTTGGATGTCAAACCATGGGATGATGAAACTGATTGGAT  
GAATTATTGACCAACGTCAAAGCTATCGAAATGGAAGGTTTGAAGTTGGGGTGCTACCAATGGATTCCA  
GTTGGTTTTCGGTATTAAAAAATTACAAATTAACCTTGGTTGTTGAAGATGCTTTAGTCTCATTGGATGAC  
TTACAAGCTGCTGTTGAAGAAGATGAAGACCACGTCCAATCTACTGATATTGCTGCTATGCAAAAATTG  
TAA

YAL003W\_homolog 230aa(SEQ ID NO 508)

MSDKEDLNLISDNNRVISMRLILQLSTTGINKKYKRYTNMFDSTTATQADVTVYKAFQKEFPQFTRWF  
NHIASTFEEDLPAGKAPAAASGSAAAAAEEDEDEDVDFGSDDEVDEEAELKQORLAEYAAKKAAGK  
PKPAAKSIVTLDVKPWDDDETDLDELLTNVKAIEMEGLTWGAHQWIPVGFQIKKLQINLVVEDALVSLDD  
LQAAVEEDEDHVQSTDIAAMQKL

YAL060W\_homolog 1185bp public: 1..1185(SEQ ID NO 509)

ATGAAGGCAATTGTATACCACGATAGAGGAGATATTAGATACGACCCCAATTTCCCTGATCCACAAATC  
ATTTCGACTGGATGATGTCAAATCAAAGTTCATTATTGTGGGATTTGCGGTACTGATTTAAAAGAATAT  
AGTGATGGGCCGATTTTTTTTCCACCAGAAAGGTGAATTGAATGAAATTTCTCAAATGGAATCAATTCAA

157/251

GTCATGGGTCATGAAATTAGTGGTGAAGTAATTGCTATTGGGGATGATGTAACCAATGTTAAAGTGGGT  
GATAAAGTTGTTGTTGAAGTGACAGGAACCTGTTTAGATAGACATCGTTACCAAGATCCTAAAAATGGC  
GATCTGCCTAAACCAAATTGTCCAAGTTGTGTTTCGGGTAACATAATGCGTGTGATTATCTTGCTTTA  
ATTGGTTGTGGATTTGCTAATGGTGGATGTGCAGAATATTTAGTTGTTGCTAGTCTGAAAGTTATTGCA  
TTCGATCAGAATAAAATCCCTATGGATATTGCCGCATTAATTCACCAATAGCTGTTAGTTGGCATGCT  
GTTAAAGTATCAAATTTTAAACCCGGTTCATATGCATTAATTTTAGGTGGTGGCCCCATTGGATTAAACA  
ACAATTTTGGCTTTGAAAGGTAATCAAGTCTCCCAAATTGTTTTAAGTGAACCAGCATTAGCAAGACGT  
CAATTGGCAGAGAAATTAGGAGTTATTACTTATGACCCACGGGTAAATCAATCGAACAATGTGTTGAA  
GACTTAAAAAATTATCCCGGGAGGTTATGGTTATGAATATTCATATGATTGTTCTGGAGTTAAGGCA  
ACTTTTGAAACTGGATTGAAAACCTTGAAAATTCGTGGATGTGCAACAAATGTTGCCATTTGGGCTCAT  
AAATCAATTCCTATATATCCCTATGGAAATTACCCTTTCAGAAAAAATGTTAACTGGATCAATTTGTTTT  
GTTAAAAAGATTTTGAAGAATCAATTAAAGCAATTGAAAAATGCTTTAATATCGATTGATGAATTGAAA  
ATGTTGATTACTCTGAAAATTCATTTACAAGATGGAATTGAAAAAGGGTTTTTGGAAATTAATTAATCAC  
AAGGAAAAACATATTAAAAATTTGTTTTCTCCGAAAAGTGAATATTTACTATGCAATGGAGTAAATGAT  
TCCAATAATAA

YAL060W\_homolog 394aa (SEQ ID NO 510)

MKAIVYHDRGDIRYDPNFPDPQIIRSDDVKIKVHYCGICGTDLKEYSDGPIFFPPKGELNEISQMESIQ  
VMGHEISGEVIAIGDDVTNVKVGDKVVVEVTGTCLDRHRYQDPKNGDSPKPNPCSCVSGNYNACDYLAL  
IGCGFANGGCAEYLVVASSKVIADFQNKIPMDIAIQPIAVSWHAVKVSNFKPGSNALILGGGPIGLT  
TIFALKGNQVSQIVLSEPALARRQLAEKLGVTITYDPTGKSIEQCVEDLKKLSPGGYGYEYSYDCSGVKA  
TFETGLKTLKIRGCATNVAIWAHKSIPLYPMEITLSEKMLTGSICFVKKDFEESIKAIENGLISIDELK  
MLITSKIHLQDGIIEKGFLLEINHKEKHILFSPKSEYLLCNGVNSNK

YBL058W\_homolog 1116bp public: 1..1116 (SEQ ID NO 511)

ATGTCTGAAATACTCCAGATTCCCAATTGATTGCTGAATTTGTATCTATAACAAATTTCTTCTACATAC  
CTTGCTGAACAGTATTTACTGAGAAACAGCAATGATTTAGTGGAAGCAGTTGAGGATTTCTATGCCAAC  
AATGAACCATCTCAAAAATCAGAAACCAAAAATCTTCTTCTTCTAATGCTAAAGGCTCTGGTGTAA  
ACATTTAGAGACTTGAACGATGAAGATGATGATGAAGAGGATGACAAGACCAATACCAATTTCTTTACT  
GGAGGAGAGAAATCAGGATTGCAAGTTGAAGATCCCAATAAAGATAAGGATAATGACAGATCAATAATT  
GATCAAAATTTTCCAAAAGCCAGAGAACAATGCAACAACCAGATGATAGACCAAGTGCTTCTCAAGAT  
GATCAACCATCACCAATTAATTTTTCAGGCAAGGGTTCAATTTGGGTGACGGGAATGAACCAAGTCAA  
GTAGTGGAGGATCCTAATGCCAGTGCTAAAAAATTCAGACCTAGTAAAGTGACTAGAGAAATTACATTT  
TGGAACAAGGTTTTCACAGTAGGTGATGGACCTTTCATAGATACGATGATCCAAAGAAACGCCAGTGTT  
TTGCAAGAATTGAACCAAGGAAGAGTTCCAATGTCAATTTTAGATGTTGAATTTGGCCAAGATGTTGAT  
GTTTCTGTATACAAGAAACCGACGAAGATTGGACACCTCCGAAAAGAAAATTTGGTGGTTATCACGGT  
GCAGGTCTAGACTAGGCTCACCAGTACCTGGGGAAGTACTTGTAAATAATGAAGCATCATCTCAACCT  
GATATCAAAACCGAACTGAAATTTCTAAACCAAAAGACGAAGGCGAAGGTGACTCCACAGTTCAATA  
AGATTTGCCAATGGTAAAGAACATCACACAAATTCATTTCTCGGATTCTATTCTCAAGGTTTATGAA  
TTTGTTAAAAATCATGAATATAATTCTGAACCTACTAGACCATTCACTTTAAGTCAATGCATTCCCAGTC  
AAACCAATAGAAGAAAGTAGTGACATTACAATTTCTGATGCTAAATGAAAAATGCAGTGATTGTTCAA  
AGATGGAAATAG

YBL058W\_homolog 371aa (SEQ ID NO 512)

MSENTPDSQLIAEFVSITNSSTYLAEQYLSRNSNDLVEAVEDFYANNEPSOKSETKKSSSSNAKSGSVK  
TFRDLNDEDDDEDDKTNTNFFTGGEEKSLQVEDPNKDKDNDRSIIDQIFQKAREQMQQPDDRPSASQD  
DQPSPIKFSKGKFLGDGNEPSQVVEDPNASAKKFRPSKVTREITFWKQGFVGDGPLHRYDDPRNASV  
LQELNQGRVPMISILDVEFGQDVDSVYKKTDEDWTPPKRKIGGYHGAGHRLGSPVPGEVLVNNEASSQP  
DIKTETEISKPKDEGEDSTVQIRFANGKRTSHKFNSSDSILKVYEFVKNHEYNSEPTRPFTLSHAFFV  
KPIEESDITISDAKLKNAVIVQRWK

YBR039W\_homolog 804bp public: 1..804 (SEQ ID NO 513)

ATGCGTCTTAAATCCATTAAAAACATTGAAAAATCACCAATACCATGAAGATTGTTGCCTCTACTAGA  
TTGAGTAAAGCTCAAAAAGCCATGGCTTCATCTCGTGTTCATGAAACTGATAAAGAATCTTGTGCT  
AATGCTGAACCAAAACCAATTGAAGAAGAAGCTTCTAAATCTGATGACAAAACCTTTATTGATTGTTGTT  
TCTTCCGATAAAGGTTTATGTGGTTCTATTCACTTCAAGTTTCCAAAGCTGCCAGAAAGAGAACTGAA  
GAATTAATGGTAATGTCGATATTGTTTGTATTGGTGATAAAGTCAAAGCACAAAATTTGAGAACTTAT  
GCTGACAAAGTTAAATTGGCATTCAATGGTGTGGTAAAGAAGAACCAATTTCACTGAAGTTGCCTTA  
ATTGCTGATGAAATTGCTAAATTAGGTAACATGAAAATGTTGAAATTTCTTTACAACAAATTTGTTTCT  
GGTGTTCATTGTAACCATCTAAATTTTCCATTTATGCTGCTGATGCCATTGCTAACTCTCCAGGTTTA  
AGCAATATGAATTGGAATGAAGAATCACTTCTGATGTTGCTCAATTTCTTTAGCTAACAACCTTG  
TTGACTGCTATGGCTGAAGGTTATGCATCTGAAGTTTCTGCTAGAAGAAATGCTATGGACAATGCCTCC

158/251

AAGAATGCTGGTGATATGATCAACAGTTACTCTATTTTGTATAACAGAACTAGACAAGCCGTCATTACC  
AACGAATTGGTTGATATCATTACTGGTGCTTCCTCATTGGACTAG

YBR039W\_homolog 267aa (SEQ ID NO 514)

MRLKSIKNIKITNTMKIVASTRLSKAQKAMASSRVFNETDKEFLSNAEPKPIEEEASKSDDKTLILIV  
SSDKGLCGSIHSQVSKAARKRTEELNGNVDIVCIGDKVKAQILRTYADKVKLAFNGVVGKEPNFTEVAL  
IADEIAKLGNYENVEILYNKFVSGVSVFEPKFSIYAADAIANSPLSKYELENEEITSQVQFSLANNL  
LTAMAEGYASEVSARRNAMDNASKNAGDMINSYSILYNRTRQAVITNELVDIITGASSLD

YBR062C\_homolog 450bp public: 1..450 (SEQ ID NO 515)

ATGTTATCTGCATCTAACGAAGAAGCCATAGCATCAGCATTGCGACAATTGAGTGAATCAGAAGGATCA  
ACACTTGCTCAATCACTCATGGATCTGCTTGGTGAACAAAAGACATCGAAGGGGGTCACTGACGAATAC  
TTGGATACCTTTGGAACGTATTCCAGTAAACAAAATTTACTGTATAAGACGCATCTTTGCAATTTGTACA  
AATCGATTCAAAGATGATAAGCATCCATTGATTGTGAGATTGCGCTTGTGGTCACTGAGTCAATCATATT  
TTTGATTTGGAATGTGTTGGGCCGTGGTTGCAATGAATCCACTTGTCCAATGTGTGCAACCAATATC  
TTAGAGGTAGAAGCTAATAGAAGGAAAATAATAGATGAAGAAATAAAAAAGGCCCAAGAAGAAGATTCC  
GAGGAAGAAGAAGAAGGTTGGGATATATATGGATAA

YBR062C\_homolog 149aa (SEQ ID NO 516)

MLSASNEEAIASALRQLSESEGSTLAQSLMSLGEQKTSKGVTDYLDTLERIPVKQITDKDASCPIC  
NRFKDDKHPLIVRLPCGHGVNHIFDLECVGPWLQMNSTCPMCRNTNILEVEANRRKIIDEIKKAQEEDS  
EEEEEGWDIYG

YBR101C\_homolog 855bp public: 1..855 (SEQ ID NO 517)

ATGGAAAAATTATTACATTGGACAATTGCACAACAATCAGGGGATAAAGCAGCTCTTGAAAAGATTGGA  
GAACCCGATCAAAAGGCACTTAATCAATTATTTGGTGGTCCCGATGAAGCCACTTTAATGAAGGAAAGT  
ATAAAAGTTGTTGAATCAACCGATGTTTCATTAGAAGATAAAGAGATCGCCTTGAAAATTTGCAAATG  
TTGATTGAAAATTTAGATAATGCAATAATATTGGTAATTTGAAATTATGGAATCCATTGATTGACATT  
TTAGCCAAAGAAGATACCCCTGTTGAATTGAAAGTACTTATTTGTGGAATAATTGGAACCGCTGTACAA  
AACAACCCCAAATCTCAAGAAGATTTCAATGAACTGAAGGATTGAGTGAATTGATAGAATTAGCACAA  
GATGACAAAAAATTTGAATTACAACCTGAAGGCATTGTTTGCTATTTCTTCATTATCAGAAAATTTTCAA  
CCTGGATATGCAAAGTTTGAGAAATTGCAAGGTTTGAACTCATTAATTTTGATAACAAGAACAACAAG  
TATCAATTGAGAATTTTATCATTAATATCATCCATTTTGAGTAATGGGTTAGACGATAGCTTGAAAGCA  
CAATTCAAAGAAGCAAAATTACCTCACTATTTAGCCTCGGTATTGAATGAGGATTCAAACACTAGTTTG  
GTGGACAAATCTTTAAACATTGTTTCTCAATTGAATCAATTAACTATGAGTTTAGCTTAGAAGAAAAA  
TATGAAATAAATAGAGGAATCCAAGTGGTTGAAGGGTTGAGTGAGAACTTAATATTGATGATCTCAAT  
AATGCCAAACAGGCCACATCCTCTTAG

YBR101C\_homolog 284aa (SEQ ID NO 518)

MEKLLHWTIAQQSGDKAALEKIGEPDQKALNQLFGGPDEATLMKESIKVVESTDVSLLEDKEIALENFEM  
LIENLDNANNIGNLKLWNPLIDILAKEDTPVELKVLICGIIIGTAVQNNPKSQEDFNETEGLSELIELAQ  
DDKKFELQSKALFAISSFIRNFQPGYAKFEKLGKLIINFDNKNKYQLRILSLISSILSNGLDDSLKA  
QFKEAKLPHYLASVLNEDSNTSLVDKSLNIVSQNLNLYEFSLEEKYEINRGIQVVEGLSEKLNIDDLN  
NAKQATSS

YBR139W\_homolog 1653bp public: 1..1653 (SEQ ID NO 519)

ATGCAATTATCTACATTAGTCACTTGGTTGGCTGCTTTAACTGTCGGTGCACAGGCAGTATCATTCGGC  
AACAATTTAAAAGATCAGATTATATTGGATTCTGAGGAAAGCTCCCAGATTTATATTGGAGTCAGTG  
TTCAAAGACTTGGGTTCAATTGCCAGTTGATTGTGATTACTGCTTGGGCAGAAATGCAATCTGAATTATCA  
CCTGAACAAATTGCCAAATTAATCAATCAATATGAGTCTAAAAATGAAAAACCAAGAAAAATAAGTTT  
AATCCAATGTCGACATTTTCTTCACCAAGTTCCAAGTTTGAAAAGCTTTCCAATGATAAATTTGCTGGT  
TATTCATGCGTGTAAAAGAGAGTTTCCAGAAATTTGGGTCTTGATACAGTGAAACAATACACTGGG  
TATTTAGATATTGACTCATTAGATAAACATCTTTCTTATTGGTTTTTTGAAAGTAGAAATGATCCAAAG  
AATGATCCTATTATTTTATGGCTCAATGGTGGTCCAGGTTGCAGCTCTTCAACGGGATTATTTTGTGAA  
TTAGGACCATCCTCGATCAACAAAACCTTTACACCCAGTTTACAACCCATATTCTTGGAATTCCAATTGCG  
TCGGTTATTTTCTTAGATCAACCCGTTGGAGTTGGATATTCGTATACAGGAGGAGATGAAGTTAAGAAT  
ACTCTCACTGCTGCTAAAGACGTTTATGTGTTTTTGGAAATTGTTTTTCCAAAAATCCCACAATTTTGTG  
ACTAATAAGTTTCACATTGCCGGTGAATCTTACGCCGGTCAATTATATACCAGCATTTGCTTCAGAAATC  
ATTAACAATGCCGATAGGTCATTTGAGTTGGCATCTGTGTTGATTGGTAACGGTATCACCGGATCCATTG  
ATTCAAGATGGTTCTTATAAACCAATGGGCTGTGGTGAAGGTGGTTACAACACTGTTTTGACAACCTGAA  
CAGTGTGATCAAATGGAAAGGGATTATCCTAGATGTGCTAAATTGACTAAATTATGTTACAGTTTCCAA  
TCTGCCTTGACTTGTGTTCCAGCTCAATACTACTGTGATTCCCGTTTATTTCAACCTTATGCTCAAACA  
GGATTAAATCCTTATGATATCAGAAAGGATTGTGCCGAGCAAGGTGGTAATTGTTACGTAGAAATGGAT

159/251

TACTTGGATGAATACTTGAATCTCGATTATGTGAAAGAAGCTGTTGGTGCTTCTAATATTGACATTTTT  
 ACTTCATGTGATGACACCGTGTTTAGAACTTTATTTTAGATGGTGATGAAATGAAACCTTTCCAACAA  
 TATGTTGCTGAGTTATTGGACAATAATGTACCTGTATTGATTTATGCTGGTGACAAAGATTATATTTGT  
 AATTGGTTGGGTAACCTGGCATGGGTAACGAATTGGAATATTCAGATAGTGAACATTTTGCACCAAAA  
 CCATTACAATTATGGAACAAGATGGCAAGAAAGCTGCTGGAGAAGTCAAGAATCACAAACATTTTACA  
 TTCTTGAGAAATTTATGACGCTGGTCACATGGTTCCCTTTTGATCAACCAGAAAATGCTCTTAGTATGGTT  
 AATACTTGGGTACAGGGAGATTATCTTTTGGTTTAGAGGGTAATAAATTATCTGAAGCTGATTAA

YBR139W\_homolog 550aa (SEQ ID NO 520)

MQLSTLVTLWLAALTVGAQAVSFGNNLKDQIILDSESSPDLYLESVFKDLGSLPVDLITAWAEMQSELS  
 PEQIAKLINQYESKNEKPKKNKFNPMSTFSSPSSKFELSNDFAGYSMRVKESFPEILGLDTPVKQYTG  
 YLDIDSLDKHLFYWFFESRNDPKNDPIILWLNNGPGCSSSTGLFFELGPSSINKTLHPVYNPYSWNSNA  
 SVIFLDQPVGVGYSYTGDEVKNTLTAADKDVYVLELFFQKFPQFLTNNKFHIIAGESYAGHYIPAFASEI  
 INNADRSFELASVLIGNGITDPLIQDGSYKPMGCGEGGYKPVLTTEQCDQMERDYPKAKLTCLCYSFQ  
 SALTCVPAQYYCDSRLFPYAQTGLNPFYDIRKDCAEQGGNCYVEMDYLDLEYLNLDYVKEAVGASNIDIF  
 TSCDDTVFRNFILDGDEMPPFQYVAELLDNNVPLIYAGDKDYICNWLGNLAWNELEYSDSEHFAPK  
 PLQLWKQDGKKAAGEVKNHKTFLRIYDAGHMPFDQPENALSMVNTWVQGDYSFGLEGKNLSEAD

YCL052C\_homolog 1446bp public: 1..1446 (SEQ ID NO 521)

ATGAGACAAAGAACAACCATTTATAATCCTTATTCTAGTCATGATGGAATCATAACTAATCTTAATCGA  
 ACAAATTTCCAATTATCAAGCATACCTAATCATTTATTCACAATTGAGAATAAATATACCATCACCACC  
 ACCACCACACAACCTAACAAATCATCATTTATATCTGGCAATTAAAGAAATTAAGAAATTCAAACGAAATTC  
 AATAAATGAATCAGGTATACCAATTTTTCTCATTTTATTATGAACCAGGACTTAATATTTATGCTGTA  
 CCACAATCTAATGTCGACAAATTAGAATTTTGGCAACAAGTTGAACAATTGATAATGGAATTTATTAGGG  
 ATTAAATTTATCTTCACAACAATGGATTGCTAATGTTAATTTCTTTTATTATCATGATATTCAACCTCAA  
 CCATTATTGAATTTGAAAGAAGGATGGAATTCATTTTACATCCTAAATCCAATTATGATTATATATAT  
 AATCAAGATAAAATTTATTTCCGGAATTTGTTAACAATGTGTCAGAAATAGAATTTAATCTTGAACCTG  
 GGTATTTATAAAGAAATTTGGTTTGT'TTTAATTTGATGAAAAATCTCAACTAATGATGATTTGAATTTA  
 AGTGGTATTAGAGTGATATTAGATGAAGATAGTAATCAATAACAAGAAGAAATCGATACATAAGACA  
 ATGTTTTCATATAAAACCAAGACATAGGAGTTTGTGATGATTCTACCACCATCACCACCACCAAGATCAT  
 CCACAAGGATTACATCCTATTTTGGAGTACTGAACTTAACACAACAACCTATTTGTTATTCCAACGATTTT  
 GATGTTGAAGAATGTAAATTTTATTATTATTGAAATTTAAATAAATCATTAATATTTGATCAATTTCAA  
 AACATTTCCAATAGGATCGCAATTAATTTAATAATGGGAATAAAAAATTTAGAATTTACCAGAATATAAA  
 ATTAATCAATGGGGTAATGAACTTTATTTGAATTTGAATTTGATAATGATAATGATATCCCTCATCAT  
 ATAAATTTAACAGTTTCAATCAAGATATCAATTACCTCAAAATAATCATTTCCCATTTCCCAATTAGTAAT  
 GTTTTAAATTCGTTACCAAAATTTTATAGTTTGTAAATGTCAAAGAAGGAAATTTATTAGATAAAATCA  
 CCTTTTGATACTAAAAGAGATGTTAAATTTGGTGGTAATTTATGAAATTTATTTTACTGAAGATACAGTT  
 TTTTATCATTTACAGAATTTCCGACAATTTCCGGCAATTTCCGGTAGTTCAACATTATTAGAAATTAATATT  
 CCTCATGGGAAAACCTACATTTGATAGAGTCAATAATATAACTTCACTTGGTTTATTAAATTTGGTGTATTG  
 ATGATTTTATATGCCATTTCAATAAGAGTTTTCATGAGTACCACCTCAAAGACGAAAAGGGATTAA

YCL052C\_homolog 481aa (SEQ ID NO 522)

MRQRTTIYNPYSSHDIITNLNRTNFQLSSIPNHLFTIENKYITTTTTQPNKSSLYSAIKELRIQTKF  
 NNNESGIPIFSFHYEPGLNIYAVPQSNVDKLEFWQQVEQLIMELLGIKLSSQQWIANVNSFYHDIQPP  
 PLLNLKEGWKFNHLPKSNYDIYNQDKIIIRELLTNVSEIEFNLESIGIYKEIGLFLIDEKISTNDDLNL  
 SGIRVILDEDSNTNNKEESIHKTMFHIPRHSFDDSTTTTKIIPQGLHPILSTELNTTTIIVIPTDF  
 DVEECKFYYYLNLNLSLIFDQFQNIPIGSQLIINNGNKNLELPEYKINQWGNELLFEFEFDNDNDIPHH  
 INLTVHSRYQLPQNNHSHSQISNVLNSLPNIFIGCNVKEGNLLDKSPFDTKRDVKIKGNYEIIYFTEDTV  
 FYHLQNSDNSGNSGSSTLLEINIPHGKTTTFRVNNITSLGLLIGVLMILYAISIRVFMSTTSKTKRD

YCR009C\_homolog 882bp public: 1..882 (SEQ ID NO 523)

ATGTGGAAAAAGAAAAGAGGGAATTTTTTTTTTGTTCATTTTTTTTTTTTCTTTTATCTCGCACAT  
 TTCTTTCTTCAACTAGACATGCTTGGGGAGGATTTAAGAAAGCAATCAATCGAGCTGGCGCATCTGTT  
 ATTGTCAAGGATGTTGACAAGACTATGGATAAGGACTTTGATGTGGAGGAGAGAAGGTACAAGACCTTA  
 AAGACTGCAGGGACGAATTTACAGAAAGCTGCCAAGGGGTATTTGGACAACATCAGAGCAATCACGAAT  
 TCCCAAGTCACAAATGCCCAGATTATTTATAACTTGTACGAGGAGTCGAAGCAGGACAAATCGCTCTAC  
 TCGAATGTTGGGACTTATTTACATGCAGAGTGTCAAGGAGTTTGTGAGGAGACTGTGAAACAGATTGAT  
 GGCCCGTATAGGGAGACTGTTTTGGATCCAATTGGAAGTTTTCCAACCTACTTTAGTGAGATTGACGAA  
 GCAATCAAAAGAGAGCACACAAGAAGATTGACATGAGCAGTGCAAAGCCAAAGTTAGACGGTTAGTC  
 GATAAACCTGCCAAAGATGCGGCCAAGTTGCCACGCGCCGAGAAAGGAATTTGTCGATGGCCAAAGGATT  
 TACGACGAGTTGAATGACCAGCTCAAGGCCGAGTTGCCGCGAGTTGATTGCATGAGGGTGCCTTTCTAC  
 GATCCGTCGTTTGGAGCGTTGGTCAAGATCCAGTTGAGGTTCTGTACTGAGGGGTACTCGAGATTGGCA

160/251

CAGATCCAACAGTACTTGGACCCAGCGTCCAGAGACGAGTATGCCAATGGGTTGTTGGACGGCAAGATT  
GATGATATGTTGGCACAAATGCAAGGTTTGGAGTATACTTCTTTAGGAAAGTAG

YCR009C\_homolog 293aa (SEQ ID NO 524)

MWKKKKREFFFFCHSFFFFFYLAHFFLQLDMSWGGFKKAINRAGASVIVKDVDMKDFDVEERRYKTL  
KTAGTNLQKAAGYLDNIRAITNSQVTIAEIIYNLYEESKQGQSLYSNVGTYYMQSVKEFDEETVKQID  
GPYRETVLDPIGKFSNYFSEIDEAIKKRAHKKIDYEQCKAKVRRLVDKPAKDAAKLPRAEKELSMKEI  
YDELNDQLKAELPQLIALRVFPYDPSFEALVKIQLRFCTEGYSRLAQIQQYLDPASRDEYANGLLDGKI  
DDMLAQMQGLSITSLGK

YCR010C\_homolog 858bp public: 1..858 (SEQ ID NO 525)

ATGTCAGCTGATTTAGAAAATCAACAACCACAAGATCATCATCTTATTATTGAAAACAAGGGTGATAAC  
AGTAGCAACCACCACCACCACAACAACAATTCAACATCACCTTATGATCCTCATCATCCAATTACTAAA  
ATTGAAACTGATGGAGATTATGTTACTTTTGGTAATGAAAGATATTTACGTTCTGATTTAGTTGAAGCA  
TTTGGTGGTACTTTAAATCCAGGGTTAGCTCCACCACCTAAAAATGATTTTGCTAATCCTGCTCCATTG  
GGATTATCGGCATTTGCTTTAACAACATTTGTTTTAAGTTTAATTAATTGTGAAGCTAGAGGGGTTACT  
ATTCTAATATTGTTGTTGGATTGGCATTCTTCTATGGTGGTGGTGGTCAATTAGTTGCTGGTATGTTT  
GAATTGGCCGTTGGTAATACTTTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT  
GCTGCTATTCAAGTTGATTCATTTGGTATTAAAGCTGCTTATGCTAATAATACTGAAGAATTACATTAT  
GCTGTGGGGATATTTTAAATTGGTTGGTTTATTTTTCAGTATTTTCTTGGATGCTTTTAAACCGTTAACT  
ACTGTGGCATTCTTTTAAATATTTTCTTTTAAAGTATTACATTTTATTATTGGCAATTTCTGATTTT  
ACTGGTAAAGTGGCAATTAAAAAGCCGGTGGAGTGGTTGGTTTAAATTACTGCTTTTGTGCTTGGTAT  
AATGCTTATGCTGGTATTGCTAATCCTCAAAATAGTTATATTACTGTTAAAGCTATTCCATTACCAGAT  
TTACAAGATCCAACAAGAAAAATAAATAA

YCR010C\_homolog 285aa (SEQ ID NO 526)

MSADLENQQPDHHLIIENKGDNSNHHHHNNNSTSPYDPHPITKIDTDGDYVTFGNERYLRSDLVEA  
FGGTLNPLGLAPPPKNDNFANPAPLGLSAFALTTFVLSLINCARGVTIPNIVVGLAFFYGGAAQLVAGMF  
ELAVGNTFGGVALSSYGGFWGAWAAIQVDSFGIKAAYANNTTEELHYAVGIFLIGWFIFTFFLMLLTVKS  
TVAFFLIFFFLSITFLLLAISDFTGKVAIKKAGGVFGLITAFVAWYNAYAGIANPQNSYITVKAIPLPD  
LQDPTRKNK

YCR021C\_homolog 1029bp public: 1..1029 (SEQ ID NO 527)

ATGTCGCGCTGCTGTTTCAACTTTATCCGATATCATCAAACGTAATGATGCTGTTAACGTGAACCCACCA  
AACCCAATTATTGATTTACATATCACTGAACATGGTAGTGATTGGCTTTGGGCTGTTTTCAGTTTTT  
GCATTATTTGCAATTGTGCATGGATTCAATTACAGTTTTACTGACGTTAGAAAATCTGGTTTGAAGAGA  
GCTTTATTGACTATCCCATTATTTAATAGTGCTGTTTTGTCCTTTGCTTACTATCTTATGCTTCTAAC  
TTGGGCTATCTGGATTTTGACAGAATTCAACCATGCTGGTACTGGTTTTAGACAAATCTTTTATGCA  
AAATTTGTTGCTTGGTTCTTGGGTTGGCCATTAGTGTGGCTATTTTCAAATTATCACCATAACCAGC  
TTTACTACTACTGAAGATGAGTCTGATTGCTTAAGAAATTCATTTCTTTGTTTGAAGCTTTGTTTACT  
AGAGTTTTGGCAATTGAAGTTTTCGTCTTGGGTTTATTGATTGGTGGTCTTTAATTGAATCTACTTACAAA  
TGGGGTTATTTCACTTTTGTCTGTTGTGTTCCAATTGTTTGTCTATTTATTAGTCATTAATGATGTGGTT  
GTTTCATTTGGTTTCATCTTCTCATTCACTGCTTTGGCAATGCTCTTATCCTTGGTTTGTATTGTTGG  
ATTTTGTACCCAGTTGCTTGGGTTTGGAGTGAAGGTGGTAATGTTATTCAACCAGATTGAGAAGCAGTG  
TTCTATGGTATTTTGGATTTGATCACTTTTGGTGTATTCCAATTATCTTGACTTGGATTGCCATTAAT  
AACGTTGATGAAGAATTCTTCAACAAAATATGGCATTTCATTGAAACCAGAAAATGAACATGCTCCA  
ACTGCTACTGAAGATGTTGAAAAAGCAGTTGGTGAAACCCCAAGACATTCTGGTGATACTGCTGTTGCT  
CCATCAGGTGTTCCAGACACTGGTGTGCTCAAGCACAAAGCCGAAGCTGAAGAACGTATTTAA

YCR021C\_homolog 342aa (SEQ ID NO 528)

MSAAVSTLSDIKRNDVNVNPPNPIIDLHITEHGSIDLWAVFSVFALFAIVHGFYISFTDVRKSLKR  
ALLTIPLFNSAVFAFAYTYASNLYTWILTEFNHAGTGFRQIFYAKFVAVFLGWPLVLAIQIITNTS  
FTTTEDESDLLKKFISLFEALFTRVLAIEVFVLGLLIGALIESTYKMGYFTFAVVFQLFAIYLVINDVV  
VSFGSSSHSVFGNALILAFVIVWILYPVAVGLSEGGNVIQPDSEAVFYGILDLTIFGVIPILTWIAIN  
NVDEEFFTKIWHFHLKPENEHAPTATEDVEKAVGETPRHSGDTAVAPSGVPDTGVAQAQAEAEERI

YDR178W\_homolog 510bp public: 1..510 (SEQ ID NO 529)

ATGATTTCAACTTATTCACGTATTGGTTTAAACCACTTAACTAAATCATCATCATCATCATTAACCT  
ACTACTGTTAGACCATTATTATTGGCCAATTTTACTAGAGGAATTAACCTATTCTCAACCACCAGGT  
TATATTGTTGGTACAGTTAATGATGCTTATGTACCACCACCACATAAATAGAAGGTTTACATTACAT  
TGGACTAGTGAAAGGATTGTTGCTATTGGTATTGTACCATTAGTTTACGACCACTTATTAAGTGGT  
GGTGGCTTCGACTTTAATTGATTCCACCATTGTCAGCATTATTATTATTTCATTGTCATACTGGTTTCCAA  
AGTTGTATTATAGATGATATTCCTAAAAGAGTTTATGGATCTTATCATAATTATGCCATGTATTTATTG

161/251

ACTTTTGGTACTGGTATTGCTGGTTATGGTATTTATCAAATTGAACTAAAGAAGGTGGTGTTCCTCAAT  
ATTATTTCAAACTTTGGAAAGCTTAA

YDR178W\_homolog 169aa (SEQ ID NO 530)

MISTYSRIGLTTTLTKSSSSSSSLTTTVRPLLLANFTRGIKTIPQPPGYIVGTVNDAYVPPPPHKLKLEGLSLH  
WTSERIVAIGMLPLVLAPFITGGGASTLIDSTMSALLLFHCHTGTFQSCIIDDIPKRVYGSYHNYAMYLL  
TFGTGIAGYGIYQIETKEGGVSNIISKLWKA

YDR202C\_homolog 387bp CDS: 1..&gt;387 public: 1..387 (SEQ ID NO 531)

ATGACAGCAAATATCTTGAATAATAAAACATTCATAGATACTGTATTATCAATACAATCAACTCAAAAT  
GATAAAGAATTACATTGGTATATTATAAATATAATTTTACCCGATTTACCTCAAATCATAGAGACTTTA  
CAGATTTGTTCAAATTTGTTGATGTACAATTCACCACAAGAACCTGATTCCAAACAATGTATTGAAAAA  
GGTCCATCTCAAGCTACCTTTGCTTTTAACCAATCAACAAGATTCTGTCAATGGGATAATAACCCGA  
GATGGACCATATATCACAGATCTTAATTTGACGGTTAAGAATCATTATTTCAACAAGCATTTCCTATAAG  
TTGCGCTTAATAAAGCCAATGGTTTTAGAACAACTTGTTAAT

YDR202C\_homolog 129aa (SEQ ID NO 532)

MTANILNNKTFIDTVLSIQSTQNDKELHWYIINIILPDLQIIE TLQICSNLLMYNSPQEPDSKQCIEK  
GPSIKLPLSLTNQQDSVNGIITRDGPYITDLNLTVKNHYFNKHFHKLRLIKPMVLEQLVN

YDR256C\_homolog 1458bp public: 1..1458 (SEQ ID NO 533)

ATGGCTCCAACATTTACGAATCTAACGGTCAACCAATTCCAGAACCATTTGCCACTCAAAGAGTTGGT  
CAACACGGTCCATTGTTGTTACAAGATTTCAACTTGATTGATTGATTGATTTGCCCCATTTGATAGAGAAAAGA  
ATCCCAGAAAGAGTTGTCCACGCTAAAGGTTCCGGTGCTTATGGTGTGTTTTGAAGTCACTGACGATATC  
ACTGATATTTGTGCTGCCAAATCTTGGACACTGTTGGTAAGAAAAGTAAAGTCTTCCACAGATTCTCT  
ACTGTTGGTGGTGAATTAGGTTCTGCTGATACTGCTAGAGATCCAAGAGGTTTTGCTACCAAATTTTAC  
ACTGAAGAAGGTAACCTTGGATTTGGTTTACAACAACACTCCAGTGTTTTTCATTAGAGACCCATCTAAA  
TTCCACATTTTCATCCACACCCAAAAGAGAAACCCAGAAACTCACTTGAAGGATGCTAACATGTTTGG  
GATTACTTGACTAGCAATGAAGAATCCATTCATCAAGTTATGGTTTTATTCTCCGACAGAGGTACTCCA  
GCTTCTTACAGAGAAATGAATGGTTACTCTGGTGCACACTTATAAATGGTCCAACAAAAAGGTGAATGG  
TTTTACGTTCAAGTTTCAATTCATCAGTGACCAAGGTATTAAGACTTTGACCAACGAAGAAGCTGGTGGT  
TTAGCTGGATCTAACCAGATTACGCCCAAGAAGATTTGTTCAAGAACATTGCTGCTGGTAACTACCCA  
TCATGGACTGCTTACATTCAAACCATGACTGAAGCCGAAGCTAAAGAAGCTGAATTTTCTGTGTTTGAT  
TTGACCAAAAGTTTGGCCACACAAGAAATACCCATTGAGAAGATTTGGTAAGTTCACTTTGAATGAAAAC  
CCAAAGAATACTTTGCTGAAGTTGAACAAGCTGCTTTCTCTCCAGCCACACTGTTCTTACATGGAA  
CCACTGCTGATCCAGTCTTGCAATCAAGATTGTTCTCCTATGCTGATACTACAGACACAGATTGGGT  
ACCAACTATACTCAAATCCCAGTGAAGTGTCTGTCAACGGTGCTGTTTTCAACCCACATATGAGAGAT  
GGTGGTATGACTGTTAATGGTAACTTGGGTAGCCATCCAACTACTTGGCCAGTGATAAGCCAGTTGAA  
TTCAAACAATTTTCTCTTCAAGAAGACCAAGAAGTTTGAATGGTGGTGGTCCACTCCATTCCACTGGAAA  
GCCACCCAGCTGATTTCAAACAAGCTCAAGAATTGTGGAAAGTGTGAAGAGATATCCAAACCAACAA  
GAACATTTGGCCCAACATTGCTGTACATGCTGCTGGTGGTGGTATGCTGCTATCCAAGACAGAGTGT  
GCATACTTTGGTAAAGTCTCTCAAGACTTGGCTGATGCTATCAAAAAGGAAGTTTGAATATCTCCA  
AGAAAATAA

YDR256C\_homolog 485aa (SEQ ID NO 534)

MAPFTNSNGQPIPEPFATQRVGQHGPLLLQDFNLIDSLAHFDRERIPERVVHAKGSGAYGVFEVTD  
TDICAAKFLDTVGKKTRIFTRFSTVGELGSADTARDPRGFATKIFYTEGNLDLVYNNTPVFFIRDPSK  
FPHFIHTQKRNPEPETHLKDANMFWDYLT SNEESI HQVMVLFSDRGTPASYREMNGYSGHTYKWSNKKGEW  
FYVQVHFISDQGIKTLTNEEAGALAGSNPDYAQEDL FKNIAAGNYPSTAYIQTMTAEAEAEAEFSVFD  
LTKVWPHKKYPLRRFGKFTLNENPKNYFAEVEQA AFSPAHTVPYMEPSADPVLQSR LFSYADTHRRLG  
TNYTQIPVNCPTVGAVFNPHMRDGAMTVNGNLGSHPNY LASDKPVEFKQFSLQEDQEVWNGAATPFHWK  
ATPADFKQAQELWKVLKRYPNQQEHLAHNIAVHAAGADAAIQDRVFAYFGKVSQDLADAIKKEVLELSP  
RK

YER103W\_homolog 1971bp public: 1..1971 (SEQ ID NO 535)

ATGTCTAAAGCTGTTGGTATTGATTTAGGTACAACCTATTCTTGTGTTGCTCATTTTGCCAATGATAGA  
GTTGAAATTATTGCTAATGATCAAGGTAATAGAACTACCCCTTCATTTGTTGCCTTCACTGATACTGAA  
AGATTGATTGGTGATGCTGCCAAGAATCAAGCTGCTATGAACCCAGCAAACACTGTTTTCGATGCTAAA  
CGTTTAAATGGGAGAAAATTTGATGATCCAGAAGTTATAAATGATGCTAAACATTTCCCATTTAAAGTC  
ATTGATAAAGCAGGTAAACAGTGATTCAGTTGAATATAAAGGTGAACTAAACATTTTCAACAGAA  
GAAATTTCTTCAATGGTTTTAAACAAAAATGAAAGAAATTGCTGAAGGTTATTTGGGTTCTACTGTTAAA  
GATGCCGTTGTTACCGTTCCAGCTTATTTCAATGATTCTCAAAGACAAGCCACCAAAGATGCTGGTACT

162/251

ATTGCTGGTTTGAATGTTTTAAGAATTATTAATGAACCTACTGCTGCTGCCATTGCTTATGGTTTAGAT  
AAAAAAGGTTCCAGAGGTGAACATAATGTTTTAATTTTCGATTGGGTGGTGGTACTTTTGTGTTTCA  
TTATTAGCCATTGATGAAGGTATTTTCGAAGTTAAAGCCACTGCTGGTGATACTCATTGGGTGGTGAA  
GATTTTGATAACAGATTAGTCAACTTCTTTATTCAAGAATTCAAGAGAAAGAACAAGAAAGATATTTCC  
ACCAACCAAAGAGCTTTAAGAAGATTAAGAAGCTGCTTGTGAAAGAGCCAAGAGAAGCTTTGTCTTCTCT  
GCTCAAACCTCAATTGAAATTGATTCCCTATATGAAGGTATTGACTTCTACACTTCAATCACCAGAGCC  
AGATTTGAAGAATTGTGTGCTGACTTGTTCAGATCCACTTTAGATCCAGTTGGTAAAGTTTGTAGCTGAT  
GCCAAGATTGATAAATCTCAAGTTGAAGAAATTGTCTTGGTTGGTGGGTCCACCAGAATTCCAAAGATT  
CAAAAATTGGTTTCTGATTCTTTAATGGTAAAGAATTGAATAAATCTATCAACCTGATGAAGCTGTT  
GCTTATGGTGCTGCTGTTCAAGCTGCCATTTTAACTGGTGATACTTCTTCCAAGACTCAAGATATTTTG  
TTATTGGATGTTGCTCCATTGTCTATTAGGTATTGAACTGCTGGTGGTATCATGACCAAATTGATTCCA  
AGAAATCTACTATTCCAACPAAGAAATCAGAACTTTCTCCACTTATGCCGATAACCAACCAGGTGTT  
TTGATTTCAAGTGTGTTGAAGGTGAAAGAGCTAAAACTAAAGATAACAACCTTTGGTAAATTTGAATTA  
TCTGGTATTCCACCAGCTCCAAGAGGCGTCCCTCAAATTGAAGTTACTTTGATATTGATGCTAATGGT  
ATCTTGAATGTTTCTGCTTTAGAAAAAGGTACTGGTAAAACTCAAAGATTACTATCACCACGATAAA  
GGTAGATTATCCAAAGAAGAAATTGATAAATGGTTAGTGAAGCTGAAAAATTCAAAGAAGAAGATGAA  
AAGGAAGCTGCTAGAGTCCAAGCCAAGAATCAATTGGAATCTTATGCTTATTCAATTGAAAAACACAATC  
AATGATGGTGAAATGAAAGATAAGATTGGTGCAGATGATAAAGAAAAATTAATAAGCCATTGATGAA  
ACTATTCTTGGTTAGATGCATCTCAAGCTGCTTCTACTGAAGAATACGAAGATAAACCTAAAGAAATTA  
GAATCAGTTTGTCTAATCCAATCATTAGTGGTGGTCTTATGGTGCTGCCGGTGGCGCTCCAGGTGCGAGG  
GGATTCCCAGGTGCTGGTGGCTTCCAGGTGGTGCCCGAGGTGCCGGTGGTCCAGGTGGTGGTCTACTGGT  
GGTGAATCAAGTGGACCAACTGTTGAAGAAGTTGATTAA

YER103W\_homolog 656aa (SEQ ID NO 536)

MSKAVGIDLGTTPYSCVAHFANDRVELIANDQGNRTTPSFVAFTDTERLIGDAAKNQAAMNPANTVFDK  
RLIGRKFPDDPEVINDAKHFPFKVIDKAGKPVIVQVEYKGETKTFSPPEISSMVLTKMKEIAEYLGSTVK  
DAVVTVPAYFNDQSQRQATKDAGTIAGLNLVRIINEPTAAAIAVGLDKKGSRGHNVLIFDLGGGTDFDVS  
LLAIDEGIFEVKATAGDTHLGGEDFDNRLVNFFIQEFKRKNKKDISTNQALRRLRTACERAKRTLSSS  
AQTSIEIDSLYEGIDFYTSITRARFEELCADLFRSTLDPVGKVLADAKIDKSQVEEIVLVGGSTRIPKI  
QKLVSDFENGKELNKSINPDEAVAYGAAVQAAILTGDTSSKTQDILLLDVAPLSLGIETAGGIMTKLIP  
RNSTIPTKKTSETFTSYADNQPGVLIQVFEGERAKTKDNLLGKFELSGIPPAPRGVPQIEVTFDIDANG  
ILNVSALEKGTGKTQKITITNDKGRLSKEEIDKMVSEAEKFKEEDEKEAARVQAKNQLESYAYSLKNTI  
NDGEMKDKIGADDKEKLTKAIDETISWLDASQAASTEYEDKRKELESVANPIISGAYGAAGGAPGGAG  
GFPAGGFPAGGAPGAGGPGATGGESSGPTVEEVD

YGR086C\_homolog 954bp public: 1..954 (SEQ ID NO 537)

ATGCATAGAAGCTTATTCTTTAAGATCCACTAGAGCTCCAAGCTGCATCTCAATTACAAGCTCCACCTCCA  
CCACCATCATCTACCAAATCCAAATTTTTTGGTAAAGGTTTCGATTAGTCATACTTTCCGTAAACAAGCT  
GCTGGTGCTTTAGGTCCAGAATTGTGAGAAAATTTGGCCATTTTAATTAATAATGAAAAAAATTTAATG  
AGATCAATTGAAATCACTTCTCGTGAAAGAAAAGATGTTGCTAAACAATTATCTTTATGGGGTGAAGCT  
AATGAAGATGATATTAGTGATATCACTGATAAATTTGGGGGTTTTAATCTATGAAGTTGGTGAATTGGAA  
GATCAATTTATTGATAGATATGATCAATATAGAATCACTTTGAAATCTATTAGAGATATTGAAGGTTCA  
GTTCAACCAAGTAGAGAAAGAAAAAATACTGATCAAAATTGCTTATTGAAATATAAAGATCCCT  
CAATCACCAAAAATTAATGTTTTAGAACAGAATTGGTTAGAGCTGAAGCTGAATCTTTAGTTGCTGAA  
GCTCAATTGAGTAATATTACTAGAGAAAAATGAAAAGCTGCTTTAATTATCAATTTGATTCTATTAGA  
GAACACGCTGAAAAAATGCTTTAATTGCTGGTTATGGTAAAGCTTTATTAGAAATTATTAGATGAAAGT  
CCAGTCACTCCAGGTGAACTAGACCAGCTTATGACGGTTATGAAGCTTCTAAACAAATATTATTATGAT  
GCTGAAAACGCTTTAGCTTCTTGACTTTTGATTCTGCCGTTGTTTCGTTCAACTTTATCATTTAGCTGCT  
CATGATGAAGAAGCAGAAGAAGATTTAGAAGGTGCTTATGAAGATGATGAATTGGCTAATGAAGCTGAA  
AATTTAAGAATTGCTGAAAAAGATTTTGATGAAGTTGAAGCTAAAATTTGCTGCTTAA

YGR086C\_homolog 317aa (SEQ ID NO 538)

MHRTYSLRSTRAPTASQLQAPPPPSSTKSFFGKGSISHTFRKQAAGALGPELSRKLAILIKMEKNLM  
RSIEITSRERKDVAKQLSLWGEANEDDISDITDKLGLVLYEVGELEDQFIDRYDQYRITLKSIRDIEGS  
VQPSRERKQKITDQIAYLKYKDPQSPKINVLEQELVRAEAESLVAEAQLSNITREKLKTAFFNYQFDSIR  
EHAEKIALIAGYGKALLELLDESPVTPGETRPAYDGYEASKQIIDAENALASWTFDSAVVRPTLSLAA  
HDEEAEEDLEGAYEDELANEENLRIAEKDFDEVEAKIAA

YGR197C\_homolog 1536bp public: 1..1536 (SEQ ID NO 539)

ATGTCTCATGATGATCAAAATCTGAATCAAAACCCAGCTCAAAATCCAACCTCCAATCCTGTGTCAAAG  
CCGTCTGATATGGGCAGATCAAGCAACGACAGTGCGCTCCGAACCATCAATACAACATTTTACGTTAGCC  
CCACTCGAACCACAAGGCGATGAAGAGGATATGGAATGGGTGAGCCAATATCACGACAATCAACCTTT  
CTTGAGAGAGTACAATCTCGATATTCATTTTCCACGAGAATTTGCGAGCTCAAAGAAAGGAATTGTCC



163/251

ATGAAATATCTTAAATTTATCTAGTCATGGCCATTGGTTGCTTAGGAGTGTTCCTATATATTGGGGT  
TCAATGTATCAAAGAGAAACCCGAATTAACAACTTGAAATGTTGGTAGTTTTAGAGATGAAGAAATT  
AATGGCATCCCTCCACTTTTTGGCAATCAGCTTCGTGATTTATTGGCCACCCCAACGGCTAGAACACTC  
GGCGATTGGAAAATATATAACACTAGCGAATTTGAAACTATTGCATCAAAACACAACAACAATAAAT  
GAAGAGGTCATTCGTCAAATTCATCATCAAAATTATTGGGCCCTCGATATATGTCAAGCAAAATTCATCT  
TATAACATATACAATGCATTAGCCAATGGTAATCAGTACAATGTCAGTGACTCTGTGTATTGTTACTAT  
GAAACAGGAAGACACCTAAC TAGTGTGGCCCATATGTGGTGGCATCTATAGATGCCATTCAAACATATG  
TGGTTGGATCAAACCTGGTGATGAGGGACATTGTGAGAATTGGTAATATAACTCTTGACAATGCAAC  
TCGGTTGCTGTGCGCCACTACCGCTTGGCATTCCAAATAATTGATATGAGACCATCTACTAGTGGAGTT  
TAGTTGCAGCTTTACAAATTGGTCTTCTTTATCTTGTCAATTGTTAGTTTTTTCAGTTTCAATTTTTTT  
GTCGATATACACCGATCAGTGGCATTAAATGGTGAAGCAAAGAACTTTTTACTTTTATCGAGTTTTTGCA  
TCAATCATATCGTATTTTTGTTATCAGTTTAAATGTTTGGTTTGGTTACTTTAGCGTTTCAAGTTGATTTT  
GCTGTTTACATTTGGTAAATCTGGCTTCTTAGTTTACTGGATGGTAACATTTTAAACAATGTGGAGTGT  
GGATTGGCTAACGAATTGGCCGCTATGCTCATACTTACTATCTATCCACCAATGGTTGGGTTTTGGTTG  
ATCTTCTGGGTAATTATAAATATCACACCCACATTACACCAATTGCTTTGTTACCTGAATTTTATCGG  
TATGGTTACGCCATGCCATTGCATAATGCTTTTGAATTTTATCTGTTATTTTTTCAACACGTATAAG  
GGATTAATAGGAAGAAGCATTTGAATCATAATTGCATGGGTGGTATTTTAAACATTAATGGCACCAATA  
GTGGTGGTTTACTTTGGTAGCATTAGTAGTAAAAAGCTGCTGCTCCCGCTGCTGCTGCAAAAAAGGAA  
AAGGAAAAGTCAAAGTAA

YGR197C\_homolog 511aa (SEQ ID NO 540)

MSHDDSNNSNPSSNPSTSNPVSKPSDMGRSSNDGSEPSIQHFTLAPLEPQGDEEDMEMGEPISRQSTF  
LERVQSRYSFFHENLRAQRKELSMKYLKIYLVMAIGCLGVFSIYWGSYQRETRIKNLKMLVLEDEEI  
NGIPPLFGNQLRDLATPTARTLGDWKIYNTSEFETIASKHNNTINEEVIRQIHQNYWASIVYKQNSS  
YNIYNALANGNQYNVSDSVYCYETGRHLTSVGPYVVASIDAIQTMWLDQNSVMRDIVRIGNITLDNAN  
SVAVATTALAFQIIDMRPSTSGVLVAALQIGLLYLIVVSFFSFNFVDIHRSVMLVKQRNFFLLYRVFA  
SIISYFVISLMLFGLVTLAFQVDFAVTFGKSGFLVYWMVFTLTMWSVGLANELAAMLILTIYPPMVGFWL  
IFWVIINITPTFTPIALLPEFYRYGYAMPLHNAFEIYSVIFNTYKGLIGRSIGIIIAWVVFLLTMAPI  
VVVYFGSTMSKAAAAPAAA KKEKEKSK

YGR250C\_homolog 1890bp public: 1..1890 (SEQ ID NO 541)

ATGCTGCTGCTGAACTAATCAACTTCAAGAATCTATGGAAAAGTTGAACATTGGTTCAACTACTGAA  
GAACAATCAGCTGCTGCTGCTACTACCACTGCTGATCAATCAGCTGAAGAACAAGGAGAATCATCTGGT  
GTTGCCGAGAAATCTGCCTCCTTGTACGTTGGTGAATTGAACCCATCTGTTAATGAAGCTACCTTGTTT  
GAAATCTTTTCTCCAATCGGTCAAGTTTCTCTATCAGAGTTTGTCTGTGATGCTGTCCTTAAAAAATCT  
TAGGTTATGCTTACGTCAACTACCACAAGTACGAAGATGGTGAAAAGGCTATTGAAGAATTGAACATC  
AACCCGATCGAAGGTGCTCCATGTCGTATCATGTGGTCTCAAAGAGACCCATCTGCTAGAAGATCTGCT  
GATGGTAATATTTTCATCAAGAATTTGCATCCAGCCATCGATAACAAAGCTTTGCATGACACCTTTTCT  
GCTTTTGGTAAAAATTTTGTCTTGTAAAGTTGCCACCGATGAATTTGGTCAATCAAAGTGTTTTGGTTTT  
GTCCACTATGAACTGCTGAAGCTGCTGAAGCTGCCATTGAAAATGTCAATGGTATGTTATTGAACGAT  
CGTGAAGTTTTCGTTGGTAAGCACATTTCTAAAAAGACCGTGAATCTAAGTTTGAAGAAATGAAAGCC  
AAGTTCACTAACATTTATGTTAAAAACATTGACTTGAACATTTAGAAGAAAGCTTTGAAAAATTTGTTT  
TCTCCATTCGGTAAGATTACTTCCATTTACTTGGAAAAAGACCAAGATGGGAAATCTAAAGGTTTTGGT  
TTTGTAAATTTTGAAGATCATGAATCTGCTGTTAAGGCTGTTGAAGAATTGAACGATAAAGAAATCAAC  
GGTCAAAAGATCTACGTTGGTAGAGCACAAAAGAAAAGAGAAAGATTGGAAGAATTGAAGAAACAATAC  
GAAGCTGTTAGATTAGAAAAATTTGGCCAAATACCAAGGTGTCAACTTGTGTTTGAAGAATTTGGATGAC  
ACTATTGATTCTGAAAAATTAGAAGAAGAATTCAAACCATTTGGTACCATTACATCTGCCAAGGTTATG  
GTTGATGAAGCTGGTAAATCAAAGGTTTTGGTTTCGTTTGGCTTCACAACCCAGAAAGAAGCCACCAAG  
GCTATCACTGAAATGAACACCAGAATGATTAACGGCAAGCCATTGTATGTTGCTTTGGCTCAACGTAAG  
GATGTTAGACGCTCTCAATTAGAACAACAAATTCAGCCAGAAACCAATGAGAATGCAAAATGCTGCT  
GCTGGTGGTTTTACCTGGTCAATTCATTCCACCAATGTTCTACGGTCAACAAGGCTTTTTTCCCACCAAT  
GGCAGAGGTAACGCTCCATACCCAGGTCCTAATCCACAAATGATGATGAGAGGTAGAGGTCAACCATTC  
CCAGAACAATGGCCAAGACCAGGTCCAAATGGCCAAACCAAGTTCCTGTCTACGGTATTCACCTCAATTT  
CAACAAGACTTTTAAACGGTCAAAAATGAGACCTCAGCAACAACAACAACAAGAGGTGGATAC  
TATCCAAACCGTAACCAAAACCAGCAAGAGAGACTTGGCTGCTATCATTTCTAGTGTTCACAGAATCA  
CAAAAGAGAATTTTGGGTGAAGAATTGTATCCAAAGATTGTTGCTACCGGTAAGGCTCAAGAACCAGAA  
GCTGCTGGTAAAAATCACTGGTATGATGTTAGGTTTAGAAAACCAAGAAATTTTGGATTTGTTAGATGAT  
GATGAATTTGTTCAATAACCATTTTCAAGATGCTTTTGAAGAGTACAAGAAGTCTGAAGCT  
GCCGTAATGCTGAAGAGCAAGCTTAA



164/251

YGR250C\_homolog 629aa (SEQ ID NO 542)  
MSAAETNQLQESMEKLNIGSTTEEQSAAAATTTADQSAEEQGESSGVAENSASLYVGELNPSVNEATLF  
EIFSPIQVQSSIRVCRDAVSKKSLGYAYVNYHKYEDGEKAI EELNYPNPIEGRPCRMWSQRDPSARRSG  
DGNIFIKNLHPAIDNKAHDTFSAFGKILSCKVATDEFGQSKCFGFVHYETAEEAAEAAIENVNGMLLND  
REV FVGKHISKKDRESKFEEMKANFTNIYVKNIDLNYSEESFEKLFSPFGKITSIYLEKDQDGKSKGFG  
FVNFEDHESAVKAVEELNDKEINGQKIYVGRAQKKRERLEELKKQYEAVRLEKLAKYQGVNLFVKNLDD  
TIDSEKLEEEFKPFGTITSKVMVDEAGKSKGFGFVCF TTPPEATKAITEMNTRMINGKPLYVALAQRK  
DVRRSQLEQQIQARNQMRMNAAGGLPGQFIPPMFYGOQGFPPNGRGNAPYPGPNPQMMMRGRGQPF  
PEQWPRPGPNGQVPVYGIPPOFQODFNGQNM RPQQQQQQQPRGGYYPNRNQT SKRDLAAI ISSVPQDQ  
QKRILGEELYPKIVATGKAQEPEAAGKITGMMLGLENQEILDLLDDDEL FNNHFEDALTA FE EYK KSEA  
AGNAEEQA

YKL117W\_homolog 666bp public: 1..666 (SEQ ID NO 543)  
ATGTCTCTCGACAACCACTCAAACCTCAACTGTATTATGGGCTCAACGTTTCATCTGAAGATGACGCTGCC  
AAAAATATCATTTATTTAACCATTCAAATATCTGATCCAATTGATTTAAAAATAGATTTAAAAAGTGAT  
CATTTAATTATTGATTCTAAATCTAATGATTTCAGTTTATTCATCAATTGATTATCATTTACAAATTGAT  
TTTTTCAAAGAAATAGATCCTGATCAATCAAAAATTAATACTGAAAATGGTTACATATTTTTATGATT  
CTTCGTAAAAAGATCAACAAGAAGAATATTGGCCACGTTTAACTAAAGAAAAAATGAAATATCATTAT  
ATTAAAACTGATTTTGATAAATGGGTGGATGAGGATGAACAAGATGAAGTTAAAGATGATCCAAATGAT  
TTTGGTGGACCTGGTGGACCTGGTGGAGCTATGGATTTCTCACAATGTTGAGCGGCATGGGCGGTTTA  
GGTGGCACTGGTGGAGTGGCGGTCTGGTGGCGTCGATCTTAGTGCATTGGCTTCTCAATTGGGTCAA  
GCTGGTGGTGGTGGTGGTGGTGCAGGTCTTGATGGTGAAGAAGGCGAAGAAGGCGATGAAGAAGCTAAA  
AAAGCGCAAGAAGAATCAAATGCCACTGCTACTGAAAAAGAATAA

YKL117W\_homolog 221aa (SEQ ID NO 544)  
MSSTTTQTPTVLWAQRSEDAAKNIIYLTIQISDPIDLKIDLKSDHLIIDS KSNDSVYSSIDYHLQID  
FFKEIDPDQSKINTENGSHIFMILRKDQEEYWPRLTKEKLKYHYIKTDFDKWVDEDEQDEVKDDPND  
FGGPGGPGGAMDFSQMLSGMGLGGTGGSGGPGGVLDLSALASQLGQAGGAGGAAGLDGEEGEEGDEEAK  
KAQEE SNATATEKE

YKR075C\_homolog 3042bp public: 1..3042 (SEQ ID NO 545)  
ATGTCGTTATCAGGAGAAGTGTTTTTCAGGAGGAGCAACCACTTCTCAACATATCGAGGCACAAGATGAT  
GACCATTTTGAAAATACAACCTTTAAATTGAAAAGAACTAGATCCATGGGTTTATTAGATGAATTTATC  
CCTGATAAACTAAAAGAACAAGATGGTAATAATTCAGAAGCAAATTCATCAACAACAGCTGCATCAACA  
ACCAGCTCAAGAACTTGGCAGCTATGGCAGCTATAGCATCACAAACAAATTCGTCATATGTTAACGAA  
ACTCCAAGCAGTCAACATCATGAACTATAGAATCCATATCTAATAACTCCGATGGCGATGAACCCAT  
TCATCAGATGTAGCGCCATCATCTACATCACCTGTCAATTCACCTTCACCAACTTCCTCACCAGCATTA  
GATTTAAAATCTCCAGAATTGTTGCCTCATGATGATACAGATTTAGCTGTTGAACCTTCACGTCATGTT  
GATTATTTATCCCAATGGGATGTTTCTGATATTTGGAAGTCTTGGCGATACGTTATTTCCAAAAGA  
AAAGATGTTGCTAATGCTGCAAGATTGGAATGCTTCATGGAGAAGCTTGGGCTCAAAGACGCTCTAAT  
CTCAAGACTATAAGTCCAGAAGTGGTGAATTGGTGCAGAAAGATAGTGATGTTACTTGGCTTTATGGACCA  
ATATTAAAAGATGATGACCATGTGAATAATGAAAATCACGACTCTGATGCTATTGAACTACTGCTACT  
AGTTCTGTTGCCGGGATATATCTATTGCCAAAAATGTTCCAGTAAGAATGGACCTAAACCAATATTG  
AAAAAGAGAACAATGGAACAACCTGATGATAAGTCATTCTAATTTATTAAAATTACAATTGGCAACACAA  
ATACATCAAAAGAAAAGAGAACAAAAATGAAACAACAAGAAGAAATTGAAAAGACAACATCAATTGAAT  
CATCCCGATGAATATTTTGATCCCGAAGCCCTTCTGAACAAATTAACAGTCAATATAAGAATACAGCT  
CCTACTCATAACACTAGTGTGGCCAAATTACAAAGCTTGTGAAAACCTCCCAATTTCTCATCTTCTGCT  
AGTTTGAAAGATTTGATGAAAGATGAAGCCGTTGTTGTGCCTTCTTCAGAACAAATCAGTCACGATCAA  
AACCAAGAAGATGGTAATGTTTCTGGGACGTTGAATCCAAAGGTGAAAGACACATACATTTTAATGAC  
GAAGTGATGCAATGTATTGCCATTGATGTGTATTTCAGATGATGAGCAACGATATAAATCTGATGAAGAA  
GATTATGATTTCTGATGATGACGATGATGATTATTATGATCAATATGAACCATCTAATGACAGTCTAGCT  
CAAAGTCACCTATATGAAGGAGACGATGAATCCATTGAGGAAGCGGATGAAGAGGTAGAGGATGATGAA  
GATGGATCTGAAGATGAAGAAGACGATGAAGGGGATTTCTTTTAAATGTGAAATCCAATTTCAATGCC  
CCAATAATTTTGGGCCAGCATTCAGTGCATCAACTTCTACTCCAGTGGCACCATCTTTAAGTCGTCAC  
ACAGATATTACTGATGATACAGCATCAATATCTACCACCAACAGTAAATCTTATAAAACAATTCAATTA  
TTACCTTCAACATCTATTAATTATGGTTCTGATGAATCTAGTGATGAGGCAACCCCTTATACGTCGAGT  
CTTTCTCATAATGTCAATAATGATATTAGTAGAGGTTATGATTATTATTATGATTACAACACTGTATAC  
ACATGTAATCCAAACAATTCAGTGTATGCATCTTATCAAAAGTCCAGATGTTGTTGATGTTCCAGAAAAT  
CTTGATATGGGATCCAATTTTGATTATGAATTTATTGAAAATAACGATAGTATCCCTGTAGATACACA  
ACATTTGAGAATAATAGTACCATTAAATAATATGCCAATTCTGTATAGTCTGCCGTCATCACCTTTATCA  
GTTGCTATTTCCGGTGGAGGTAAAAATCTGGTGTCACTGTTAATCCCCAAATTTCCCATAGTTAAT  
GTCAACTCTAACCACAACAACAACAATCACAAGCAAAACCAAGCCAAAGACAAAGGCATCTCTCT

165/251

TTCCAATTGAGTGATTGAGAAGATGATTCAAATAGTGATTCCGGATGATGATGGTATTTTCAGGATTATCA  
ATAGGTACAAGAAGATCTAGTCAAGCTTTAGCTGAACTGGTATTTCAATCATCATTGACAAGTTCTACA  
CAAGAAACAGCACCACAACATTTCCCGGATGCTAAAGAGATTGAACCGGTTGCTGAACATGTTTCGAGT  
ATTAACCCACGATATTCTTCGACTTCGATTTCTAAGCAACCTACAAGTTCAAGTTCACTTTTCACAACTG  
TTTTTCGGAGGTGCTGGTGGGTTAAGTAGTACTGATAAAGAGTTGTGCGAACTGTTTTTAGGAGGATCA  
ACGTCAGCATCAACATCAACATCGCATGATGAGAAGACTACTACTATTGATTCTTCAAGTACTGGGTTT  
TTCCAAGTACCAAATAGAGATTATACTCCTTCTCCAGATAATAATACTTTGACTCGTACATTATCTAAT  
ACATCCAAGAAATCTTCACCATTACCACCACAAACAACCTTCAGAGAATGCATTTCAGAGGTGATGGACAA  
CAATCACAATCACAATCACAATCACAATCACAGTTGCCACTGCAACAACAACCTGCAACCACGACGGGGA  
TTATTATTTGATGAAGAAGATTCTGAAGATTCTGAAGATGAAGGAATGGTTATTGGTGGTAAAAAGAGAA  
GAAAGAAATTACATGGACAAGGATATAATGCATTAAAGTCAAGTTGCAGGTAGAAATGGTATCCATAGT  
CCAAGTCCACAATTGGTAAATGCTAGTGCACATCTTCAAGATCAAGATCAAGGTCAAGGTCAAGGTCAAGGT  
GAACATGAACATGAAGAAAATCATAAGAATCTTGTGGTCAAGCTAGAGGTTTAGCTAAACACTTCTTT  
GGATAA

YKR075C\_homolog 1013aa (SEQ ID NO 546)

MSLSGEVFSGGATTSQHIEAQDDHDFENTTFKLKRTSRMGLLDEFIPDKLKEQDGNNSSEANSSTTAAST  
TSSRNLAAMAAIASQTNSSYVNETPSSQHETIESISMNSDGDVTHSSDVAPSSSTSPVNSPSPSTSSPAL  
DLKSPPELLPHDDTDLAVEPSRHVDYLSHQWVSDIWKSWRYVISKRKDVANAARLENASWRTWAQRRSN  
LKTISPVVNWSKSDSVTWLYGPILKDDHVNENHDSDAIETTATSSVAGDISIAKKCSSKNGPKPIL  
KKRTMEQSMISHSNLLKLQLATQIHQKKREQKLKQEELEKRQHQLNHPDEYFDPEALSNKLNQSYKNTA  
PTHNTSVAKLQSLKTPNSSSSASLKDLMKDEAVVPSSEQISHDQNOEDGNVSGDVESKGERHIHFND  
EVMQCIADIVYSDDEQRYNSDEEDYSDDDDDDDYDQYEPSNDSLQSHLYEGDDSEIEADEEVEDEDE  
DGESEEDDEGGFFLNVKSNSNAPIILGQHSSASTSTPVAPSLSRHTDITDDTASISTTNSKSYKTIQL  
LPSTSINYGSDESSDEANPYTSSLSHNVNDISRGYDYDYDYNTVYTCNPNNSVYASYQSPDVVDVPE  
LDMGSNFDYEFIEENNDIPVVDTTFENNSTINMPIISYSSPSSPLSVAISGGGKNSGVTVNSPNFPIVN  
VNSNPQQQQSQAKPKPKTKASFFQLSDSEDDNSDSDDDGISGLSIGTRRSSQALAESVQSSLTSSST  
QETAPQHFPDAKEIEPVAEHVSSINPRYSSTSISKQPTSSSSLSQSFFGGAGGLSSSTDKELSKSFLGGS  
TSASTSTSHDEKTTTIDSSSTGFFQVFNRYDTPSPDNNTLTRLNNTSKKSSPLPPQTTSENAFRGDGQ  
QSQSQSQSQSLPSQQSQPRRGLLFDEEDSEDSDEGMVIGGKREEKKLHGQGYNALSQVAGRNGIHS  
PSPQFGNASAHLQDQDQGHENEHEHEHENHKNLVGQARGLAKHFFG

YLR216C\_homolog 1221bp public: 1..1221 (SEQ ID NO 547)

ATGTGTAAAGTGGTGAGTGTGTTCGAGAACATTCCACCAGTATTTTTTCCAAATTTATATAAAAAATGAG  
ATAAAATTTTCTGTTTCTGGTATTTTCTTTTCCACCAACTCATGACTGCCACACCTGTTTATTTTGAT  
ATTTTCATGCAACGGCAAACCCAAGGGCCGTGTTGTTTCAAACCTCTACGATGATGTGTTCCTAAAAACA  
GCAGCTAATTTCCGTTCTTATGTACTGGTGACAAAGGTATATCACCAAAATCTGGTAAACCACTTTCC  
TATAAAGACTCAATTTTCCACAGAGTGATCAAAGACTTTATGTGCCAAGGTGGTGACTTTACCGCTCCT  
TCCGACCATTTTGGGAAGTGGTGGTGAGTCCATTTACGGAGAAAAGTTTGAAGATGAAAACCTTTAAGTTG  
AACCATAACAAACCAATTTTGTGTCAATGGCTAACTCTGGACCAAAACCAATGGCTCTCAATTTTTT  
ATCACAACAGTTTCCAACACCACACTTGGACGGTAACACGTTGTGTTTGGAGAAGTCATTGAAGGGAAA  
TCAATTGTACGTCAATTAGAGAGAAGCGAAAAGGGTGCCAAATGACAGACCAGTAGAAGATTGGAAAAT  
GCTGATTGTGGTGAGCTTCCAGCCAACTATGAGCCGGTTGCACTGGGTGCCGATGATGGAAGTGGTGAT  
ACGTACGAAGAGATTTAACCGACAACGACACTATCGACATCAACAACCCGAATCTGTTTTCGCGGCT  
GTCAGCAAAATCAAGGATATTGGTACCAAACTTTTGAAAGAAGGGAAATTAGAAAAATCATACGAAAAG  
TATACCAAGGCCAATAGCTACTTGAATGATTACTTTCCGAAGGTTTGTCTCCAGAAGACTTATCAACA  
TTGCATGGCCTCAAATTATCGTGTTACTTGAACGCTGCGTTAGTGGCATTGAAATTGAAACACGGCAAA  
GATGCAATTGCTGCTGCAACAATGCATTAGAAGTAGAGCAAAATCGACGACAAATCCAAAACCAAGCA  
TTATACAGAAAAGGTATGGGCTATATCCTAGTCAAAGACGAAGAACAGGCTCAAAAGATTCTTGAAGAA  
GCTCTCGAATTAGAACCTAACGATGCTGCTATCCAAAAGGATTACAAGAAGCTAAACACAACATCAAG  
TTGCGTCTGTGACAAACAAAAGAAGGCAATGGCCAAGTTCTTCTCATAA

YLR216C\_homolog 406aa (SEQ ID NO 548)

MCKVVSFENIPPVFFPNLYKNEIKFSFSVFFFFHQLMTATPVYFDISCNGKPKGRVVFVKLYDDVVPKT  
AANFRSLCTGDKGISPKSGKPLSYKDSIFHRVIKDFMCQGGDFTAPSDHLGTGGESIYGEKFEDENFKL  
NHNKPFLLSMANSGPNTNGSQFFITTVPTPHLDGKHVVFEVIEGKSIVRQLERSEKGANRPFVEDWKI  
ADCGELPANYEPVAGSADDGTGDTYEEILTDNDTIDINNPQSVFAAVSKIKDITGKLLKEGKLEKSYEK  
YTKANSYLNDYFPEGLSPEDLSTLHGLKLSCYLNALVALKLKHGKDAIAAANNALEVEQIDDKSKTKA  
LYRKMGYIILVKDEEQAQKILEEAELEPNDAIQKGLQEAHNIKLRRDKQKKAMAKFFS

YMR009W\_homolog 537bp public: 1..537 (SEQ ID NO 549)

ATGGTCAATTTTATTTTCATGATAACAAAGATACACTTGAAAATTTTACTGAAGATCACAATTCAGGA  
GAACCAGTTAGTTTTGATCAACTAGCTGAAATTGGTGTATTATTACAAGTACATTACTACCCAGGAAGAA

166/251

TTAGACGCATTGGCTACTGAAAGAGAATACAAGAATAGAGATGTTGTTACTTTTAACTTACCAGCCTTC  
AATAATGATATTGATGCTTATAATGCCAAAATGCAACAGTTTACAAAGAACATTATCATGAAGATGAG  
GAAATTAGATATATTGCTGAAGGTGAAGGTTATTTTGATGTTAGAGATAAACAAAGATCGTTGGATTAGA  
GCTAAATTATCACCTTACGATTTGTTGATTTTACCAGCAGGAATTTATCATCGTTTACATTGACTAAT  
GCTGCAAAACACGTCAAGGCAGTTAGATTATTTAAAGATGAACCTAAATGGGAAGCTATCAATAGAGAC  
ACAGGAAAAAATACCGAAGCTCGTGAACCTATGCTAAGACTATTGCAGTATAG

YMR009W\_homolog 178aa (SEQ ID NO 550)

MVEFYFHDNKDTLENFTEDHNSGEPVSFDQLAEIGVIYKYITTTQEELDALATEREYKNRDVVTLLNLP  
AFNNDIDAYNAKMQQFYKEHYHEDEEIRYIAEGEGYFDVRDKQDRWIRAKLSPYDLLILPAGIYHRFTLTN  
AAKHVKAVRLFKDEPKWEAINRDTGKNTEARELYAKTIAV

YMR011W\_homolog 1641bp public: 1..1641 (SEQ ID NO 551)

ATGTCCTCAAGACAACGTCATCAACATCTACAGCTGAGGCTGTAAATAATGAAATCAAAGTCAAAGAT  
GAATTTTCGACAAGAAGAACAAGCTCATACCTAGTTTGAAGATAAACCTGTGAGTGCATACATTGGTATC  
ATCATTATGTGTTTCCCTTATTGCCCTTTGGTGGTTTCGTTTTCGGTTTCGATACCTGGTACTATTTCCGGT  
TTCATTAATATGTCTGACTTTTGTAGAAAGATTCCGGTGGTACTAAAGCTGACGGTACTCTTTACTTTTCC  
AATGTCAGAACTGGTTTAAATGATTGGTTTGTTCACGCTGGTTGTGCCATTGGTGCATTATTCTTGTCT  
AAAGTCGGTGATATGTATGGTAGAAGAGTTGGTATCATGACTGCTATGATTGCTATATTGTTGGTATT  
ATTGTTCAAATTGCTTCTCAACATGCTTGGTATCAAGTCATGATTGGTAGAATTATCAGTGGTCTTGGC  
GTTGGTATGTTATCAGTTTATGTCTTTTGTTCATTTCAGGTTTCTCCAAAACATTTGAGAGGTACT  
TTGGTGTGCTGTTTCCAAATTGATGATTACCTTGGGTATCTTCTTGGGTATTGTTACTACCTATGGTACT  
AAGAGTTACTCAGACTCTAGACAATGGAGAATTCCATTAGGTTTATGTTTGTCTTGGGCTTTATGTTTGT  
GTGCTGGTATGGTTAGAATGCCAGAATCTCCACGTTACCTTGTCCGTAAAGACAGAATTGAAGATGCT  
AAAATGTCACTTGTCTAAAACCTAACAAAGTTTCCCCAGAGGACCCAGCCTTATACCGTGAACCTCAATTA  
ATTCAAGCTGGTGTGAAAGAGAAAGATTAGCCGGTAAGGCATCTTGGGGTACTTTATTCAATGGTAAA  
CCAAGAACTCTTTGAAAGGGTTGTTGTTGGTGTCTGTTACAAGCCTTACAACAATTGACTGGTGATAAC  
TATTTCTTCTACTACAGTACCCTATTTTCAAGTCCGTTGGTATGAATGATTCTTTCCAAACCTTCTATC  
ATTATTGGTGTATTAACTTTGCGTCCACTTTTGTGGTATTTATGCTATTGAAAGAATGGGTAGAAGA  
CTCTGTTTGTAACTGGTTCCGTTGCCATGCTGTCTGTTTCTTAATCTATTCCTTGGTTGGTACTCAA  
CATCTTTATATTGACAAACCAGGTGGTGTCTAGTAGAAAACCCAGATGGTGATGCCATGATCTTTATGACT  
TCACTTTATGTGTTCTTCTTTGCTTCTACATGGGCTGGTGGTGTCTTACTCCATTATTTCTGAACCTTAT  
CCATTGAAAGTTAGAAGTAAGGCTATGGGTTTAGCTAATGCTTCCAATTGGACCTGGGGTTTCTTAATT  
TCTTTCTTTACTTCAATTATTACTGATGCTATCCACTTCTACTACGGTTTCGTTCTTTATGGGATGTTTA  
GTTTCTTCACTTTTCTTTGTCTACTTTATGGTTTACGAACTAAAGGCTTACCTTGGGAAGAAATTGAT  
GAATTGTACTCCACCAAGTCTTCCATGGAATCAGCTGGTTGGGTGCCACCTTCCGAAGAAGAAATG  
GCAACCTCTACGGGATATGCTGGTGTATGCCAAACCAGAGAGGAACACGTTTAA

YMR011W\_homolog 546aa (SEQ ID NO 552)

MSQDNVSSTSTAEAVNNEIKVKDEFQRQEEQAHTSLEDKPVSAIYIGIIIMCFLIAFGGFVFGFDGTISG  
FINMSDFLERFGGTKADGTLTYFSNVRTGLMIGLFNAGCAIGALFLSKVGDYGRRVGIMTAMIVYIVGI  
IVQIASQHWYQVMIGRIITGLAVGMLSVLCLPLFISEVSPKHLRGLTVCCFLMITLIGFLGYCTTYGT  
KSYSDSRQWRIPGLCLFAWALCLVAGMVRMPESPRLVVGKDRIEDAKMSLAKTNKVSPEDPALYRELQL  
IQAGVERERLAGKASWGTLENGKPRIFERVVVGVMQLALQQLTGDNYFFYYSTTIFKSVGMNDSFQTSI  
IIGVINFASTFVGIYAIERMGRRLCLLTGSVMSVCFLLYSLVGTQHLIDKPGGASRKPDGDAMIFMT  
SLYVFFFFASTWAGGVYSIISELYPLKVRSKAMGLANASNWTWGFLISFFTSFITDAIHFYGYFVFMGCL  
VFSIFVYFMVYETKGLTLEEIDELYSTKVLPWKSAGWVPPSEEMATSTGYAGDAKPEEHV

YMR110C\_homolog 1986bp public: 1..1986 (SEQ ID NO 553)

ATGAGTAAACCATCTTCCATCAAAAAGTCTAAGGCATCTGCTATTAAACCTCGGCTAATTCAAATCA  
AAAACCCCAAAAATTGAGACCCCAAAATTGCAACAGTTGAAACACGATTAGAAGGCGAAGTTCCAACA  
ACTAAAGTTTCAATTAAAGAAACAGTATTACTACTGAATCTGTAAAGGCTTCAGAAGATAAGTCTACT  
CCACAAAGCTAACACCCCTGCTGCTGCTGTAGCAAAGTCTAATCCAAATACCAATGCAGAGCCAGCT  
AAAATTCCAAACGAAAACTGTAAAAACAGAAATCAGCACTGAGTCAAAAACAAAACGGTGCAACAACA  
ACAAAGGAAAAATCTGATGTTCTGTTGGAGACAAAATCGACGTCATCAACTACTGTCTAGCAACAATAAC  
TCGGTCTTACAATATACCGAGTTGTCCGAGATCCCTATTGGTGTGTTGAAAGAATTACTAAGGCCCTCCAT  
AGTGGCAAAACACACTCTTTACAGTTTGAATGAAACAAATACGAAACTTGTACTTTACAATGAAAGAC  
AACCAGGAAGCTTTGTGTGACGCTTTGCAAAAGGACTTTACCCGCTCTTCTTCCGAAACAAGAACTAT  
GAATTGCCCAGTGGATTGAATGAGCTAGTGTATTATTATGTCACAGCTCCACAAATGGAGCAAAACACAA  
CCTGTTGACAGAGTTGCCATTGAATTTGTCTTTTGAATCCAGTTTACATTGAGAGAATTCCCTTTGGGAACA  
ATTTTAGTCATTGCTGCTTTCAATTATCCGTTTTTTGTCTCGATCTCACCATAAGTTGGTGCAATAGCA  
AGTGGCAACACAGTTGCACTCAAGCCTTCTGAGTTAACACCCCGTTTTTCCAAGCTTTTACTGACTTG  
TTGTCAAAAAGCATTTGACCCAGAGATATTTTTTGTGTTCAATGGGGCCATTCTTGAACAACATGCTTG

167/251

TTGGAACAAAAATTTGACAAAATTGTTTATACTGGTAGCGGTTTGGTAGGTACAATAATTGCGAAAAAG  
GCTGCGGAAACCTTGACACCAGTTATTTTGGAGTTGGGAGGAAAGTCACCTGCTTTTGTGTTTGGATGAC  
ATTTCTGACAAGGACTTGGAACCTGTTGCTCGAAGAATTGCTTGGGGTAGATTTGTAAATGCTGGTCAA  
ACATGTATCGGTGTTGACTATGTATTGGTGGCAAAGTCCAAGCACGACAAATTTATCCTGGCCTTGCAA  
GAGGTAATTGAAAAAGAGTTTTTTCAAGACGTTGACAAGACGAGAACTTTACCCATATGATCCATGAC  
CGGGCATTGAGAAAATGGAGAGTATACTCAACACTACTTCTGGTAATGTGATAATTGGAGGCAAGCTT  
GATCATGGCACAAGATATGTGGGACCTACCGTGATTGATAACGTAACCTGGACAGATTCCCTCTATGAAA  
GACGAGATTTTCGGTCCAATTTTACCAATTTTAACCTACACTGATCTTGAAAAATCCTGTCGTGAAATT  
ATTGCTAACCACGATACTCCCTTGGCACAATATATCTTTACAAGTGGACCTACATCTAGACAGTATAAT  
TCCCAAATTAACACTATTACCACTTTGGTTAGATCTGGGGGATTGGTTATCAATGACGTTTTGATGCAT  
ATTGCTTTGCACAATGCTCCGTTTGGTGGTGTGGAACCTCGGGAACGGTGCCTATCATGGAGAGTTC  
TCATACAGAGCTTTTACACATGAGAGGACCGTTCTCGAACAACATTTGTGGAATGATGGGTACTCAA  
TCAAGATATCCCCCATATGCCAATAAAAAAGACAAATTGATCGCCAGCTCCCAACAAAAAGTACGGTGCT  
AGAGTTTGGTTCAATAGAGAAGGAATGTGAGAATTGGAGGTCCACCCCTCTTGTGTTTCTGCTTGGAAAC  
AATGCTCTTGGGGTAGCTGAATTAGTACGTGATTTTATTGGAGCTGGTTTGTGA

YMR110C\_homolog 661aa (SEQ ID NO 554)

MSKPSSIKKSKASAIKPSANSKSKTPKTIETPKLQVETRLEGEVPTTKVSIKRNSTTESVKASEDKST  
PQSTNTPAAAVAKSNPNTNAEPAKIPNEKSLKTESPSSQKQNGATTTKEKSDVSLETKSTSSTTVSNNN  
SVLQYTELSEIPIGVERITKAFHSGKTHSLQFRLKQLRNLFTMKDNQALCDALQKDFHRLPSETRNY  
EFATGLNELVFIMSQLHKWSKPQPVDELPLNLSLNPVYIERIPLGTILVIAAFNYPFFVSIPIVGAIA  
SGNTVALKPSLTPRFSKLFTDLLSKALDPEIFFVNGAIPETTCLEQKFDKIVYTGSGLVGTIIAKK  
AAETLTPVILELGGKSPAFVLDDISDKDLATVARRIAWGRFVNAGQTCIGVDYVLVAKSKHDKFISALQ  
EVIEKEFFQDVKTRNFTHMIHDFEKMESILNTTSGNVIIGGKLDHGRYVGPVVIDNVWTWDSSMK  
DEIFGPILPILTYTDLEKSCREIIANHDTPLAQYIFTSGPTSROQYNSQINTITTLVRSGLVINDVLMH  
IALHNAPFGGVGTSGNGAYHGEFSYRAFTHERTVLEQHLWNDWVLKSRYPYANKKDKLIASSQQKYGG  
RVWFNREGNVRIGGPPLLFSAWNNALGVAELVRDFIGAGL

YNL031C\_homolog 411bp public: 1..411 (SEQ ID NO 555)

ATGGCTAGAACAAAACAAACAGCAAGAAATCTACTGGTGGTAAAGCCCCAAGAAAACAATTAGCTTCC  
AAAGCTGCTAGAAAATCTGCTCCATCTACTGGTGGTGTCAAGAAACCACACAGATATAAGCCAGGTACT  
GTTGCCTTGAGAGAAATTAGAAGATTCACAAAATCTACTGAATTATTGATTAGAAAATTACCATTCCAA  
AGATTAGTCAGAGAAATTGCTCAAGATTTCAAACTGATTTAAGATTCCAATCTTCTGCTATTGGTGCT  
TTACAAGAGCGGTTGAAGCTTACTTGGTTGGTTTATTTCGAAGATACTAAGTTGTGTGCTATCCATGCT  
AAGAGAGTTACCATTCAAAAGAAAGATATGCAATTAGCTAGAAGATTGAGAGGTGAAAGATCTTAG

YNL031C\_homolog 136aa (SEQ ID NO 556)

MARTKQTARKSTGGKAPRKQLASKAARKSAPSTGGVKKPHRYKPGTVALREIRRQKSTELLIRKLFPQ  
RLVREIAQDFKTDLRQSSAIGALQEAVEAYLVGLFEDTNLCAIHAKRVTIQKKDMQLARRLRGERS

YNL134C\_homolog 1086bp public: 1..1086 (SEQ ID NO 557)

ATGAAAGCAGCTATCATTTCTGGATCTTTTCAACCTTATCAATTAGCGGAAATTAAGATATTCTCTCAA  
CAAAAAATAAAAGAAAATGAAATATTAATCAAAGCAGTAGCTTTTGCAATAAACCCAACTGATTGGAAG  
CACATTGTTTATCAATTGGGCAGCCCAGGTGATGTTGTTGGTTGCGATGTTAGTGGGATCATTGAAGAA  
GTGGGTTCTCAAGTAACTGGGTTTGCAAAAGGTGACACTGTAAGTGCTTTTATACTGGTAATAGATCA  
CCTCGCACTGGAGCTTTTGCAGAAATATGTAGCTGTTGATCCTGCTACTTCGATAAAGTACAATAAGAAT  
TTTGAACATTTGACTAATTTACAAGTATCTGAAATCCACTCATTTGAAGGGGCAGCAAGTATTAATTTA  
GGTTTGGTTACCGTTGGGCTTTTCATTTTCTCATTACTTACGAATTGACAACAAAAAGCAACCTGGGGAT  
AGTATTTTGATTGTTGGGGAGGAGCAACTGCAACTGGAGTTCTAGCCATTGAGGTTGCCAACTAGTGAT  
AATCTCAAAGTAATCACACAGCATACCCAAAAACACACCTCTTGAAACAATTAGGGGCAGATTAT  
GTTTTCGATTATGGAGACGCTGATGTTGTCAATAAAATTAAGAATATTGGCCAAATTAATTTGCTCTT  
GATACGATTGCAACACCAGAAAACGTTTCAAAAAGTTTACGACTCAACAGAGGGGTCTCAAGAAGTATTT  
ATTGATTCTTTAGCAGGTTTAGACTATCGATCAATTGCTGCCAATGATGCCAGAGGAGATCAAGTACAT  
TGGGGGCACACCATTGCTTGTGTTGGCATCTTTAAAGAGAAAAGTGTGTTTAAATGAAAATTATGTTCAA  
ACACCTGAATTGTTAGATGATTTTACTCAGTGGTGGCAAAAGGTGGTCCCTCAAATAATTGATCGTATT  
AAACATACAAATTTAAAGTTATTAATGAAGGATTAGACTCCGTAAGTGAAGGGTTAGAATTGTCTAGA  
AATAATAAACTCTCTGCTGAAAAGGTTGTATTTAGAGTTCTGGATCTGTGA

168/251

YNL134C\_homolog 361aa (SEQ ID NO 558)  
MKAIIISGSFEPYQLAEIKDIPQQKIKENEILIKAVAFAINPTDWKHIVYQLGSPGDVVGCDVSGIIEE  
VGSQVTGFAKGDPTVSAFITGNRSPRTGAFAEYVAVDPATSIKYNKNFEHLTNLQVSEIHSFEGAASINL  
GLVTVGLSF SHYLRIDNKKQPGDSILIWGGATATGVLAIQVAKLVYNLKVITTASPKNHTLLKQLGADY  
VFDYGDADVNNKIKNIGQIKFALDTIATPETFQKVYDSTEGSQEVFIDSLAGLDYRSIAANDARGDQVH  
WGHTIACLASLKEKTVFNENYVQTPPELLDDFTQWWQKVVPQIIDRIKHTNLKLNEGLDSVSEGLELSR  
NNKLSAEKVVRVSDS

YNR002C\_homolog 798bp public: 1..798 (SEQ ID NO 559)  
ATGACGCTCTTCATCTTCTCAAAAATCTGTTGGATCTTCAATCATAGATGCAAACCAAGGACCAATAAAA  
AAAGTTGAAATTGCTGGAGAGGGTGGTGAATTTGTTATTATCAATCGTCACAAGTACTACAGACATGAC  
TTGATGGCTGCCCTTCGGGGGTACTTTAAACCCAGGTGCCTTCTCCTTGCCCAAAGATCAATATCAACCCT  
GCTCCCCCTCGGGTTATGTGGGTTTGCCATGACCACCTTTTGTCTTATCCCTTTTACAAATGCCCAAGCTATG  
GGTATCAAAGTTCCAAATGTGGTAGTTTCACCTTGCATGTTTCTACGGTGGTGCAGCTCAATTTTTTGTCT  
GGATGTTTTTGTAGTTTGTGACTGGAAATACATTTGGTATGACTGCATTGACATCTTACGGTGCCTTCTGG  
TTGAGTTATTTCAGCAATCTTGGTTGATAGTTTGGTATCGCTGCAGCCTACGAAGCTTCTGAAGAAACA  
GCTTCACAGTTACCAAATGCCATTGGATTTTTCTTACTTGGCTTGGGGTATCTTTACATTTATGTTGTGG  
TTGAACACTTTTAAATCTACAGTTACTTTTACAGTTCCCTTGTGTTTCTTATTGTTTGTAAACATTCCTTTT  
TTAGCTGGTGGTGAATTTAGTGGAAAGAGTCGGTGTACTAGAGCTGGTGGTGTGTTTTTGGTGTATTACACA  
GCCATTGTTGCTTGGTGGAAATGCCCTTAGCCGGTACTGCTACTCCAACCAACTCTTACTTCCAACCTGTT  
TCTATTCCATTGCCAGGTAACGTTGTTTTCAAGAAATAG

YNR002C\_homolog 265aa (SEQ ID NO 560)  
MTSSSSQKSVGSSIIDANQGPIKKVEIAGEGGEFVIINRHKYRHDLMMAAFGGTLPNGASPPWPKNINP  
APLGLCGFAMTTFVLSLYNAQAMGIKVPNVVSLACFYGGAAQFFAGCFEFVTGNTFGMTALT SYGAFW  
LSYSAILVDSFGIAAAEASEETASQLPNAIGFLLAWGIFTFMLWNLTKSTVTFSSLFLLFVTFLL  
LAGGEFSGRGVTRAGGVFGVITAIVAWWNLAGTATPTNSYFQPVSIPLGNVVFKK

YOL139C\_homolog 630bp public: 1..630 (SEQ ID NO 561)  
ATGCTGAAGAAATTAGCTCAAAAACTGAAGAAATTGTCAATTAGATTCCAAGACTGTTTTTGTATTCCAAA  
GAAGAATTTAATGCAAAGCATCCATTGAACAGTAGATGGACATTATGGGTACACTAAACCACAAACCAAC  
AAGAGTGAAAACCTGGCATGATTTATTAAAGCCAGTTATAACTTTCTCATCTGTTGAAGAATTTTGGGGA  
ATTTACAACTCGATTCCACCAGCAAATCAATTACCTTTGAAATCAGATTATCATTGTTTCAAAGAAGGA  
ATTAGACCGGAATGGGAAGATGAGGCTAACTCAAAGGTGGTAAATGGCAATTCTCCTTCAACAAAAA  
CTGGAAGTCAATCCAATCATAAATGATTTGTGGTTAAGAGGTTTGTGTCAGTTATTTGGTGAACCAATT  
GAGGATGAAGAAAACGAAGTCAATGGGATTTGTGTTGAATATCAGAAAGCAAGCTTACAGAGTCGGTATT  
TGGACCAAAGATTGTGATGAATCCAAATTTAAAGACTGTCTGGTGAGAGATTGAAGAAAGCTTTGCAATTA  
AACGATGAACAAAAAGTTGAATTCATGTCGCATGATGCTTCCAATACTAGAGGCGCTGAACCTCAAATT  
GTTTTGTAA

YOL139C\_homolog 209aa (SEQ ID NO 562)  
MSEELAQKTEELSLDSKT VFD SKEEFNAKHPLNSRWTLWYTKPQTNKSENWHDLLKPVITFSSVEEFWG  
IYNSIPPANQLPLKSDYHLFKEGIRPEWEDEANSKGGKWQFSFNKKSEVNPIINDLWLRGLLAVIGETI  
EDEENEVNGIVLNIRKQAYRVGIWTKDCDESKLKT VGERLKKVLQLNDEQKVEFM SHDASNTRGAEPQI  
VL

YOR120W\_homolog 888bp public: 1..888 (SEQ ID NO 563)  
ATGCCAGCTCAATTGCAAGTTAACTGATTTATTTTCACTTTTAAACAAATGGAAAACAAAATCCCAGCTGTT  
GGATTAGGTACTTGGCAAGCAACCAATGAAGACGAAGCTTACAGAGCCGTCTTAGCAGCTCTTAAGAAC  
GGATACAAGCACATTGATACCGCTGCAATTTATGGAATGAAGAACAAAGTCGGTAAAGCCATCAAGGAC  
TCTGGAGTTCCAAGAGAAGAAATTGTTGTTACTACTAAATTTGTGGAAATGCTGACCATAAAAAATATTGAA  
GAAGCCTTAGAGACTTCATTGAAAAAATTGGGTCTTAACTATGTTGACTTGTACTTGTATCCATTGGCCA  
GCTTCAATTGACAAAGTCAACTAATAAACCATAGACTGATTTTGTATTATGTTGATACCTTATAGAGGTTTA  
CAAAAAGTTTATAAGAACAGCAAGAAAAATCAGAGCAATTTGGTGTGTTCTAAATTTTCAACCAAAAAGAAATG  
GAAAGGTTATTGTCTTCGGAAGGTGTCGATGTTGTTTCTGCTGCTCAACCAAATTTGAAGCTCACCCATTG  
TTGACTCAGCTTGAAATGTATGATTTATTTGAAAGAAAAAGGTATCGTTTTTGAAGCTTATTCACCATTG  
GGTTCTACAAACTCTCCATTATTCAAGAACGAAACCATCGTTAAATTCGCTGAAAAGAAATGGTGTGAA  
CCAGCTCAAGTTTTTGGTATCTTGGGCAATTCAAAGAAAGACTGTGGTTTTTGCCTAAATCCGTCACCGAA  
TCAAGAGTTATTCTTAACCTTGAAGAAATTCACCTTTACCTTCAGAAGATTTTCGAAACATTGAACAAATG  
TCTGAAAAAGATGGTGTGTCAGAACTTGTAAACCCAGCTTTCAACAACTTTGATGATTAA

169/251

YOR120W\_homolog 295aa(SEQ ID NO 564)

MPAQLQVNTDYFTLNNGNKIPAVGLGTWQATNEDEAYRAVLAALKNGYKHIDTAAIYGNEEQVGKAIKD  
SGVPREELFVTTKLWNADHKNIEEALETSLKKLGLNYVDLYLIHWPASIDKSTNKPYPDTDFDYVDTYRGL  
QKVYKNSKKIRAIIGVSNFTKKKLERLLSSEGVDDVPAVNQIEAHPLLTQPELYDYLKEKGIVLEAYSPL  
GSTNSPLFKNETIVKIAEKNQVEPAQVLVSWAIQRKTVVLPKSVTESRVISNLKFTLPSDFETLNKL  
SEKDGVVVRTCNPAFNNFDD

YOR122C\_homolog 381bp public: 1..381(SEQ ID NO 565)

ATGTCTTGGCAAGCCTACACTGATAACTTAATTGCTAACGGTAAAGTCGATAAAGCAGCCTTATATTCA  
AGAGCCGGTGACGCATTATGGGCCCAATCGGGATCATTCGAATTACAACAACAGAAATCACTGAAATTT  
GCCAAAGGTTTCGATAGTGCTGAAGGTTTGCAAACCAGCGGTTTACACGTTCAAGGCCAAAAGTACTTT  
TTGTTAAGAGCTGACGACAGATCAATTTATGGTAAACACGAAGCCGAGGGTGTATTGTGTTAGAACT  
AAACAACTATTTTGTATCGCCCATTTATCCAAGTGGTGTTCACCAGGTGAAGCTACCACTCTTGTGTGAA  
AAATTAGCCGATTACTTGATCAATGTGCGTTATTAG

YOR122C\_homolog 126aa(SEQ ID NO 566)

MSWQAYTDNLIANGKVDKAALYSRAGDALWAQSGSFELQQPEITEIAKGFDSAEGLOTSGLHVQGQKYF  
LLRADDRSIYGKHEAEGVICVRTKQITILIAHYPSGVQPGEATTLVEKLADYLINVG

YOR261C\_homolog 993bp public: 1..993(SEQ ID NO 567)

ATGTCAACAACCTGCAACTAGCACAAATGAATTGGCCCTTTTGGATAAGTCAGTAGTAGTTTCTCCGTTG  
GTTTTACTATCTGTGGTGACCATTTATAATAGAGTTGCCAAAGATTCTAAGAAGAGAGTTGTTGGGGTA  
ATATTAGGAGATAACTCTACTGACACAATCAAAGTTACAACTCGTACGCAATTCCTTTTGAAGAAGAC  
GAGAAGAACCCTGGAGTATGGTTTTTGGACCACAATTTTATAGATTCAATGGGAGAAATGTTTAAAAAA  
ATTAATGCCAAAGAGAAATTGATTGGCTGGTACCATTACAGGACCTAAATTGAAACCATCAGATTTGAAA  
ATTAATGAGGTTTTTCAGAAGATACACCGACAACCCATTGTTGTTAATTGTTGACGTTCAACCAAGAGAA  
GTTGGTATTCCAACAGATGCATATTTTGGCGTTGATGATATTAACCAACGATGGCTCTGCTGCTGAAAAG  
ACATTTATTTCATGTCCCTTCCTTGATTGAAGCAGAAGAAGCTGAAGAAATTGGAGTTGAACATTTGTTA  
AGAGACATCAGAGACCAAGCTGCTGGTAACTTGTCTTAAAGAGTTTCTGAAACACATCAATCATTATTG  
GGTTTACATCAGAAGCTTGGAGAAATTGCAAATTATTTGGATAAGGTTTACCAAAAGAAATTACCTATG  
AATCATACTATTTTGGGAAATTACAGAATGTTTTTAATTTGTTGCCAACTTGATGCAACAACCTGGGG  
AGTGATCTCGATGGTGGTTCAGACTCGTCTCATGCATTAGCCACTGCATTTACTGTCAAGACAAATGAC  
GAATTGATGATCATATACATTAGTACATTAGTTTCGAGCTATTATTGCATTCCATGATTTGATCGAAAAC  
AAGTTAGAAAATAAAAAGTTGAACGAAAATAAAGCACAAGCTTCCGTGGCTGAAGTGTCAATTAATAGC  
GAAAAGAAAGATTCTATAGAAGATTAA

YOR261C\_homolog 330aa(SEQ ID NO 568)

MSTTATSTNELALLDKSVVVSPLVLLSVVDHYNRVAKDSKKRVVGVILGDNSTDTIKVTNSYAIIPFEED  
EKNPGVWFLDHNFIIDSMGEMFKKINAKEKLIGWYHSGPKLKPSDLKINEVFRRYTDNPLLLIVDVQPRE  
VGIPTDAYFAVDDIKNDGSAAEKTFIHVP SLIEAEAEIEIGVEHLLRDIRDQAAGNLSLRVSETHQSLL  
GLHQKLGEIANYLDKVYQKKLPNMHTILGKLQNVFNLLPNLMQQSGSDLDGGSDDSHALATAFTVKTND  
ELMIIYISTLVRAIIAFHDLIENKLENKLNENKAQASVAESSLNSEKDSIED

YPR035W\_homolog 1122bp public: 1..1122(SEQ ID NO 569)

ATGACTACTTCCCTTACAGAACAACTGCTATTTTGGCCAAATATTTGGAATTGTCTCAAAATGGTAAA  
ATCTTAGCTGAATACGTCTGGATTGATGCTGAAGGTAACACTAGATCCAAATGTAGAACTTTATCCAAA  
AAACCAACTAGTGTGATGATTACCTGAATGGAATTATGATGGTTCATCTACTGGTCAAGCTCCAGGC  
CATGATTCTGATGTGTATTTAAGACCAGTTGCTTTTTATCCTGATCCATTTAGAAAAGGTGACAATATC  
ATTGTTTTAAATGAATGTTGGAACAATGATGGTACTCCAAACAAATTTAATCATCGTCATGAATGTGCT  
AAATTGATGAAGGCTCATGCTAGTGAAGAAGTTTGGTTTGGTTTAGAACAGAATATACTTTATTTGAT  
CAATATGATTATCCTTATGGTTGGCCAAAAGGTGGATTCCAGCTCCTCAAGGTCCATTCTACTGTGGG  
GTTGGTACTGGTAAAGTTGTTGCTAGAGATGTCATTGAAGCTCATTATCGTGCTTGTCTTTATGCTGGT  
ATCAACATTTCTGGTATTAATGCCGAATTATGCCATCTCAATGGGAATTTCAAGTTGGTCCATGTGAA  
GGTATTGAAATGGGTGATCAATTATGGATTGCTCGTTATTTATTACAAAGAGTTGCTGAAGAATTTGGC  
GTCAAGATTTCTTCCATCCAAAACCTTTGAAAGGTGATTGGAATGGTGCTGGTTGTCATACTAATGTT  
TCTACCAATCTATGAGAGTGCCTGGTGGTATGAAAGTTATTGAATCTGCTTTGAGTAAATTGGCCAAA  
AGACACAAGGAACATATGTTATTGTATGGTGCCGATAATGATCAAAGATTAAGTGGTCGTCATGAACT  
GGTCATATGGATACTTTTTCATCAGGTGTTGCTAACAGAGGTGCATCTATCAGAATTCCAAGACAAGTT  
GCTAAAGAAGGATATGGTTATTTTCGAAGATAGAAGACCAGCTTCTAACATTGATCCATACTTGGTCACT  
GGTATCATGGTGGAGACAATCTGTGGTTCTATTCCAGATGCTGATATGGCTAAAGAATTCCTTAGAGAA  
AGCAGTGATGATACTAA

170/251

YPR035W\_homolog 373aa (SEQ ID NO 570)

MTTSLTEQTAILAKYLELSQNGKILAEYVWIDAEGNTRSKCRTLSKKPTSVDLDPEWNYDGSSTGQAPG  
HDSVYLRPVAFYPDPFRKGDNIIVLNECWNNDGTPNKFNRHECAKLMKAHASEEVWFGLEQEYTLFD  
QYDYPYGWPKGGFPAPQGPFFYCGVGTGKVVARDVIEAHYRACLYAGINISGINAEVMPQSQWEFQVGPCE  
GIEMGDQLWIARYLLQ RVAEEFAVKISFHPKPLKGDWNGAGCHTNVSTKSMRVPGGMKVIESALSKLAK  
RHKEHMLLYGADNDQRLTGRHETGHMDTFSSGVANRGASIRIPRQVAKEGYGYFEDRRPASNIDPYLVT  
GIMVETICGSIPDADMAKEFLRESSDDN

YMR099C\_homolog 900bp public: 1..900 (SEQ ID NO 571)

ATGCCAGTTGAAGAGCTTGAAGACCGTGTATCATTACTGATCCAAATGACTCAACTAACAGAGCCACC  
ATTTTGAAATTTGGTGCTACTGTAGTTTCTTGAAAAACAATAATCAAGAAAAATTGTGGTTATCAGAA  
GGTGCTCATTTAGATGGAAGTAAAGCCGTTAGAGGTGGTATCCCATTAGTTTTCCCGTAAA  
CAAAAAGATTCAAATCATCCAACCTTTCAAATTACCTCAACATGGATTGCTCGTAATTCAAATTGGGAA  
TTCTTGGGACAAACTCAAGAAAGTCTATTACGGTTCAATTTGGATTAGGTCCAGAAAATGTTGATCCA  
GAACTTTGAAATTATGGAATTATGATTTCACTTTGATTTTAACTGTTAGTTTGACTAAAGATAAATTG  
GTTACTTCAATTGACGTGGAAAACTGGTAAAGAAGCATTGAATTTAATTGGTTGTTCCATACATAT  
TATAGAATCCATGACATCACCGATACATTAGTTACCAATTTAATTGACCAACAATGTTACGATCAATTG  
ATTGGTGAATCATATATCGAAAAGGCACCAGTTATCAGTTTCCATGAAGAATTTGATAGAATTTATTCA  
AAAGTCAGTTTGGAAAAATCCATTCAAGTCGTTGATAAAGGTCAAGTCTTTTCAATCTTCATAGAAAA  
AACTTGCCTGATTCCGTTGTATGGAATCCATGGACTAAGAAAGCTGAAGGTATGGCTGATTTCCAACCA  
AAATCAGGGTTTCATCAAATGGTCTGTGTTGAGCCAGGTGATGTTAACTCAATGGTCTCTTTACCAGCT  
GGTGGGAAATGGTCAGGTGGTCAAGAAATCACTATTGGCGGTGAGATTAAAGTTCAAGCTAATATTTAT  
TAG

YMR099C\_homolog 299aa (SEQ ID NO 572)

MPVEELEDRIITDPNDSTNRATILKFGATVVSWKNNNQEKWLWSEGAHLDGSKAVRGGIPLVFPVFGK  
QKDSNHPTFKLPQHGFARNSTWEFLGQTQESPITVQFGLGPENVDPETLKLWNYDFTLILTVSLTKDKL  
VTSIDVENTGKEAFEFNWLFTYYRIHDITDLVTNLIDQQCYDQLIGESYIEKAPVISFHEEFDRIS  
KVSLEKSIQVVDKGQVLFNLHRKNLPDSVWNPWTKKAEGMADFQPKSGFHMVCVEPHVNSMVS LPA  
GGKWSGGQEITIGGEIKVQANIY

YBL085W\_homolog 3519bp public: 1..3519 (SEQ ID NO 573)

ATGGATGGTGGCGATACTTATATATGTATAAAACAATTTAATGCCAGATTAGGCGATGAATTGAGTCTT  
AAAATTGGCGACAAAATTCAAGTATTGGCTGACGATAGAGAATATAATGATGGTTGGTACATGGGCAAA  
AATTGTTGACTGGAGAAGCAGGCTTATATCCAAAACATTTACTCAATTAATAACCAACAATGATAGT  
AAAACACTTCTTAGATCGAGGTCAAGAAGAATGATGGCACCTAAAAGTTCCGACCAAGAAACAACACCA  
AAGGACACCACTACTCCCGTGGTGTGAGTAATCTCAATCCCAACACTCCTCCAAATTACCCTCCAACA  
TTGTCTATCTTCAACAGAACCTTCCCATTTAGCTGAACCAATGTCTCAGTTAAATTTAAATAAAGATTCT  
CAATCTTCTCAATATACTGGGTCTCATTTGAACAGCCAAATTGATAGAGCATTACAAGAATTCAAGGG  
TCTAATGCCGACTTGACCAATTCTGGCAATGATTTTAAATGAGCACAGAAACCACCACTACAATAACAAC  
ACTAATAATAATAATAATAATAATAATAGTGTCTACTAGTAATAATTACAACAACCAACAGTTAATG  
TCGAAGAAATCAAATGATAGTCTTTCTAGTCAATATCAATATCAATCACAATCCCAACAACCAAAACAT  
TTGAGTGGAGATAAATCTCGACAATCCTTAAGTACGATTTGGACCCTTTGAAAGCAAATACTTGGACA  
CCAAAGCAAGTTTCTTCTTATTTTGCCTTGGTGTAGGGTTTGATATGGATGTGGCTGGGAAATTTGCT  
CAACACAAAATCACTGGAGAAATCTTGTGTAATTGGATTTAAATCTTTTGAAGAATTGGATATTGAT  
TCATTTGGTACCAGATTCAAATTATATAAAGAAATGGGAAATTAAAGGAATTGAATACTGAAGGAGTT  
AAAGATAAACAATTGAGAACAGATTCTCTGTGCTGACTGGATCAACTGGTAAAAATGACACTACGTCATCA  
GCATTAAATTTCTCCACCAACTGCTTCCACAACCTTTACACGATGCCGTGCCTCATATCGATGATAATAAT  
ATGTTAAATAATACTGGCAACAACAACAACAATAATGCCATCAGCCGTTTTGACCAACACTTCTGAC  
TACAATAATAATAGTCAACAACAAGTGGTTCTCAACATCATCAGAGGAAAAGGTCACTGTGGTGGAT  
GTTGCCCCACAACAATACTTGGCTTCTGATTCTACATTTATGTGCGCTAGAAGAGCTCCTCAACCACCA  
CTTGGTGAGAGCCCAATTGATACAAGTTATAAATTTGGTGCTGGAAGCGAATACGATAGACCAAGTTCA  
CACTATGGCATGTACATGACACGTACTAACGCTTCAAGTCATGCCTTGGGAAGTTTCACTACCAAGTAATC  
AACTCAGACCAAGCTTCAATTTATGATCTGTTTTCCAATCATAATAGAAATGGATCATCAACTTCA  
AAACAACACCACAAGAGAAATTCATCAGTAACCAACAATAACAATAACAATAACGGTAACAGCAACCAC  
AAGCATCATCACAGACGTCAATCTTCGGTATTCTCATACCTTTCTGCTGGTAATGATGATTGGGCAAAA  
CCAACACCAAAATTTAGTAGTAAGTTCCAAAGTAACAATTTGTACAAGGGTGGTATGATGGTCAAT  
GGAGATTTCACTTCTTCAAGCAATAACAACAACAGTAAGTTAGTGTGCGCCAGCCAGATCAAG  
AGAGAAACCACTAGTGGTCAATCGTCTCTTCATGAATCAGGATCCAAATCGAAAGGAAAATCACAATTT  
TTTGATTTATCCAATTCACCAAGTTGATATTGATGATGCCAAGTTTTCTCCAAAAAACTGAATTCGGTA  
TCAGTTCCGACCAAGTCAATGGATGCAATTTGGTGGTAATGGAGACGATAGACGTGTTGCTAGTGATTCT  
ACAGGATTGAGTCAATCAAAACCTAATAATTCATCAAGACTTAAAGGCATTCTGTCACGTCACACTCAA



171/251

AGTTTCCGAAGTTTAAACAGGGTCGAAGAACTGAAAAACATCAGCATTTCAGAAGGTATACGTGAGATT  
ACTCCTGATGAAGCCATTAAACTGCCAGTCATAGTGGTTATATGTCTAAACGTTCAAATAACAATTTA  
GCGTGGAGAACAAGATATTTACATTACACGGTACCAGATTATCATATTTCCAATCTTTGAAAGATAAA  
AAGGAAAAAGGTTTGATTGATATTACTGCTCATAAAGTGATACCTATTGATAGTGCTAGTGATGATACT  
GATAAAGCTGATAGATATGCTGCGATGTATGCCTCGACAACATTTGCTGGTAATTATTGTTTTAAATTG  
GTTCCACCGGTCCAGGGTTTAAAAAGGGTTAACGTTTACGCAACCGAAAACTCATTATTTGCTGTT  
GAAACAGAAGAAGAAATGAGAGCTTGGGTCAAAGCATTAAATGCAAGCCACTATTGATATTGATGATTCT  
GTTCTGTTGTGAGTAGTTGTTCTACCCCACTGTCAGTTTGAATAAAGCTCAAGAATTGTTAGCTAAA  
GCCAGAGAAGAAACCAATTACGAGATGAACAATAAAGCTAATGGCTACATTAGAAGCTTAGAAGAT  
ATCAATGATACTTCATTTCTGGCATCTTTGGATTATCCTGATATGAGTGGAGATATTGGTTTTGGTAGT  
ACTTCTCCAGTAGCAGCAACTTCAGCACCTAAATTGACTCTTGATACTAATTTTAATAGGAAAAAGTTCT  
GGAACCTATGGGAACAACGGGGACAATAGGTACTCCAGGAACATCAGGTGGTACGGTACCAACAACACCA  
CAAAATACCAGGATCATCAAGTCAAAGTGGTGGGTTTGCTTACCTTATTTATTAGCTTCTGGGTTATTA  
TCACCCAAATCAGGAGGTGGTGCCGGTCCAGGAGGAATTGTATCATCGTCTTCTCCAATTAATGAAAAAT  
GGACCTTTAAGAAATTCAACTTCAAATTCAGAATATTTTGGTGATATTACTTATAAAAGTTTAAAAACCA  
CCATCTCGACAAAATTTCCAATATGCAAGTATCACTAGTGGTGGTGGCAGTATTGGGTTTGGATATGGT  
TCCAACAATAGTGGCCTAGGTGGACCAGCAACAGCAATTGGAGGAGGAGGAGGAGGAGTATTATCATCA  
TCCACTCCATATTCTACTGGTCTTGATCAACAGTAAGTTCAATGAATTATAAATCATAACAACAAC  
AACAACAACAACAATTCTGTTAATAGTCCGATTAAATGAATTTAGATCTTCAAGGGATTGAAATCATCA  
TCGTACCAACGACAACAACAGGTACATCTTCAACATCAGGGAAAAAACCCCAATCACGTAGAACATCA  
GATAAAATGTTGGGATTTTCAAGTGATGCTTCAGGTAGTCATACTTTTGTATTAAACCGAAAAATAA

YBL085W\_homolog 1172aa (SEQ ID NO 574)

MDGGDTYICIKQFNARLGDLSLKIGDKIQVLADDDREYNDGWYMGKNLLTGEAGLYPKTFTQLITNND  
KTLRLSRSRMMAPKSSDQETTPKDTTPVVSNNLNPNTPPNYPPTLSSSTEP SHLAEPMSQLNLNKDS  
QSSQYTGSHLNSQIDRALQELQGSNADLTNSGNSFNEHRNHYNNTNNNNNNNNNAATSNNYKQPQLM  
SKKSNDLSQYQYQSQQPKHLSGDKSRQSLTDDLPLKANTWTPKQVSSYFALVLGFDMDVAGKFA  
QHKITGEILFELDLNLLKELDIDSFGTRFKLYKEIGKLKELNTEGVKDKQLRTDSSSTGSTGKNDTTSS  
ALNSPPTASTTLHDAVPHIDNMLNNTGKQQTQLMPSAVLNTSDYNNSQSQSGSQHHQRKRSSVD  
VAPQQYLASDSTFMSPRRAPQPPSGESPIDTSYKFGAGSEYDRPPSHYGMYTRTNASSHALGSSSPGI  
NSRPASSIYDSFSNHNRRNGSSTSKQHHKRNSSVTNNNNNNNGNSNHKHHHRRHSSVFSYLSNGNDDSAK  
PTPKLLSSKFQSNLYKGGDDGHGDFTSNNNNNNNSKLVSPAQIKRETTSGQSSLHESGSKSKGKSQI  
FDLSNPVDIDDAKFSPKKSNSVSVRTKSM DAIGNGDDRRVASDSTGLSQSKPNNSSRLKIRATSTQ  
SFRSLTGSKSKTSFAQEGIREITPDEAIKTASHSGYMSKRSNNNLAWRTRYFTLHGTRL SYFQSLKDK  
KEKGLIDITAHKVIPIDSASDDTDKADRYAAMYASTTTFAGNYCFKLVPAPGFKGLTFTQPKTHYFAV  
ETEEEMRAWVKALMQATIDIDSVPVVSSCPTVSLNKAQELLAKAREETKLRDEQLKANGYIRSLD  
INDTSFSASLDYPDMSGDIGFGSTSPVAATSAPKLTLDTNFNKRKSSGTMTGTTGTIGTPGTSGGTVPTTP  
QIPRSSSQSGGFASPYLLASGLLSPKSGGAGPGGIVSSSSPINENGPLRNSTSNSEYFGDITYKSLKP  
PSRQNSQYASITSGGSGIFGYGSNNSGLGGPATAIGGGGGVLSSTPYSTGSGSTASSMNYNNNNNN  
NNNNNSVNSPINEFRSSRDLKSSSSPTTTTGTSSSTSGKKPQSRRTSDKMLGFSSDASGSHTFVIKPKK

YBR019C\_homolog 2028bp public: 1..2028 (SEQ ID NO 575)

ATGTCAAACGAATATATTCTTGTTACTGGTGGTGCAGGTTACATTGGTTCTCATACAGTTATTGAATTA  
ATCAGTAATGGATATAAAGTAGTCATTGTTGATAATTTAAGTAATCTTCCTATGATGCAGTTGCTAGA  
ATTGAATTCATTGTCAAACAACATGTTCCATTCTATGATGTTGATATCAGAAATTATGAGCAATTGAAT  
AAAGTTTTCCAAGATTATAAGATCTCTGGAGTCATTCATTTTGCTGCTTTGAAAGCTGTTGGTGAATCA  
ACAAAAATCCCTTAGCATATTATGATAATAATGTATCAGGTACTGTCAACTTATTGGAAGTATGTAAA  
GCCAATGATGTGAAGACAATTGTTTTTCAGTTCTTCAGCTACTGTCTATGGTGATGTGTTAGTATGGT  
GATAATTCAATGATTCTCTATCCCTGAACATTGTCCAATGGATCCAACAAATCCATATGGAAGAACAAAA  
TTCATTATTGAGTCGATTTTAAAAGATATTTATAATAGTGATGATGCTTGGAAAGTAGCAATTTTGAGA  
TATTTCAACCCAATTGGTGCTCATCCATCTGGTTTATTAGGTGAAGATCCATTGGGGATCCCAAATAAC  
TTATTACCTTATTTGGCTCAAGTTGCTATAGGTAGACGTGAAAAATTGTCTATTTTCGGAAATGATTAT  
AATAGTCTGATGGTACCCCTATTAGAGACTATATTCATGTGGTTGATTGGGCAAAGGGTCACATTGCT  
GCATTGGCGTATTTGAAAAACTTGCAATCTAAAGGCTTGATCGTGAATGGAATTTAGGTACTGGTAAA  
GGATCCACTGTTTTTGAAGTTTATCATGCATTTAGTAAAGTTGTTGGTAGAGAATTGCCCAATGAAGTT  
GTTGGAAGACGTGCTGGGGATGTCTTGGATTTGACTGCTAAGCCAGACAGAGCAAACAAGGAATTGCAA  
TGGAAACTGAACTTACCATTGATGATGCTTGTAAGATTTATGGAATGGACTACTGAGAACCCTTTT  
GGATTCAACATTGAGAATTATTCTTGGAAAGAATTTGATGGGTTCATAACCGTTTGCACAGTTTGTGTT  
CTGGTGACTTGAAGTTAACTTAGCGAATCGTGGTGCAATGATCCAAGCTATCACGTTGAAGGATTC  
AATATGGTCAAAGCTTATAAATAGCTGAAGATTTTCAATCTGAAACTAACCCTTTTTCGGTACCCT  
GTTGGTAGATATGCCAATAGAATTTCCAATGGAGAATTTAAATTTGAATGGAAAAGTGTAACAATTAAC  
AAAAATGAAGGAGCAAACAACCTGCATGGTGGTGCAATGGATTTCGATAAACAAGATTTCTTTGGTCCA  
GTTGTGAAAAGTCGTGATGGTAAGTTTTTCTGTTGATTCTTGTGTTGTTGATAAAGATGGTAATGATGGG



172/251

TTCCCAGGTGAGCTTGAAGCTATCGTACATTACACAATTGATGACTCCTCAGTGGAAATTGAATATGAA  
TGTCAATTATTATCTGGTGAAGCAACAATTGTCAATATGACTAACCATAGTTATTTCAATGTTTCCAAC  
TCAGACACTATTGAAGGAACCGAGGTAAATTTGATTACTGATAAAATGTTAGAAGTGGATTACACAATTA  
TTACCAACTGGTAAATTTATTGAAAATGAAAAAGCTGCTAGCCCAATTGTGTTAAATGAGAATGACGTA  
TTTGACAATTGTTTTATTGTTGATGAAGAATGTGGTATAGATACTCGTGATAAACCTTTGAAACAAGTC  
TTTGAAGCACTAGTTTTGTGACAAACAACAATTGAAGATATCCACCACTGAACCAGCTTTCCAATTT  
TACACTGGTGACGGTGTAAATACTAAAGGTTTTGGGAAAAGATGTGGTTTTCTGCGTGGAACCAAGTAGA  
TTTATTAATGCAATCAATCACAAGAATGGTCTAATCAAGTCATCTTGAAAAAGGTGATGTTTATGGA  
AGTAAATTAATATGAATTTCAATAG

YBR019C\_homolog 675aa (SEQ ID NO 576)

MSNEYILVTGGAGYIGSHTVIELISNGYKVVIVDNLSSSYDAVARIEFIVKQHVFPYDVIDIRNYEQLN  
KVFQDYKISGVIHFAALKAVGESTKIPLAYYDNNVSGTVNLLLEVCKANDVKTIVFSSSATVYGDVTRFG  
DNSMIPPEHCPMDPTNPYGRTKFIIIESILKDIYNSDDAWKVAILRYFNPIGAHPSGLLGEDPLGIPNN  
LLPYLAQVAIGRREKLSIFGNDYNSRDGTPIRDYIHVVDLAKGHIAALAYLKNLQSKGLYREWNLTGK  
GSTVFEVYHAFSKVVGRELPHVVGRRAGDVLDTAKPDRANKELQWKTELTIDACKDLWKWTENPF  
GFNIENYSWKEFDGFNNRLHSFVAGDLKVNLANRGALIQAITLKDSNMVKAYNNAEDFKSETNPFPGTT  
VGRYANRISNGEFKLNKQVYKLTKNNEGANNLHGGANGFDKQDFGFPVVKSRDGKFFVDFLLVDKDGNDG  
FPGELEAIVHYTIDSSVEIEYECQLLSGEATIVNMTNHSYFNVSNSDTIEGTEVKLITDKMLEVDSQL  
LPTGKFIENEKAASPIVLNENDVFDNCFIVDEECGIDTRDKPLKQVFEATSFVTNNKLKISTTEPAFQF  
YTGdGVNTKGFGRKCGFCVEPSRFINAINHKEWSNQVILKKGdVYGSKIKEYEQ

YCR005C\_homolog 1194bp public: 1..1194 (SEQ ID NO 577)

ATGAGAGGTATCAAAGGTTTAGTTTGGGAAGGTTCTGTTTTGGACCCAATTGAAGGTATCCGTTTCAGA  
GGAAGAACCATCCCAGACATTCAAAAAGAATTGCCAAAAGCACCAGGTGGTGAAGAACCATTACCAGAA  
GCTCTTTTCTGGTTGTTGTTGACTGGTGAAGTTCCAAC TGACGCCCAAAC TAAGGCTTTATCCGAAGAA  
TTTGCTGCTAGATCAGCATTACCAAAGCACGTTGAAGAATTGATCGACAGATCTCCATCTCACTTGCAC  
CCAATGGCTCAATTCTCCATTGCCGTTACTGCTTTGGAATCTGAATCCCAATTTGCCCAAGCTTATGCT  
AAAGGTGCCAACAAATCCGAATACTGGAAATACACTTACGAAGATTCCATCGATTGTTAGCTAAATTTG  
CCAACCATTTGCTGCTAAGATTTACAGAAACGTTTTCCACGATGGTAAATTGCCAGCTGCCATTGACTCC  
AAATTGGATTACGGTGCTAACTTGGCCAGTTTGTGTAGTTTTGGTGACAACAAGGAATTTGTTGAATTA  
ATGAGATTGTACCTTACCATCCACTCTGACCACGAAGGTGGTAACGTCTCTGCACACACCACCACTTG  
GTTGGTTCCGCTTTATCTTCCCCATTCTTGTCTATTAGCTGCTGGTTTGAATGGTTTAGCTGGTCCATTA  
CACGGTAGAGCTAACCAAGAAGTTTTGGAATGGTTGTTCAAATTAAGAGAAGAATTAAACGGTGACTAC  
TCCAAGGAAGCCATTGAAAAATACTTGTGGGAAACCTTGAAC TCCGGTAGAGTTGTCCCAGGTTACGGT  
CACGCTGCTTTGAGAAAGACCGATCCAAGATACACTGCTCAAAGAGAATTTGCTCTTAAACATATGCCA  
GACTACGAATTTGTTCAAATTTGGTTTCAAACATTACGAAGTCGCTCCAGGTGTTTTGACCAAAACACGGT  
AAGACCAAGAACCCATGGCCAAATGTGGACTCCCACTCTGGTGTCTTGTACAACTACTACGGTTTGACT  
GAACAATCTTTTCACTGTCTTGTTCGGTGTTCAGAGCCTTTGGTGTCTTGCCACAATTGATCTTG  
GACCGTGGTATCGGTATGCCAATTGAAAGACCAAAATCTTTCTCCACTGAAAAATACATTGAATTGGTC  
AAAAACATCAACAAAGCTTAA

YCR005C\_homolog 397aa (SEQ ID NO 578)

MRGIKGLVWEGSVLDPIEGIRFRGRTIPDIQKELPKAPGGEEPLPEALFWLLLTGEVPTDAQTKALSEE  
FAARSALPKHVEELIDRSPSHLHPMAQFSIAVTALESSESQFAQAYAKGANKSEYWKYTYEDSIDLLAKL  
PTIAAKIYRNVFHDGKLPAAIDSKLDYGANLASLLGFGDNKEFVELMRLYLTIHSDHEGGNVSAHTHL  
VGSALSSPFLSLAAGLNLGAGPLHGRANQEVLEWFLKREELNGDYSKEAIEKYLWETLNSGRVVPYG  
HAVLRKTDPRYTAQREFALKHMPDYELFKLVSNIEVAPGVLTKHGKTKNPWPNVDSHSGVLLQYYGLT  
EQSFYTVLFGVSRAFGVLPQLILDRGIGMPIERP KSFSTEKYIELVKNINKA

YDR345C\_homolog 1653bp public: 1..1653 (SEQ ID NO 579)

ATGTCATTAGATAATTCAACAGAAAACCGTGATTTGGAAGAAAAGGAAGAAATTCCAAAGAACGAACAT  
AACGAACAAGGCGAACAACGAGAACATAGCATATACCTACTTTGGAAGATAAACCATTTGAAGGAA  
TATATTGGTATTAGTATTTTGTGTTTCCTTATTGCTTTTGGTGGTTTCGTTTTTCGGTTTCGATACGTGGT  
ACCATTTCTGGTTTTCATTAACATGACTGACTTTTTAGAAAGATTTGGTGGTACTAAAGCTGACGGTACT  
CTTTACTTTTTCCAACGTTAGAACTGGTTTATTGATTGGTTTGTTCATGTGGGTTGTGCCATTGGTGCA  
TTATTCTTGTCTAAAGTCGGTGATATGTATGGTAGAAGAGTTGGTATCATGACTGCTATGATCATTTAT  
ATTGTTGGTATTATTGTTCAAATTTGCTTCTCAACATGCTTGGTATCAAATCATGATTGGTAGAATTATC  
ACTGGTCTTGTCTGTTGGTATGTTATCAGTTTTGTGTCCATTATTTATCTCAGAGGTTTCTCCCAAACAT  
TTAAGAGGTACATTAGTTTATTGTTTCCAATTTGATGATTACCTTGGGTATTTTCTTGGGTTACTGTACC  
AGTTACGGTACTAAGAAATATTCTGACTCCAGACAATGGAGAATTCCATTGGGTTTATGCTTTGCTTGG  
GCCTTGTGTTTGGTGGTATGGTAAGAATGCCAGAATCTCCACGTTACCTTGTGCGGTAAAGATAGA  
ATTGACGATGCTAAGATTTCACTTGCCAAAAC TAACAAGGTTTCTCCAGAGGACCCTGCATTATACCGT

173/251

GAACTTCAATTAATCCAAGCTGGTGTGAAAGAGAAAGATTGGCCGGTAAGGCATCTTGGGGTGCTTTA  
ATCACTGGTAAACCAAGAATCCTTGAAAGAGTTATTGTTGGAGGTATGTTGCAATCATTGCAACAATTG  
ACTGGTGATAACTATTTCTTCTACTACAGTACCACCATTTTCAAGTCTGTCCGGTTTAAATGATTCCTTC  
GAAACATCTATTATCCTTGGTGTCACTCAACTTTGCTTCCACTTTTGTGGTATTTATGCCATTGAAAGA  
TTGGGTAGAAGACTCTGTTTATTAAGTGGTTCGGTGGCCATGTCCATTTGTTTCTTAATTTACTCATTG  
ATTGGTACTCAACATCTTTACATTGATCAACCAGGTGGTCCAACCAGAAAACCAGATGGTAACGCTATG  
ATTTTCATTACTGCACCTTTATGTTTTCTTCTTCGCTTCTACATGGGCTGGTGGTGTCTACTCCATTGTT  
TCTGAACCTTTATCCATTAAGTCAGAAGTAAGGCTATGGGTTTTGCTAATGCATGTAAGTGGTGTGG  
GGTTTCTTGATTTTCTTCTTCACTTCATTTATCACTGATGCTATCCACTTCTATTATGGTTTTGTGTTT  
ATGGGCTGTTTAGTGTTCCTTTCTTTGTTTACTTTATGATTTACGAACTAAAGGTCTTACTTTA  
GAGGAAATTGATGAATTATACTCTACCAAGGTGTTCCATGGAAATCAGCCGGTTGGGTTCCACCTTCT  
GACGAAGAAATGGTTCGTGCAAAAGGCTATACTGGTGATATCCACGCAGATGAAGAGCAAGTTTAA

YDR345C\_homolog 550aa (SEQ ID NO 580)

MSLDNSTENRDLEEKEEIPKNEHNEQGEQNENNEHIPTLEDKPLKEYIGISILCFLIAFGGFVFGFDTG  
TISGFINMTDFLERFGGTKADGTLFYSNVRTGLLIGLFNVGCAIGALFLSKVGDVGRVVGIMTAMIY  
IVGIIVQIASQHAHYQIMIGRIITGLAVGMLSVLCPLFISEVSPKHLRGTLVYCFQLMITLGIPLGYCT  
SYGTTKYSDSRQWRIPLGLCFAWALCLLGGMVRMESPRLVGVKDRIDDAKISLAKTNKVSPEDPALYR  
ELQLIQAGVERERLAGKASWGALITGKPRILERVIVGGMLQSLQQLTGDNYFFYYSTTIFKSVGLNDSF  
ETSIIILGVINFASFTVGIYAIERLGRRLCLLTGSVAMSICFLIYSLIGTQHLIYDQPGGPTRKPDGNAM  
IFITALYVFFFASTWAGGVYSIVSELYPLKVRSKAMGFANACNLWGLISFSTFITDAIHFFYGFVF  
MGCLVFSIFFVYFMIYETKGLTLEEIDELYSTKVVPWKSAGWVPPSDEEMVRAGYTGDIHADEEQV

YDR545W\_homolog 1194bp public: 1..1194 (SEQ ID NO 581)

ATGGCATCCGAAGGTATTACTGAAATCGACTCTGGTTTAATTGAAACCAATTACGATAACGTCGTCTAC  
AAGTTCGACGATTTAACTTGAAACCAAAACATTGTTAGAGGTATTTTGGTTACGGGTATGAAACTCCA  
TCCGCTATTCAACAAAGAGCCATCTTGCCAATCACTGAAGGTAGAGATGTTTTGGCTCAAGCTCAATCC  
GGTACTGGTAAAACCGCTACCTTTACCATTTCTGCATTACAAAGAATCAATGAAAATGAAAAAGCCACT  
CAAGCTTTAATCTTGGCCCCAACAGAGAATTGGCTTTGCAAATCAAGAATGTTATCACTGCTATTGGT  
TTGTACTTGAAGGTTACTGTCCATGCTTCTATTGGTGGTACCTCAATGAGTGACGATATTGAAGCTTTC  
AGATCTGGTGTTCAAATTGTCTGGTACTCCAGGTAGAGTCTTAGACATGATTGAAAGAAGATATTTTC  
AAAACCGATAAAGTCAAGATGTTTCTTTGGATGAAGCTGATGAAATGTTATCAAGTGGATTTAAAGAA  
CAAATTTACAACATTTTCAGATTATTACCAGAAACCACCAAATTGTCTTATTATCTGCCACCATGCCA  
CAAGACGTTTTTGAAGTCACCACCAAATTCATGAACAACCCAGTCAGAATCTTAGTCAAAAAAGATGAA  
TTGACTTTGAAGGTATCAAACAATTCTATATTAATGTTGAATTAGAAGATTACAAATTCGATTTGTTG  
TGTGATTTTGTACGATTCTATTTCTGTCAACCAAGCCGTCATTTTCTGTAAACACTAGATCCAAAGTTGAA  
TTTTTAACCAACAAATTGAGAGAACAACACTTTACTGTCTCTGCCATCCACGCTGATTTGCCACAAGCC  
GAAAGAGACACCATTATGAAAGAATTGAGATCTGGTCTTCAAGAATCTTGATCTCTACTGATTTGTTA  
GCTAGAGGTATTGATGTCCAACAAGTTTCTTTAGTTATCAACTACGATTTGCCAGCCAACAAGGAAAC  
TACATTTCATAGAATTGGTAGAGGTGGTCTGTTTCGGTAGAAAGGGGGTTGCCATCAACTTTGTCACTGAC  
AGAGATGTTGGTATGATGAGAGAAATTGAAAAATTCTACTCTACTCAAATCGAAGAAATGCCAGCTGAT  
ATTGGTGCCTTTATTTGCTTAG

YDR545W\_homolog 397aa (SEQ ID NO 582)

MASEGITEIDSGLIETNYDNVVKFDDLNLKPNIVRGIFGYGYETPSAIQQRAILPITEGRDVLAAQAS  
GTGKTATFTISALQRINENKATQALILAPTRELALQIKNVITAIGLYLKVTVHASIGGTSMSDDIEAF  
RSGVQIVVGTGPRVLDMIERRYFKTDKVKMFIIDEADEMLSSGFKEQIYNIFRLLPETTQIVLLSATMP  
QDVLEVTTKFMNPNVRILVKKDELTLLEGIKQFYINVEDELYKFDCLCDLYDSISVTQAVFCNTRSKVE  
FLTNNKLREQHFTVSAIHADLPQAERDTIMKEFRSGSSRILISTDLLARGIDVQVSLVINYLDPANKEN  
YIHRIGRGGFRGRKGVAINFVTDVDRVGMREIEKFYSTQIEEMPADIGALFA

YIL057C\_homolog 606bp public: 1..606 (SEQ ID NO 583)

ATGGCGGGAAAGAAAAGTCTAAGTCTGAAGCTTTACCATTAGATTAGACAATATTAACCAATGGAT  
CATTTACAACCAGTCCCTAAAACAAGATCATCATCAATTACCTCAATTGAAAGTGCTGATGAACCAGGT  
ACTATGAAACAAGTGTTGTTACCACCTACAATCAAAGAATTTGACGAATTGGAACAATTTGAATCATTT  
GTTTCGTGATGAACTTGGGATAATGATTTTGATTATTTCCATGGTAGATTACATTATTATCCACCATTT  
GTTATGAAGAGTTGTCAAATAATCTTGAAAAATCAAGCCTACCATGAATAAAAACTCCAAGAAATTT  
AGACGTGATTTACAACATCATATTTCAAAAACATTTAATTAAAGATTTAGAAAAATGTTGTGGTTACGAG  
TTGAATTTTGGTAAAGGAGAAGTTGTTGAGACTGATAATAAGTTACTTGGAAATTTAAAGACGAAACT  
GATCATGGTTTTAGTAAAGAAGAAGAAGATATGTATGATAGACATTGGAGATTGGAATTTGGATGTTTCT  
TGTACAAATGAATCAGCTATGGTTGATGTTGAATATAAATCCATTCCAATGTAA

174/251

YIL057C\_homolog 201aa (SEQ ID NO 584)

MAGKKKSKSEALPLDLNPKMDHLQVPKTRSSSITSIESADEPGTMKQVLLPPTIKEFDELEQFESF  
VRDETWDNDFDYFHGRLHYYPFVMKSCQNNLEKIKPTMKNKSKFRRDLQHHIQKHLIKDLEKCCGYE  
LNFGKGEVVETDNKVTWKFKDETDHGFSSKEEDMYDRHWRLDVSCTNESAMVDVEYKSIPI

YKR097W\_homolog 1662bp public: 1..1662 (SEQ ID NO 585)

ATGGCTCCTCTACTGCTGTTGAATCTTCAATCAATTTTCGGAGGTCACCCAATATCAAATCCACTCAA  
GACCCATTGGTCCAAAAGTTGTCTCTTAATACCGACACTGTGATCAGACACAATGCTCCACCTCCAACC  
TTATACGAAGATGGTTTATTAGAAAAAGGTACTACTATCTCATCTACTGGTGCTTTAATGGCTTACTCT  
GGTAACAAAACCGGTAGATCTCTTAAAGACAAGAGAATTGTCGACGAATCCACCTCATCCCATAACATT  
TGGTGGGGTCCAGTGAATAAACAAGTTGACGAATTAACCTTGAAGATTCTAGATCAAGAGCTTTGGAT  
TACTTGAGAACTAGAGAAAAGTTGTTTGTGTTGACGCTTATGCTGGTTGGGATCCAAGATACAGAATC  
AAGGTCAGAATTATCTGTGCTAGAGCTTACCATGCTTTGTTTCATGACCAATATGTTGATCAGACCAACT  
GAAGAAGAATTAAAAAACTTTGGTGAACCAGATTTACCATCTACAATGCTGGTCAATTCCCAGCCAAC  
ATCCACACTAAAGGTATGACTTCTGCCACTTCTGTTGAAATCAACTTTAAAGATATGGAAATGGTTATC  
TTGGGTACTGAATATGCTGGTGAAATGAAGAAAGGTATCTTTACTGTTATGTTCTACTTGATGCCAATC  
AAACACAAGGTTTTGACTTTGCACTCTCATGTAACCAAGGGGTGAAAAAGGTGATGTCACCTTTGTTC  
TTTGGTCTTTCTGGTACTGGTAAGACCACTTTGTCTGCTGATCCACAAAGAAAGTTGATTGGTGATGAC  
GAACATTGTTGGTCCGACAATGGTGTGTTCAACATTGAAGGTGGTTGTTACGCCAAATGTTTGGACTTG  
TCTGCTGAAAAAGAACCAGAAATTTCAACTCCATCAAGTTTGGTGTATTTTGGAAATGTTGTCTAC  
GACCAATACCAAGGTTGTTGACTACGAAGATTCAATCAATCACTGAAAACACTAGATGTGCATACCCA  
ATTGATTTTCAATCCATCTGCCAAGATTCCATGTTTGGCCGACACCCATCCAACCAATATTTATCTTGT  
ACATGTGATGCTTCCGGTGTGTTGCCACCAGTCTCCAAATTGACTAATGCTCAAGTTATGTATCATTTT  
ATTTCTGGTTACACCTCCAAGATGGCAGGTACTGAAGAAGGTGTTACTGAACCACAAGCTACATTCTCC  
GCATGTTTTCGGTCAACCATTTCTTGGTGTGTCACCCAATGAAATATGCTCAACAATTTGCTGACAAGATT  
TCCGAACACAATGCCAACGCTTGGTTGTTGAACACTGGTTGGGTGGTTCTTCTGTTGCTCAAGGTGGT  
AAGAGATGTCCATTGAAATACACCAGAGCTATCTTGGATGCTATCCACTCTGGTGAATTGTCTAAAGTC  
GAATACGAAAAAGTTCCAGTTTCAACCTTAATGTTCCAACCTCTTGTCTGGTGTGTTCAAGTGAATTT  
TTGAACCCAATAAAGCTTTGGACCAAGGTACTGATTCATTCAACAAGGAAATCAATCTCTTGCTACC  
AAGTTTGCTGAAAACCTCAAGACATACGCTGATCAAGCTACTGCTGAAGTTAAAGCTGCTGGTCCAGAA  
GCATAA

YKR097W\_homolog 553aa (SEQ ID NO 586)

MAPPTAVESSINFGGHPTIKSTQDPLVQKLSLNTD TVIRHNAPPPTLYEDGLLEKGTTSSTGALMAYS  
GNKTRGRSPKDKRIVDESTSSHNIWWGPNKQVDEL TWKISRSRALDYLRTREKLFVVDAYAGWDPRYRI  
KVRIICARAYHALFMTNMLIRPTEELKNFGEPDFTIYNAGQFPANIHTKGMTSATSVINFKDMEMVI  
LGTEYAGEMKKGIFTVMFYLMPIKHKVLT LHSSCNQGVKGDVTLFFGLSGTGKTTLSADPQRKLIGDD  
EHCWSDNGVFNIEGGCYAKCLDLSAEKEPEIFNSIKFGAILENVVYDPITKVVDYEDSSITENTRCAYP  
IDFIPSAKIPCLADTHPTNII LLTCDASGVLPPVSKLTNAQVMYHFISGYTSKMAGTEEGVTEPQATFS  
ACFGQPFVLVHPMKYAQQLSDKISEHNANAWLLNTGWVGSSVAQGGKRCPLKYTRAILDAIHSGLSKV  
EYKVPVFNLNVPTSCPGVPSEILNPTKAWTQGTDSFNKEIKSLATKFAENFKTYADQATAEVKAAGPE  
A

YOL126C\_homolog 1014bp public: 1..1014 (SEQ ID NO 587)

ATGGTCAAAGTCGCTATTTTAGGAGCTGCTGGTGGTATTGGTCAACCATTATCTTTATTGACCAAATTA  
AACCCAAATGTTGATGAATTGGCATTATTTGATGTCTGTCATGTTCCAGGAGTTGGTGCTGATTTATCT  
CATATCAATTTCTGATTCTAAACTCAATCATATTTACCAAAAGATAAAGAAGATAAACTGCATTAGCT  
GCTGCATTAAAAAGGTTCTGATTTTAGTCATTATCCAGCTGGTGTTCAGAAAACCAGGTATGACCAGA  
GATGATTTATTCAATATTAATGCATCAATCGTTCAAGGTTTAGCTGAAGGTATTGCTGCCAATTTCTCCA  
AAAGCTTTTGTCTTGGTGATTCTAATCCAGTCAATTTCTACTGTACCAATTGTTGCCGAACTTTACAA  
GCTAAAGGTGTTTATGATCCAGCTAGATTATTTGGTGTACTACTTTGGATATTGTTTAGAGCCAATACT  
TTTATTTCTCAATTATTCCTAGATCAAACATAACCATCTGATTTCAATATTAATGTTGTTGGTGGCCAT  
TCTGGTGAAACCATTTGTTCCATTATATTCATTAGGTAACCTAAACAATATTATGATATATTATCTGAA  
GAACAAAAGAAGGAATTAATCAAAAAGGTTCAATTTGGTGGCGATGAAGTTGTTTCAAGCCAAGAATGGT  
GCTGGTTCGCCCACTTTATCCATGGCTTATGCCGTTATAGATTAGCCGAATCAATTTTAGCTGCTGTT  
AATGGTAAAACGATATTGTTGAATGTACTTTCTTGAACCTGGATTCTTCAATTAAAGGTGCTTCTGAA  
GCTAGAAAAATTGGTTAAAGATTTAGATTTCTTTTCAATTACCAGTTCAATTAGGTAAAAACGGTATTACT  
GAAGTTAAATATGATATCTTAAATCAATTTCTGATGATGAAAAGAAATGTTTAGAAGTTGCCATTGAA  
CAATTACAAAAGAATATTGAAAAAGGTGTTTCATTGCTAAGAAATAA

175/251

YOL126C\_homolog 337aa (SEQ ID NO 588)

MVKVAILGAAGGIGQPLSLLTKLNPVDELALFDVVNVPVGADLSHINSDSKTQSYLPKDKEDKTALA  
AALKGSDLVIIIPAGVPRKPGMTRDDLNFNINASIVQGLAEGIAANSPKAFVLVISNPVNSTVPIVAETLQ  
AKGVYDPAFLFGVTTLDIVRANTFISQLFLDQTKPSDFNINNVGGHSGETIVPLYSLGNSKQYYDILSE  
EQKKELIKRVQFGGDEVVQAKNGAGSATLSMAYAGYRLAESILAAVNGKTDIVECTFLNLDSSIKGASE  
ARKLVKDLDFSLPVQLGKNGITEVKYDILNQISDDEKKLLEVAIEQLQKNIEKGVSFARK

YBL072C\_homolog 621bp public: 1..621 (SEQ ID NO 589)

ATGGGTATTTCTAGAGATTCACGTCACAAAAGATCCGCCACTGGTGCCAAAAGAGCCCAATTCAGAAAG  
AAGAGAAAGTTTGAATTAGGTAGACAACCAGCCACACCAAGATTGGTCCAAAAGAAATTCACCTCTGTC  
AGAACCAGAGGTGGTAACCAAAAATTCAGAGCTTTGAGAGTTGAAACCGGTAACTTCTCTTGGGGTTCC  
GAAGGTGTTTCCAGAAAACCAGAAATTTGCTGGTGTCTGTTTACCATCCATCTAATAACGAATTTGGTTAGA  
ACCAACACCTTACCAAAATCTGCTGTTGTTCAAATTGATGCTACTCCATTCAGACAATGGTACGAAAAAC  
CACTACGGTGTCTACTTTAGGTAAAAAGAAGGGTGGTGTCTCATGCTGCTCACGCTGCTGAAGTTGCCGAT  
GCCAAGAGATCAAGAAAAGTCGAAAGAAAATTTGGCTGCTAGATCTGGTGTCTGCTGCCATTTGAATCCGCT  
GTTGACTCTCAATTCGGTTCTGGTAGATTATACGCTGTCAATTTCTTCAAGACCAGGTCAATCTGGTAGA  
TGTGATGGTTACATCTTGAAGGTGAAGAATTAGCCTTCTACTTGAGAAGATTAACTGCTAAGAAATAA

YBL072C\_homolog 206aa (SEQ ID NO 590)

MGISRDSRHKRSATGAKRAQFRKKRKFELGRQPANTKIGPKRIHSVRTRGGNQKFRALRVETGNFSWGS  
EGVSRKTRIAGVVYHPSNNELVRTNLTLSAVVQIDATPFRQWYENHYGATLGKKKGGAHAHAHAEEVAD  
AKRSRKVERKLAARSGAAIESAVDSQFGSGRLYAVISSRPGQSGRCDGYILEGEELAFYLRRLTAKK

YBR009C\_homolog 318bp public: 1..318 (SEQ ID NO 591)

ATGTCAGGTACCGGTAGAGGAAAAGGTGGTAAAGGTTTAGGAAAAGGTGGTGTCTAAACGTCACAGAAAA  
ATTTTAAGAGATAACATTCAGGTATTACAAAACCAGCTATCAGAAGATTGGCCAGAAGAGGTGGTGT  
AAACGTATTTCTGCTTTGATTTATGAAGAAGTCAGAGTTGTCTTGAAACAATTTTGGAAAACGTTATC  
AGAGATGCTGTACTTACACTGAACATGCTAAAAGAAAAACCGTCACTTCATTGGATGTTGTTTACGCT  
TTGAAGAGACAAGGTAGAACCCTTGATGGTTTCGGTGGTTAA

YBR009C\_homolog 105aa (SEQ ID NO 592)

MSGTGRGKGGKGLGKGGAKRHRKILRDNIQGITKPAIRRLARRGGVKRISALIYEEVRVVLKQFLENNI  
RDAVTYTEHAKRKTVTSLDVVYALKRQGRITLYGFGG

YBR189W\_homolog 489bp public: 1..489 (SEQ ID NO 593)

ATGGCCGGTGAAATACCGGTTTAAAAACAAGGGGGAATCTACAGAATTGGGGTTCCAAATGTCCTAAA  
ATCAGAAGAGCTGCTCGTGAAATTTGTAACCAAGAGGTGAAAAAGGCCCCAAAAAGATTATTTCGGAAGGTA  
ATGGCTTTGATCAGAAGATTAGTCAGATTCGGTTTCTTGTCTGAGGACAAAATGAAATTTGGATTATGTC  
TTGGCTTGGAAACCCAGAAGTTTCTTGAACAGAAGATTCCAACCCCAAGTTTTCAAATTAGGTTTAGCT  
AGATCTATCCCCACGCCAGAGTTTGTATCACCACCAAGCCACATTTGCTGTTGGTAAACAAATTTGTTACC  
ATCCCATCATTTACTGTCTAGATTGGACTCTCAAAAACACATTGACTTTGCCCAACAATCTCCATACGGT  
GGTGGTAGACCCGGTAGAGTTAAGAGAAAGAACCAAGGTAAAGGTGGTGAAGAAGGTGCCGAAGAAGAA  
GAATAA

YBR189W\_homolog 162aa (SEQ ID NO 594)

MAGEYRFKKQGGNLQNWGSKCPKIRRAAREFVTRGEKGPKKIIRKVMALIRRLVRFGLSEDKMKLDYV  
LAWNPEVFLNRRFQPQVFKLGLARSIPHARVLITQSHIAVGKQIVTIPSFTVRLDSQKHIDFAHNSPYG  
GGRAGRVRKRNQKGGEGEAE

YBR191W\_homolog 330bp public: 1..330 (SEQ ID NO 595)

ATGCCACACAAATACTACCACGGTAAGACTGGTATTGTTTACAACGTTACCAAATCCTCCGTTGGTGT  
ATCATTAACAAAGTTGTTGGAAACAGATACATTGAAAAGAGAGTTAACTTGAGAGTTGAACATGTTAAA  
CACTCTGCTTGTCTCAAGAAATCTTGAACAGAGTTAAATCTAACGCTGCTAAAAAGAGAGAAGCTAAA  
GCTAACGGTGAACCGTTTACTTGAAGAGACAAGCTGCCAAGCCAAGAGGTTCAAGAATTATCTCCACT  
GAAGGTAACATTCCTCAAACCTTTGGCTCCAGTCGCTTACGAAACTTTTCATTTAA

YBR191W\_homolog 109aa (SEQ ID NO 596)

MPHKYYHGKTGIVYNVTKSSVGVIIINKVVGNNRYIEKRVNLRVHVKHSACRQEFNLNRVKSNAKKREAK  
ANGETVYLKRQAAPRGSRIISTEGNIPQTLAPVAYETFI

YCL035C\_homolog 384bp public: 1..384 (SEQ ID NO 597)

ATGATAGACAAAATGCTGCTGATTCTTGCCTGGGGATTCAATTTGTGGTATCAACCACCTCCACCTACT  
GCACAAACTGAGAAAAGAAATCGAACACACTATTAACCTCTCAAGATTGTTATTTATCTAAAACCTTAT

176/251

TGTCCATTTTGTGACCAAACCAACATCTATTAAATGAACAATATCCACAAGAATCGTACGAAGTCATA  
AACTTGAATATTCTCGATGACGGATTGACTATTGAGAATCAATTGTATGCTAATACTGGTCAATATATG  
GTGCCATAATCTTCATAAACGGACAACACGTTGGAGGAAATTCAGAAGTTCAGCAATTGCACACCAAT  
GGGAAATTGCAAGAATTATTGAATCCTCAGAAATATTGA

YCL035C\_homolog 127aa (SEQ ID NO 598)

MIDKMSSILAWGFNLWYQPPPTAQTEKEIEHTINSHKIVYISKTYCPFCDDQTKHLLNEQYPQESYEVI  
NLNILDGLTIQNQLYANTGQYMPVPIIFINGQHVGGNSEVQQLHTNGKLQELLNPQKY

YDL004W\_homolog 486bp public: 1..486 (SEQ ID NO 599)

ATGTTTCAGACAAGTTTTCCGTCAAGTTACCAAACAATCATTCACTGGGGTTAAGAGAACTTATGCCACC  
GAGGCCGCCGTGTCTACAGATGCTTTGAAATTATCCTTGGCATTGCCACACCAAACCTTATACAACGAC  
TCCGAAGTCCAACAAGTAAACTTGCCATCTGTCAACGGTGATTGGGTATTTGGCCAACCACATTCCA  
ATTGTGCAACAATTGAGACCAGGATTGTTAGAAATCATTTCAAAAACGGAGACTCTGACCAATACTTT  
GTCAGCGGCGGTATCGCCATGGTCCAACCAGGAAACAAGTTGACTATTTCCGCCATCGAAGCATTTCAAG  
ACCGACCAAATTGATCTCTGCGGTCAAAACTTGATTGCCGATGCCCAAAGAGAGCTGAATCTAGT  
GATGAAAAGGTGCTGCTGAAGCCAACATCGAATTGGAAGTGTTAGATGCTTTACAACATTTTACTAAG  
TAA

YDL004W\_homolog 161aa (SEQ ID NO 600)

MFRQVFRQVTKQSFTGVKRTYATEAAVSTDALKLSLALPHQTLYNDSEVQQVNLPSVNGDLGILANHIP  
IVEQLRPLLEIIISKNGSDQYFVSGGIAMVQPGNKLITISAIEAFKTDQIDLSAVKNLIADAQKRAESS  
DEKVAEEANIELEVLDAHQHFTK

YDR099W\_homolog 795bp public: 1..795 (SEQ ID NO 601)

ATGCCAGCCTCCCGTGAAGATTCCGTTTACCTTGCTAAATTAGCCGAACAAGCAGAACGTTATGAAGAA  
ATGGTTGAAAACATGAAAGCCGTTGCTTCCTCTGGCCAAGAATTGTCTGTTGAAGAACGTAATTTATTA  
TCTGTTGCTTACAAGAATGTCATTGGTGCTCGTCGCTTCTTGGAGAATTGTTTCATCAATGAACAA  
AAAGAAGAAGCCAAAGGAAATGAGAGCCAAGTTGCTTTGATCAGAGATTACCGTGCCAAGATTGAAGCT  
GAATTGTCTAAAATTTGTGAAGATATTCTCTGTGTTGAGCGACCATTTAATTACATCTGCCCAAAC  
GGTGAATCAAAAGTATTTTACTACAAGATGAAAGGTGATTACCACAGATACTTGGCTGAATTTGCTATC  
GCTGAAAACGTAAGGAAGCTGCTGATTTATCATTAGAGGCTTATAAAGCTGCTTCTGACGTTGCTGTG  
ACCGAGTTGCCACCAACCCATCCAATCAGATTAGGTTTAGCATTGAACTTCTCTGTTTCTACTATGAA  
ATTTTGAATCCCCAGATAGAGCTTGTCAATTTAGCTAAACAAGCTTTTCGATGATGCTGTTGCTGATTTA  
GAAACCTTATCTGAAGATTATACAAGGATTCAACTTTGATTATGCAATTATTGAGAGATAACTTGACT  
TTATGGACCGATTTATCTGAAGCCCCAGCTGCCACTGAAGAACAACAACATCCAGTCAAGCTCCAGCT  
GCTCAACCAACAGAAGGTAAGGCTGATCAAGAATAG

YDR099W\_homolog 264aa (SEQ ID NO 602)

MPASREDSVYLAKLAEQAERYEEMVENMKAVASSGQELSVEERNLLSVAYKNVIGARRASWRIVSSIEQ  
KEEAKGNESQVALIRDYRAKIEAELSKICEDILSVLSDHLITSAQTGESKVFYKMKGDYHRYLAEFBI  
AEKRKEAADLSLEAYKAASDVAVTELPPTHPIRLGLALNFSVFYFEILNSPDRACHLAKQAFDDAVADL  
ETLSEDSYKDSTLIMQLLRDNLTLWTDLSEAPAATEEQQSSQAPAAQPTGKADQE

YDR399W\_homolog 642bp public: 1..642 (SEQ ID NO 603)

ATGTCTGAATCTGAGAAAATGTACATTTTCGTACAATAATATACACCAGTTATGTCAAGAAATAGCCCC  
AAGATCAAAGAATTTAAGCCTGACTTGATCATTTGCTATTGGTGGCGGTGGTTTTATTCAGCTAGAATG  
TTGCGTTTCCTTCTTGAAAGAACCAGGTCAACCAAACGTTAGAATTATGGCTATCATATTTGCTTTATAC  
GAAGAGATTGAGAGTGAAAACGGTATTGAAAAGCCAGGTACCCAAGTTGTGCGTACTCAATGGATTGAT  
TATCATCAATCTAAAATTGACTTGGTTGGTAAAAATGTGTTAATTATTGATGAGGTTGATGATACCAGA  
ACCACTTTGCATTACGCAGTCAGTGAATTGAAAAAGATGTGGAAGAGCAATCAAAAGCCAAAGGTGCA  
GATCCTAAAGATACCAAGTTTGGTATTTTGTGTTGCACGACAAGCAAAAGCAAAAGAGAAAGCAGAAATG  
CCAGATGATATTATGAAGACTGGTAATTATTTGCTGCTCGTTCTGTCCCAGATAGCTGGATTGCATAC  
CCATGGGAGTCTACTGACATTTTATCATCAAATGAAAGCTGAAGAACAAGGAAACGATGTGTTTCCTT  
CCTTCATCCACTTTAGAGTAA

YDR399W\_homolog 213aa (SEQ ID NO 604)

MSESEKMYISYNNIHLQCEIAPKIKEFKPDLIIAIGGGGFIPARMLRSFLKEPGQPNVRIMAILLSLY  
EEIESENGIEKPGTQVVRTQWIDYHQS KIDLVGKNVLIIDEVDDTRTTLHYAVSELKQDVEEQSKAKGA  
DPKDTKFGIFVLHDKQKQKKAELPDDIMKTGNFYFAARSVPDSWIAYPWESTDIVYHQMKAEEQNDVFL  
PSSTLE

177/251

YDR418W\_homolog 498bp public: 1..498 (SEQ ID NO 605)  
ATGCCCTCCAAATTTGATCCAAATGAAGTTAAATTCCTTTACTTAAGAGCTGTTGGTGGTGAAGTTGGT  
GCTTCATCTGCTTTAGCTCCAAAGATTGGTCCATTAGGTTTATCCCCAAAGAAAGTTGGTGAAGATATT  
GCCAAAGCCACCAAGAATACAAAGGTATTAAAGTTACTGTTCAATTGAGAATTCAAAACAGACAAGCT  
ACTGCTTCTGTTGTTCCATCCGCTTCATCTTTAGTCATCACCAGCTTTGAAAGAACCAGTCAGAGACAGA  
AAGAAGGAAAAAGACGTCAAACACTCTGGTAACAATTCATTAGATGAAATCTTTGAAAATTGCCAGAAAA  
ATGCAACACAAATCATTCGGTAAGAATTTGGCATCTGCTTCCAAGGAAATCTTGGGTACTGCTCAATCT  
GTTGGTTGTAGAGTTGATGGTAAGAACCCTCATGACATCATTGACGCCATCAACGCTGGTGAATTTGAT  
GTTCCAGAAAAC TAG

YDR418W\_homolog 165aa (SEQ ID NO 606)  
MPPKFDPNVVKFLYLRAVGGVEVGASSALAPKIGPLGLSPKKVGEDIAKATKEYKGKIKVTVQLRIQNRQA  
TASVVPSSASLVITALKEPVRDRKKEKNVKHSGNIPLDEIFEIARKMQHKSFGKNLASVSKEILGTAQS  
VGCRVDGKNPHDIIDAINAGEIDVPEN

YDR513W\_homolog 360bp public: 1..360 (SEQ ID NO 607)  
ATGTTTCGTACATTATTAACCAAAGACTATTCAATACATCAACAATGGTTTCATCTCAAGTTAAGAAC  
AAGGTCGAACAATTGATCAAAACCAAACCAGTTTTCATTGGCTCCAAATCCTATTGTCCATACTGTAAG  
GCTACCAAAGACACAATTGAAGCTATAACAAAGGATGCTTACATTCTTGAATTAGACGAAGTTGACGAC  
GGTGTGAAATCCAAGAAGCATTTATTGGAATCCTGGTCAAAGAACCCTTCCAAATGTCTTTATTGGT  
GGTCAACATATTGGTGGCAATTCGGATGTGCAAGCTTTGAAGTCTAGTGACAAATTAGATGACAAAATC  
AAAGCTGCTTTATAA

YDR513W\_homolog 119aa (SEQ ID NO 608)  
MFRLLTKRLFNTSTMVSSQVKNKVEQLIKTKPVFIASKSYCPYCKATKSTIEAITKDAYILELDEVDD  
GAEIQEALLEITGQRTVPNVFIGGQHIGGNSDVQALKSSDKLDDKIKAAAL

YEL009C\_homolog 972bp public: 1..972 (SEQ ID NO 609)  
ATGCCTGCTACTACTCCTATTATTTATGAAGATTCTTTATTTGAATCTCAAGATTTATTTGCTTCTCCA  
GTTAAACAACAACATCAAAAGGTTGATACGTTGGCTACCAAAAACGAAATTGGTTTGGAAATTAATTTA  
GGTTTACCAGAAATGCAAAAGGCTTCAGAACTGTTTCCACTCCATTTCAAATCCATTCCAGTGATTTG  
GAGTCGGGTTTTCAGCACCAATTTGGATGGAGTCAATGATATTGATCATACTCCAATGTTTGTGAATTTG  
GATTTGATTATGGACGGAGCCAAAGTCAATTCATCAGAAGATTGGGTTGCTCTTTTTGGAGATGACAAT  
GATGATGGTGTGCTATAGCTGGTGTCTACTAGCAAAGAACCAATGTTATCATTTGAATGAAGATAACGAG  
AACAAATGATGACGACGCTGATGACGCTGATGATGATGATGCTCTTGTTCGAAGAGAAGATACATATT  
GAAGCTTTTATTATTGGAACCATCACCAATCGTACCATTCTGCTGCTACTTCTGCTTCTCATCTCA  
TTAAACAGTCCAGAAAGTACTATTGCTACCACAGTCACTGCTGGTGGTGAAGTTGTTGTTGCAAGTAAA  
AAGCAATTTCAATTGGTAACACCAAATCCTTCATCCACTTTACCAACACCATTATTGGATTCTAAAAAT  
TCTAAAAAAGAGTTAAAGTTGATCATTTGGGTTGTGTTACCTATTTCGAAAAAACATAGATCTCAACCT  
TTACAACCGATTGTTGTTGATGACATTAAGATGCTGCTGCTTTTGAAAAGAGCTAAAAATACCTGAAGCT  
GCTAGAAGATCCAGAGCTCGTAAAAATGGAAGAATGAGTCAATTGGAAGATAAAGTTGAGAATTTGATT  
AATGAAAAGCAAGCTTTTACAAGATCAAGTTGAAAGATTACAAGAAATTGTTAAGAGTTAATGGTATTCAA  
TTTTAA

YEL009C\_homolog 323aa (SEQ ID NO 610)  
MPATTPPIIYEDSLFESQDLFASPVKQQHQKVDTVATKNEIGLELNLGLPEMQKASETVSTPFIHSSVL  
ESGFSTNLDGVNDIDHTPMFDELIDLMDGAKVNSSDWDVALFGDDNDGVAIAGATSKEPMLSLNEDNE  
NNDDDDADDADDALVPREDTIEALLLEPSNRTISAATSASTSSLNSPESTIATTVTAGGEVNVASK  
KQFQLVTPNPSSLTPLPLDSKNSKKRVKVDHLGCVTYSKKHRSQPLQPIVDDIKDAAALKRAKNTA  
ARRSRARKMERMSQLEDKVENLINEKQALQDQVERLQELLRVNGIQF

YGL123W\_homolog 750bp public: 1..750 (SEQ ID NO 611)  
ATGTCAGCTGAAGCCCCAAAAGACAATTTGGTGATAGAAGAAGAGGTGGTGAAGAGGTGGTAGAAGA  
GATGGTGAAGAAAAAGGTTGGACTCCAGTCACCAAGTTAGGTAGATTAGTCAAAGCTGGTAAAAATCACC  
AGTGTGTAACAAATCTACTTGCCTCTTTGCCAGTCAAGGAATACCAAATCATTTGATTTGTTATTGCCA  
GACTTGAAAGATGATGTCATGAAGATCAGATCTGTCCAAAAACAAACCAGAGCTGGTCAAAGAACCAGA  
ATGAAGGCTGTTGTCGTCAATTGGTGACTCTAACGGTCACGTTGGTTTGGGTATCAAGACCGCTAAAGAA  
GTTGCTTCTGCCATTAAAGCTGCTATTGTTATTGGCAAATTTATCCATCATCCCAATCAGAAGAGGTTAC  
TGGGGTTCTAACTTGGGTCAACCACACTCTTTGCCATGTAAGTCACTGGTAAATGTGGTTCCGTTGCC  
GTTAGATTAAATCCCAGCCCCAAGAGGTAAAGGTATTGTTGCTTCTCCAGTTGTCAAGAGATTAAATGCAA  
TTGGCTGGTGTGTAAGATGCTCTATACTTCCTCTTCTGGTTCTACCAGAACTACCGAAAACACCTTGAAA  
GCTGCTTCTCGCTGCTATCGGTAAACACTTACAGTTTCTTGACTCCAAACTTGTGGGCTGAAACTCCATTA  
GCTGCTTCTCCATTGGAAGTTTACGCTGAAGAAGCTGCTGCTGGTAAAAAGAGATAC TAA

178/251

YGL123W\_homolog 249aa (SEQ ID NO 612)  
MSAEAPKRQFGDRRRGRRRGRRDGEKGWTPVTKLGRLLVKAGKITSVEQIYLHSLPVKEYQIIDL LLLP  
DLKDDVMKIRSVQKQTRAGQRTRMKAVVVGDSNGHVGLGIKTAKEVASAIAAIVIAKLSIIPIRRGY  
WGSNLGQPHSLPCKVTGKCGSVAVRLIPAPRGKGIVASPVVKRLMQLAGVEDVYTSSSGSTRTTENTLK  
AAFAAIGNTYSF LTPNLWAETPLAASPLEVYAEAAAAGKKRY

YGR209C\_homolog 312bp public: 1..312 (SEQ ID NO 613)  
ATGGTTTCACGTTGTCACTGAAGTTAACGAATTCCTAAACCTTTTAAAGGAAAACAACCTTAGTTATTGTT  
GACTTTTTTGGCACTTGGTGTGGTCCATGTAAAATGATTGCTCCATTATTAGAAAAATTCCTAAATGAA  
TATTCTAATATTAAATTTTTGAAAATTGATGTTGATCAATTGGGTTCTTTAGCACAAGAATATAATGTT  
AGTTCTATGCCAAGCTTTGATTTTATTCAAAAATGGTGAAGAAGTCAATCGTGTCAATTGGTGTCAACCA  
GCTGCTATTAAACAAGCTTTGGCTTCTCTTGCTTAA

YGR209C\_homolog 103aa (SEQ ID NO 614)  
MVHVVTVEVNEFQTLLENLIVVDFVATWCGPCKMIAPLLEKFQNEYSNIKFLKIDVDQLGSLAQEYNV  
SSMPTLILFKNGEEVNRVIGANPAAIKQALASLA

YHR039C-B\_homolog 342bp public: 1..342 (SEQ ID NO 615)  
ATGTCATCTGGTATCCAATCATTATTGAAAACCGAAAAAGAAGCTGCAGAAATTGTTAATGAAGCTAGA  
AAATATAGAACCACACGTTTGAAGTCTGCAAAACAAGATGCTCAAGCTGAAATTGATAACTATAAAAAAG  
CAAAAGGAAGAAGAATTAAAAAATTTGAAAAAGAACACGAAGGGTTAAATGAAAAGATCGATAAAGAA  
GCTGATGCTGAAGTTGAAAAGGAATTGACCAGTATCAAATCCACTTTTGAAAAGAAAAAGAGTGCAGTT  
GTTAAATTGTTAGTTGACGCTACTGTCAAGCCAACACCAACTTTACACATAAATGCATCTCAATAA

YHR039C-B\_homolog 113aa (SEQ ID NO 616)  
MSSGIQSLKTEKEAAEIVNEARKYRTTRLKSAKQDAQAEIDNYKKQKEEELKNFEKEHEGLNEKIDKE  
ADAEVEKELTSIKSTFEKKKSAVVKLLVDATVKPTPTLHINASQ

YJL138C\_homolog 1194bp public: 1..1194 (SEQ ID NO 617)  
ATGGCATCCGAAGGTATTACTGAAATCGACTCTGGTTTAAATTGAAACCAATTACGATAACGTCGTCTAC  
AAGTTCGACGATTTAACTTGAAACCAAAACATTGTTAGAGGTATTTTGGTTACGGGTATGAACTCCA  
TCCGCTATTCAACAAAGAGCCATCTTGCCAATCACTGAAGGTAGAGATGTTTTGGCTCAAGCTCAATCC  
GGTACTGGTAAAACCGCTACCTTTACCATTCTGTCATTACAAAGAATCAATGAAAATGAAAAAGCCACT  
CAAGCTTTAATCTTGGCCCCAACAGAGAATTGGCTTTGCAAATCAAGAATGTTATCACTGCTATTGGT  
TTGACTTTGAAGGTTACTGTCCATGCTTCTATTGGTGGTACCTCAATGAGTGACGATATTGAAGCTTTC  
AGATCTGGTGTTCAAATTGTCGTTGGTACTCCAGGTAGAGTCTTAGACATGATTGAAAGAAGATATTTTC  
AAAACCGATAAAGTCAAGATGTTTCTTTGGATGAAGCTGATGAAATGTTATCAAGTGGATTTAAAGAA  
CAAATTTACAACATTTTCAGATTATTACCAGAAACCACCCAAATTGTCTTATTATCTGCCACCATGCCA  
CAAGACGTTTTTGAAGTCACCACCAAATTCATGAACAACCCAGTCAGAATCTTAGTCAAAAAAGATGAA  
TTGACTTTGGAAGGTATCAACAATTCATATTAATGTTGAATTAGAAGATTACAAATTCGATTGTTTG  
TGTGATTTGTACGATTCTATTTCTGTCAACCAAGCCGTCATTTTCTGTAACACTAGATCCAAAGGTTGAA  
TTTTTAACCAACAAATTGAGAGAACAACACTTTACTGTCTCTGCCATCCACGCTGATTTGCCACAAGCC  
GAAAGAGACACCATTATGAAAGAATTCAGATCTGGTTCTTCAAGAATCTTGATCTCTACTGATTGTGTA  
GCTAGAGGTATTGATGTCCAACAAGTTTCTTTAGTTATCAACTACGATTTGCCAGCCAACAAGGAAAAC  
TACATTCTAGAAATTGGTAGAGGTGGTCTGTTTCCGGTAGAAAGGGGGTTGCCATCAACTTTGTCACTGAC  
AGAGATTGTTGGTATGATGAGAGAAATTGAAAATTTCTACTCTACTCAAATCGAAGAAATGCCAGCTGAT  
ATTGGTGCTTTATTGCTTAG

YJL138C\_homolog 397aa (SEQ ID NO 618)  
MASEGITEIDSGLIETNYDNVVKFDDLNLKPNIVRGIFGYGYETPSAIQQRAILPITEGRDVLAAQAS  
GTGKTATFTISALQRINENKATQALILAPTRELALQIKNVITAIGLYLKVTVHASIGGTSMSDDIEAF  
RSGVQIVVGTGPRVLDMIERRYFKTDKVKMFIIDEADEMLSSGFKEQIYNIFRLLPETTQIVLLSATMP  
QDVLEVTTKFMNPNVRILVKKDELTLLEGIKQFYINVELEDYKFDCLCDLYDSISVTQAVIFCNTRSKVE  
FLTNNKLREQHFTVSAIHADLPQAERDTIMKEFRSGSSRILISTDLLARGIDVQVSLVINYDLPANKEN  
YIHRIGRGRFRGRGVAINFVTD RDVGMREIEKFYSTQIEEMPADIGALFA

YKL060C\_homolog 1080bp public: 1..1080 (SEQ ID NO 619)  
ATGGCTCCTCCAGCAGTTTAAAGTAAATCCGGTGTATCTACGGTAAAGACGTCAAAGACTTGTGTTGAC  
TATGCTCAAGAAAAAGGTTTTGCCATTCCAGCTATCAATGTCACTTCATCTCAACTGTTGTTGCTGCT  
TTAGAAGCTGCCAGAGACAACAAGGCTCCAATCATCTTGCAAACCTCTCAAGGTGGTGTGCTGCTACTTT  
GCCGGTAAAGGTGTCGACAACAAGATCAAGCTGCTTCCATTGCTGGTTCAATTGCTGCCGCTCACTAC  
ATTAGAGCCATTGCTCCAACCTTATGGTATCCAGTTGTTTTACACACTGATCACTGTGCCAAAAAATTA



179/251

TTGCCATGGTTTGGATGGTATGTTGAAAGCCGATGAAGAATTCTTTGCTAAGACCGGTACTCCATTGTTCTCATCCACATGTTGGATTATCTGAAGAAACCGATGACGAAACATTGCTACTTGTGCCAAATATTTTGAAAGAATGGCTAAAATGGGTCAATGGTTAGAAATGGAAATTTGGTATCACTGGTGGTGAAGAAGATGGTGTCAACAACGAACACGTTGAAAAAGATGCTTTATACACTTCTCCAGAACTGTTTTCGCTGTCTACGAATCTTTTACACAAGATTTCTCCAACTTTTCTATTGCTGCTGCTTTTGGTAACGTCCACGGTGTTTACAAACAGGTAATGTGCAATTGAGACCAGAAATCTTGGGTGACCACCAAGTTTACGCTAAGAAACAAATTGGTACTGATGCTAAACACCCATTATACTTGGTTTTCCACGGTGGTTCTGGTTCTACTCAAGAAGAATTCAACACTGCTATCAAGAATGGTGTGTCAAGGTCAACTGGACACTGATTGTCAATATGCTTACTTGACTGGTATCAGAGATTACGTCACCAACAAGATTGAATACTTGAAAGCACCAGTTGGTAACCCAGAAGGTGCTGACAAACCAACAAGAAATACTTTGACCCAAGAGTCTGGGTTAGAGAAGGTGAAAAGACCATTGTCCAAGAGAATTGCTGAAGCTTTGGATATTTCCACACCAAGGACAATTGTAA

YKL060C\_homolog 359aa (SEQ ID NO 620)

MAPPVAVLSKSGVIYKDVKDLFDYAQEKGFAPAINVTSSSTVVALEAARDNKAPIILQTSQGGAAAYFAGKGVNDKQDAASIAGSIAAAHYIRAIAPTYGIPVVLHTDHC AKLLPWFDGMLKADEEFFAKTGTPLFSSHMLDLSEETDDENIATCAKYFERMAKMGQWLEMEIGITGGEEDGVNNEHVEKDALYTS PETVFVAYE SLHKISPNSFISIAAFGNVHVYKPGNVQLRPEILGDH QVYAKQIGTDAKHPLYLVFHHGSGSGTQEEFN TAIKNGVVKVNLDTDCQYAYLTGIRDYVTNKIEYLKAPVGNPEGADKPNKKYFDP RVVWVREGEKTM SKRIAALDIFHTKGQL

YKL150W\_homolog 906bp public: 1..906 (SEQ ID NO 621)

ATGTTGACTCATCATTTATCGAAATTGGCTACTCCAAAATTCTTAGTACCATTTCGCTGGTGCCACTGCTTTGTCAATTGGTTTGGCATTGCAATATTCTACTTCCAACAATTACATTGCTAACGAAACTGGTAAAACTTCACTGATAGCAATGAATGGGTGGACTTGAAATTATCTAAGTCAATTGATTGACTCATAACACCAAA CACTTGGTTTTCAAGTTAAAAGATGAGAATGATGTTTTCTGGTTTGATCACTGCTTCATGTTTGTGACC AAATTTGTGTACACCAAAGGGTAACAATGTTATTCGTCCATATACCCCTGTCTCTGATGTTAACCAATCT GGTGAAATTGATTTCTGTGATTAAAAAATACGACGGAGGTAAAATGTCAAGTCACATTTTCGATTTGAAA GAAGGTGAAACCTTATCATTTCAAAGGACCAATTGTTAAATGGAATGGGAACCAATCAATTCAAGTCC ATTGCTTTGATTGGTGGTGGTACTGGTATTACTCCATTATACCAATTGTTGCATCAAATCACTTCTAAT CCAAAGGACAAACCAAAGTTAATTTGATTTACGGTAACCTTGACTCCAGAAGATATCTTGTTAAAGAAA GAAATCGATGCTATTGCTTCTAAACACAAGGACCAAGTTAAAGTTCATTACTTTGTTGACAAGGCAGAT GAAAAGAAATGGGAAGGTCAAATTGGTTTCAATTACTAAAGAATTCTTACAAAAAGAATTAGAAAAACCA GGTTCGTGATTTCAAGGTTTTTGTGTTGGTCCACCAGGTTTATACAAGGCTATATCAGGTCCATAAGTT TCCCCAACTGATCAAGGTGAATTGACTGGTGCTTTGAAAGATTTGGGTTTCGAAAAAGAACATGTCTTT AAATTTTAG

YKL150W\_homolog 301aa (SEQ ID NO 622)

MLTHHLSKSLATPKFLVPFAGATALSIGLALQYSTSNYIANETGKTFTDSNEWVDLKLKSIDLTHNTKHLVFKLKDENDVSGELITASCLLTKFVTPKGNVIRPYTPVSDVNQSGEIDFVIKKYDGGKMSSHIFDLKEGETLSFKGPVWKWEPNQFKSIALIGGGTGITPLYQLLHQITSNPKDNTKVNLIYGNLTPEDILLKKEIDAIASKHKDQVKVHYFVDKADEKKWEGQIGFITKEFLQKELEKPGSDFKVFVCGPPGLYKAISGPKVSPTDQGELTGALKDLGFEKEHVFKF

YLR029C\_homolog 615bp public: 1..615 (SEQ ID NO 623)

ATGGGTGCCTACAAATATTTAGAAGAATTGCAAGAAAGAAGCAATCTGATGTTATGAGATTCTTGTATCGTGTGATGATGTTGGGAATACAGACAAAAGAATGTCATCCACAGAGCTTCCAGACCATTAGACCAGACAAGGCTAGAAGATTAGGTTACAAAGCTAAACAAGGTTTCGTTATCTACAGAATCAGAGTTAGAAGAGGTGGTAGAAAGAGACCAGTTCCAAAGGGTGCCACTTACGGTAAACCAACCAACCAAGGGGTTAACCAATTGAAATACCAAAAATCATTGAGATCTACTGCTGAAGAAAGAGTTGGTCGTGCTGCTTCTAACTTGAGAGTCTTGAACCTCATACTGGGTAAACCAAGATTCCACCTACAAATACTTTGAAGTTATTTTAGTCGACCCATCTCACAAAGCTATCAGAAGAGATGCTAGATACAACCTGGATCGTTAACCCAGTTCACAAACACAGAGAAGCCAGAGGTTTGACTTCTGCTGGTAAGAAATCCAGAGGTATTAACAAGGGTCATTTGTTCAACAAAACCAAA GCTGGTAGAAGACACACCTGGAAGAAGCACACACCTTATCTTTATGGAGATACAGATCTTAA

YLR029C\_homolog 204aa (SEQ ID NO 624)

MGAYKYLEELQRKKQSDVMRFLYRVRCWEYRQKNVIHRASRPSRPDKARRLGKAKQGFIYRIRVRRGRKRPVPKGATYGPPTNQGVNQLKYQKSLRSTAEERVGRRASNLRLVNSYVWNQDSTYKYFEVILVDPSHKAIRRDARYNWI VNPVHKHREARGLTSAGKKS R GINKGHLFNKTKAGRRHTWKKHNTLSLWRYRS



180/251

YNL030W\_homolog 318bp public: 1..318(SEQ ID NO 625)  
ATGTCAGGTACCGGTAGAGGAAAAGGTGGTAAAGGTTTAGGAAAAGGTGGTGCTAAACGTCACAGAAAA  
ATTTTAAGAGATAACATTCAAGGTATTACAAAACCAGCTATCAGAAGATTGGCCAGAAGAGGTGGTGT  
AAACGTATTTCTGCTTTGATTTATGAAGAAGTCAGAGTTGTCTTGAAACAATTTTTGGAAAAACGTTATC  
AGAGATGCTGTTACTTACACTGAACATGCTAAAAGAAAAACCGTCACTTCATTGGATGTTGTTTACGCT  
TTGAAGAGACAAGGTAGAACCCTTGATGGTTTCGGTGGTTAA

YNL030W\_homolog 105aa(SEQ ID NO 626)  
MSGTGRGKGGKGLGKGGAKRHRKILRDNIQGITKPAIRRLARRGGVKRISALIYEEVRVVLKQFLENI  
RDAVTYTEHAKRKTVTSLDVVYALKRQGRTRYLGFGG

YOR285W\_homolog 546bp public: 1..546(SEQ ID NO 627)  
ATGTTTGCATTTAAAAAATCTACTACTTCAATTCTCAAAACAGTGGTCGCCCCAACATCATCTCGTTAT  
TTATCCACCGTCACATTAAGATCAATCCCAAGAACATTCCATAATGCCACTAAAGTTTCATTATTCAAT  
GGATTAAGAAGTACACCAAGATTTTATAGTGATTTGACTGAATCTCCAGAGGCAAAAGTATATAAATAT  
GCCGATGTTAAGGATGTGGCCGTACACCCGTGAAAACACCCCTGATTCTGTTTTAGTGGATGTTAGAGAA  
CCAACTGAATTTGGAGATGGTCATATACCAGGAGCTTTGAATATTCATTTAAAGTAGTCCCGGCGCA  
TTGGATTGTGCAGAAGAAGATTTCCAAGAACATTTTGGATTTCCTAAACCAAGTACTGATAAAGAATTG  
ATTTTCTATTGTCTTGGAGGTGTTAGATCTACTGCAGCTGAAGAATTGGCCAATACTTTTGGTTATAAG  
AAAAGAGGAAATTATCTTGGAAGTTGGGAAGATTGGGTAAAACATGAAAATAAAAAGAACTAA

YOR285W\_homolog 181aa(SEQ ID NO 628)  
MFAFKKSTTSILKTVVAPTSSRYLSTVTLRSIPRTHFNATKVSILFNLRTTTPRFYSVLTESPEAKVYKY  
ADVKDVAVHPENHPDSVLVDVREPTEFGDGHIPGALNIPFKSSPGALDLSEEDFQEHFGFPKPSTDKEL  
IFYCLGGVRSTAAEELANTFGYKKRGNYLGSWEDWVKHENKKN

YOR327C\_homolog 603bp public: 1..603(SEQ ID NO 629)  
ATGAAGATTTATTACATTGGTATTTTAAGATCAAGTGGAGACAAGGCTTTAGAGTTAACTTCAGCCAGA  
GATTTATCAGATTTTCCTTTTCGAAAGAAATGGGGTATCCCAATTCATGACTTTTTTCGCAGAAACC  
GTATCCCAAAGAACTCAACCTGGACAGAGACAAAGTGTTGAAGAAGGTAATTATATTGGTCATACCTTAT  
ACCAGATCAGAAGGAATTTCTGGTATCATTATAACGGACAAAGATTACCCTGTAAGACCAGCATATACA  
TTAATAAATAAAATCTTGAAGAATATTTATCATTGCATCCTAAATCTGATTGGGAAAACATTGATAAA  
GCAATGAAACTTTACAATATGGACAATTAGAAGCATATTTGAAAAAATATCAAGATCCCACTCAAGCT  
GATTCAATCATGAAAGTTCAACAAGAATTAGATGATACTAAGGTTGTTTTACACAAAACATTGAAAGGG  
GTTTTACAAAGAGGAGAGAAATTAGATTCAATTGGTTGACAAATCAGAAGCATTTGCAAGTCTTCAAGA  
ATGTTTATATAACAAGCAAAGAAAACCAATTCCTTGTGTGTGATTATGTGA

YOR327C\_homolog 200aa(SEQ ID NO 630)  
MKIYYIGILRSSGDKALELTSARDLSQFSFFERNVGSQFMFFAETVSQRTQPGQORSVEEGNYIGHTY  
TRSEGISGIIITDKDYPVRPAYTLINKILEEYLSLHPKSDWENIDKANETLQYQGLEAYLKQYQDPTQA  
DSIMKVQQELDDTKVVLHKTIEGLVLRGEKLDLSLVDKSEALSSSSRMFYKQAKKTNSSCCVM

YPL037C\_homolog 474bp public: 1..474(SEQ ID NO 631)  
ATGCCAGTCGATCCAGAAAAATTAGCTAAATTGCAAAAGTCATCTGCCAAAAAAGTTGGTGGTTCAAGA  
GTTAAAGCCAAGAAGAACATCAAGACTGAACAAGATGACACCAAATTGATTGAAGCTTTGGGTAAATTG  
AAAGCTACCAAAATCGAAGGTGTTGAAGAAGCCAATTTCTTCAGAGAAGATGGTAAAGTTTTACATTC  
AACAGAGTTGGTGTTCAGGTGCTCCAGCTTCTAATACTTTGCTTCACTGGTTACCCACAAGAAAAG  
AATATTACTCAATTGATCCCACAAAATTTACCACAATTTGGGTGCTGAAAACCTTGGAAATCTTGAGACAA  
TTGGCTGAACAAATCCAAGCTGGTAAAACCTCAAAAGACTTCAACACTGGTTCTGCTAACGCTGCTGCT  
GATGCCGGTGGTGAAGATATTCCAGACTTGGTTGACCAAAAATTTGACGATGTAGAATAA

YPL037C\_homolog 157aa(SEQ ID NO 632)  
MPVDPEKLAKLQKSSAKKVGGSRVKAKKNIKTEQDDTKLIEALGKLKATKIEGVVEANFFREDGKVLHF  
NRVGVQGAPASNTFAFTGYPQEKNTITQILPQLGAENLEILRQLAEQIQAGKTPKDFNTGSANAAA  
DAGGEDIPDLVDQKFDDVE

YPL079W\_homolog 330bp public: 1..330(SEQ ID NO 633)  
ATGCCACACAAATACTACCACGGTAAGACTGGTATTGTTTACAACGTTACCAAATCCTCCGTTGGTGT  
ATCATTAACAAAGTTGTTGGAAACAGATACATTTGAAAAGAGAGTTAACTTGAGAGTTGAACATGTTAA  
CACTCTGCTTGTCTGCAAGAATTTCTTGAACAGAGTTAAATCTAACGCTGCTAAAAAGAGAGAGCTAAA  
GCTAACGGTGAAACCGTTTACTTGAAGAGACAAGCTGCCAAGCCAAGAGGTTCAAGAATTATCTCCACT  
GAAGGTAACATTCCTCAAACCTTTGGCTCCAGTCTGCTTACGAAACTTTCATTAA

181/251

YPL079W\_homolog 109aa (SEQ ID NO 634)

MPHKYVHGKGTGIVYNVTKSSVGVIIINKVVGNRYIEKRVNLRVEHVKHSACRQEFNLNRVKSNAKKREAK  
ANGETVYLKRQAAKPRGSRIISTEGNIPQTLAPVAYETFI

YBR089C-A\_homolog EMBL\_entry 279bp public: 1..279 (SEQ ID NO 635)

ATGGCTCCAGGTGAAAAGAAAGAGTCTCTAGAAAAGAAAGGATCCAGATGCTCCAAAAAGATCCCTTA  
TCTGCTTATATGTTTTTCGCTAATGAAAACAGAGATATTGTTAGAGCTGAAAACCCAGGTATCTCTTTT  
GGTCAAGTTGGTAAATTATTAGGTGAAAAATGGAAGGCTTTAAACAGTGAAGATAAATTACCTTACGAA  
AACAGGCTGAAGCTGATAAAAAGAGATATGAAAAAGAAAAGGCTGAATACGCTAAAAAGAAATTCGCC  
TAA

YBR089CA\_homolog SWISS-PROT\_entry 92aa (SEQ ID NO 636)

MAPGERKKSSRKKKDPDAPKRSLSAYMFFANENRDIVRAENPGISFGQVGKLLGEKWKALNSEDKLPYE  
NKAEDKKRYEKEKA EYAKKNSA

YBL092W\_homolog EMBL\_entry 396bp public: 1..396 (SEQ ID NO 637)

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YBL092W\_homolog SWISS-PROT\_entry 131aa (SEQ ID NO 638)

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YDL059C\_homolog 2791bp PathoSeq: 1..2791 (SEQ ID NO 639)

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182/251

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YDL059C\_homolog\_1 67aa PathoSeq: 1..67 (SEQ ID NO 640)

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YDR377W\_homolog 24076bp PathoSeq: 1..24076 (SEQ ID NO 641)

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183/251

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184/251

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185/251

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187/251

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YDR377W\_homolog\_1 80aa PathoSeq: 1..80 (SEQ ID NO 642)

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YGR008C\_YLR327C\_homolog\_1 79aa PathoSeq: 1..79 (SEQ ID NO 644)

MTRTNKWTVEHKRPQEPKWFTHNGHSDTDPTKVKNKGAGKNNWGQPGDELDDNEVRHYQKSSGRNNSNHEMNQER  
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YGR034W\_homolog 2004bp PathoSeq: 1..2004 (SEQ ID NO 645)

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190/251

ATAGCTATTTGTAAAACTTGAACACATAAGCAGCAATTACAAAGACGTAGATTGTATGACAGTAAACCAAATCG  
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YGR034W\_homolog 120aa PathoSeq: 1..120 (SEQ ID NO 646)

VSSSRSKARKAYFTASSVERRVLLSAPLSKELRQQYNVKSLEPIRQNDVLLVVRGSKKGSEKVN SVYRLKFAIQV  
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YMR273C\_homolog 935bp PathoSeq: 1..935 (SEQ ID NO 647)

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YMR273C\_homolog\_1 98aa PathoSeq: 1..98 (SEQ ID NO 648)

IKRTSRANQPIEFDSAFGFPLPPPSQSTLVMLDYRFPVHVERAIYRLSHLKLANKRSLREQVLLSNFMYAYLN  
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YPR028W\_homolog 3616bp PathoSeq: 1..3616 (SEQ ID NO 649)

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191/251

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YPR028W\_homolog 149aa PathoSeq: 1..149 (SEQ ID NO 650)

VLDQFEQRSGLPYSYAVLGAGGLYFFLLILLNFGGIGQLLSNIAGFVIPGYYSVLVALKTTTKDDDTKLLTYWVVF  
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YFR033C\_homolog 24142bp PathoSeq: 1..24142 (SEQ ID NO 651)

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YFR033C\_homolog 114aa PathoSeq: 1..114 (SEQ ID NO 652)  
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YHR001WA\_homolog 1949bp PathoSeq: 1..1949 (SEQ ID NO 653)  
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YHR001WA\_homolog 63aa PathoSeq: 1..63 (SEQ ID NO 654)  
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YJL166W\_homolog 15790bp PathoSeq: 1..15790 (SEQ ID NO 655)  
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[illegible]

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201/251

YJL166W\_homolog\_1 93aa PathoSeq: 1..93 (SEQ ID NO 656)

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YPL271W\_homolog 7123bp PathoSeq: 1..7123 (SEQ ID NO 657)

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202/251

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203/251

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204/251

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208/251

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209/251

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211/251

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212/251

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213/251

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214/251

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216/251

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[illegible]



[illegible]



[illegible]

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YDL075W\_homolog 513bp PathoSeq: 1..513 (SEQ ID NO 661)  
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YDR064W\_homolog 5975bp PathoSeq: 1..5975 (SEQ ID NO 663)

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222/251

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YDR064W\_homolog 143aa PathoSeq: 1..143 (SEQ ID NO 664)

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YKL156W\_homolog 2002bp PathoSeq: 1..2002 (SEQ ID NO 665)

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TGTAAGAAATAGCTTTTCAATGGTTGAGCCAATATTTTATTGATCAGTAAACTCATTTTAAAGCAGAGAATACTG  
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CACATTCTACACAATGCCACAAATGAAAAAGTACTCACTATGATAGAGTATTCTGTTTACGACTACTAAATAT  
GCACCAGAGTTTACATCTATCGTAATTGTAATCTTTATGAAATTTTATCAAATAAACAGAATCAGTTTTTGGTT  
GGCAAGTTTTCTTAATTTGACTGGTCTCATCTTGAATATTTTTTATTCTAACTATGCTTAGGTACTGATGGGAA  
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TGAACATCGACCAATCTTGTTTCAATTTTCATATTTGACTCTGTAGATTGTCTTATCCTTATCCTTGTCC  
CTTGTCTTTATCTTTATCTTCTGTTTCCAAATATCCTGCCACAGTGTTCCAAATGATAGTTTTCGACTCAAC  
ATCTTTCTCAATTTTGATTTCTGTCCGTGAGTGTCTGTTTTTGTCTAGTAGTTCAGTGTATTCTTGAGGATG  
TATGGCATTGGCAAATTGATCATCTAATAAATGTTGTGGACAAGTATAGAAA

YKL156W\_homolog\_1 81aa PathoSeq: 1..81 (SEQ ID NO 666)

VLVQDLLHPSFATEAKQHKLKTLVQQPRSFMDVKCQGLNITTVFSHAQTAVTCDSCSTVLCTPTGGKAKLTEG  
CSFRRK

YLR038C\_homolog 8469bp PathoSeq: 1..8469 (SEQ ID NO 667)

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TTCTACATATTGATAGTACAGTAAATCCTAGTTATAAACCCATACCGGAGAAAGAAAACAAGAAAGTCGATACAA  
AACAATTGGAGAAAGAAGCTTTACAAGAAATCAAAGGTCCCAAAATCTATACATTGCCTGTGTTGTACATTTGTGA  
TAGGTAACATTCAATTTGTGTCAAATATAGAGTTAGTTAATTGGACAAAACAAGACAAATAATATGTAAATGTAT  
AGTATATAGCATTCCCATCCAATACAATTCGAGTTAGAGGGACAGAAAAGAGAGACGGAATAAACAACATACTAT  
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AAGATGGCAGAAAACCTTTAAAGGAAGAAGAAAGAAAAAACAACACGCCCCTATCAAGAAATCTTCT  
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GTGTCAATGTGAAGGTGAAGAATTTGAACCATGCAAAATCTTTTCAAACCTTCACTTCATTATGTCCTTTGG  
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CACAAGCTTATTGTTCTTGAAAGTGACTGTACCTATATCCATTGACCCATCTGTATGCAAAATCTCAACCGGAGT  
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224/251

ACATTACAGTGATAATCTACCTACAACATCTAGATAATCACTGAAACATATCCCTCGTTTATAGAAAGAATAAAC  
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ACCCTATTGTTATTAACAATTATTACGAAAACTTGTAGTTTTATTAGATTTAGCGATTATTCTAATACCAAAAT  
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CAACTATTGAACCCGTCACAATAATCTATCAAAATATATTAAAGATGTTCATTCAAAGAATTATTAATCGAAATTG  
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GGTGGTTCAATAAGACGTGTGTGATATATTGCACCTCACTGGATGCATCCAGGGTGGTTATGATATATCGTTGC  
TGCTAATTTAGCTTATTGTTTTGAGGAAGATAAAACCACTCCCCAAACAAGAAGAAACATTTTGAAATTTATTA  
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TCTTTCCACCTCTGTTGAAATGGAAATGAAGCTTATTATCGAAATGTATAACAAGAGCTTGAGATTAAAG  
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ACCAACCGCAAGATTCACATTTGTTCAATTTGCGGTACAATCATTGTACAACCTCAAATCAAGATTGCATGAGT  
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225/251

CTTTGGATACCAGTTTCAGCACGTTAATTGGGAACCTCTATTTTCACTCAGCATGCAAATTTGCGCAGAGCATTTTC  
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CCATTACATCGTTTGGCACTGAACATGAATTACGTTCAAGAACTCAACATGAAACATACTTTGCCGTTGATACAT  
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YLR038C\_homolog\_1 74aa PathoSeq: 1..74 (SEQ ID NO 668)

DPATFKFETPQFDFRPNQNSKHCAQAYVDYHKCVNVKGEEFEPCKIFFKFTTSLCLDWVEKWDDQRAAGKF

YNL131W\_homolog 15251bp PathoSeq: 1..15251 (SEQ ID NO 669)

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TACTTCAACATGTTCAATCAGTTACAAATTCGGGTCAATTTCAAATAGATCTGATTAAACTTCAAATACTATTTC  
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TTGGATGTTATCAAATATCATCAACTAAACAATGTAAATTCGTTTAGATTATCCAAATAATGAAATCAAATAT  
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TCCCATTTGGAAATTAATTAATAAAATCCTCATCATGTAATAAACAACAACTTATCTCATGGCAAAAAATAAAT  
CCCCAAGTACTGCTACTACTGCTACTAATGATGTGGTTGCTATTAATTGGGATGGATTAAAGATGATGAACCAT  
TAAATTTAATCAATTTACAAGAAAATGATAATTTACATACATTATATATTTTACCAGGAATTTGGAATCAAGAAT  
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CTCCAGAATGGGAAATCACTTTACCATTATCTGAACCAAGAGTTTATTTCGTATTATTGAACAAGAACAAGAAC  
AAGAGCAAGAGCAAGAGCAAGATGCTAAACACAATAATGGTTATAAATTACAATATATTTTAGAAAAATCCAAC  
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CAGCACTGGAAGGTATGAGTGATTCTAATTTCAATTTAGGGTGTGGGTCTGAGTCTGGGTGTGGGTGGGATTGA  
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CCAGCATACCTAAGAATACTGGGAATTTATATTACAACCAAAATAAATAAATAAATAAATAAATAAATAAATAA  
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TGGACCATAAGCCAAATTTGGTGAATAGTTAAATTTGCTTTAGTTCCCTTTGAAATTTTAGGTAAATTAGCACC  
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[illegible]

YNL131W\_homolog 150aa PathoSeq: 1..150 (SEQ ID NO 670)  
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 AFGNENKK

[illegible]

230/251

TCTTTAAGTCTCACAGTTAAAGTTGTAGTACCCTTCCATAAGAGCCTGATGATGTCGTGTACGAAAACCTTGTGA  
TTGATTCCATGAAATACCTT

YHR161C\_homolog 609aa PathoSeq: 1..609 (SEQ ID NO 672)

MTTYEKIVKGATKVVAAPKPKYIEPILMATSLNHSLSKENFNTIMRTLQARLHDSSWSVYKALIVIHLMIRE  
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GRLRLLDVDKGLLREVESVQKQIDSLLKNNFMENEINNDIVLTAFRLLVNDLLALFQELNEGVINILEHYFEMSK  
IDAERSLKIYKFFVDQTKFVIDYLRVAKHLEYATKLHVPTIKHAPTALTSSLEEYLDPPNFEINRKQYLAEEKGK  
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TNPFANTRFASTSHTTAFTLDNGSIQPPQQQQQONQKIQANATGNNPFKVSQTTLLQFDNYALTQQQNQHQQQLKP  
QATAGGLEH

YDR544C\_homolog 1700bp GeneSeq: 1..1700 (SEQ ID NO 673)

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TGGTGTGCAGATTAAATTTCAAGTTAAGGATCCACAAGTCAAGTACTGTAGTATTTACAGTGAGAATGGCGAAGAG  
ATTCTTACGTTTAGAAATTTGGTTAGCGGTAGTTATAGTGGTCATCTTTAAGTTATCTGTTTTGAGATTAGTCTCT  
TGTTGAATTGAAAAAATAAAGCTGA

YDR544C\_homolog 548aa GeneSeq: 1..548 (SEQ ID NO 674)

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DDSNPISATPRSEQNVFGQMPDPNLSPEKTLAPPPPPSRKVLHHEEPTVRDSALFHNLPAAHSHGRDSVMAPLASQ  
DRGHSLLKNDPFKHENLASTLGLSSSIAEVINASFKDGLIKSQVVGEVAFNYNGNASDPLVVTIPNSFDKVLVNKT  
FIEDLGQSKYKVNPTSITSKTLGGLKYLKPTQVPVIIQQIWKFEHPHQSSLMVSIRSTTPLVLENFVVSVALNQDI  
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IPTFRNLVSGSYSGHL

YHR094C\_homolog 1653bp public: 1..1653 (SEQ ID NO 687)

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GCCTTGTTGTTTGTCTGGTGGTATGGTAAGAATGCCAGAATCTCCACGTTACCTTGTCCGTAAAGATAGA

231/251

ATTGACGATGCTAAGATTTCACTTGCCAAAACCTAACAAGGTTTCTCCAGAGGACCTGCATTATACCGT  
GAACTTCAATTAATCCAAGCTGGTGTGAAAGAGAAAGATTGGCCGGTAAGGCATCTTGGGGTGCTTTA  
ATCACTGGTAAACCAAGAATCCTTGAAAGAGTTATTGTTGGAGGTATGTTGCAATCATTGCAACAATTG  
ACTGGTGATAACTATTTCTTCTACTACAGTACCACCATTTTCAAGTCTGTCCGGTTTAAATGATTCCTTC  
GAAACATCTATTATCCTTGGTGTCATCAACTTTGCTTCCACTTTTGTGGTATTTATGCCATTGAAAGA  
TTGGGTAGAAGACTCTGTTTATTAAGTGGTTCCGTTGCCATGTCCATTTGTTTCTTAATTTACTCATTG  
ATTGGTACTCAACATCTTTACATTGATCAACCAGGTGGTCCAACCAGAAAACCAGATGGTAACGCTATG  
ATTTTCATTACTGCACCTTTATGTTTTCTTCTTCGCTTCTACATGGGCTGGTGGTGTCTACTCCATTGTT  
TCTGAACTTTATCCATTAAAAGTCAGAAGTAAGGCTATGGGTTTTGCTAATGCATGTAAGTGGTTGTGG  
GGTTTCTTGATTTCTTCTTCACTTCATTTATCACTGATGCTATCCACTTCTATTAGGTTTTGTGTTT  
ATGGGCTGTTTAGTGTTTTCCATTTTCTTCTTACTTTATGATTTACGAAACTAAAGGCTACCTTTA  
GAGGAAATTGATGAATTATACTCTACCAAGGTTGTTCCATGGAAATCAGCCGGTTGGGTTCACCTTCT  
GACGAAGAAATGGTTCGTGCAAAGGCTATACTGGTGATATCCACGCAGATGAAGAGCAAGTTTAA

YHR094C\_homolog 550aa (SEQ ID NO 688)

MSLDNSTENRDLEEKEEIPKNEHNEQGEQNNENHIPTLEDKPLKEYIGISILCFLIAFGGFVFGFDTG  
TISGFINMTDFLERFGGTKADGTLYFSNVRTGLLIGLFNVGCAIGALFLSKVGDYGRRVGIMTAMIY  
IVGIIVQIASQHAWYQIMIGRIITGLAVGMLSVLCPFLISEVSPKHLRGTLVYCFQLMITLGLIFLGYCT  
SYGTTKYSDSRQWRIPLGLCFAWALCLLGGMVRMPESPRYLVGKDRIDDAKISLAKTNKVSPEDPALYR  
ELQLIQAGVERERLAGKASWGALITGKPRILERVIVGGMLQSLQQLTGDNYFFYYSTTIFKSVGLNDSF  
ETSIILGVINFASFVGIYAIERLGRRLCLLTGVSAMSICFLIYSLIGTQHLYIDQPGGPTRKPDGNAM  
IFITALYVFFFASTWAGGVYSIVSELYPLKVRSKAMGFANACNWLWGFLISFFTSFITDAIHFFYGFVF  
MGCLVFSIFFVYFMIYETKGLTLEEIDELYSTKVVPWKSAGWVPPSDEEMVRAKGYTGDIDHADEEQV

YBL099W\_homolog 1344bp public: 1..1344 (SEQ ID NO 717)

ATGGCTTTGAACTTGGAAGCTGACCAAGTCGGGGTTGTGTTGTTCCGTTCTGATAGATTAGTCAAAGAA  
GGTGAAACCGTCAAGAGAACTGGTCAAATTGTTTCCGTTCCAATTGGTCCAGAATTGTTAGGTAGAGTT  
GTTGATGGTTTTAGGTAACCAATTGATGGTAAAGGTCCAATCAAGGCTGCTGCTTACTCCAGAGCTCAA  
GTTAAAGCTCCAGGTATTTTACCAAGAAGATCCGTCCACGAACCAATGCAACCGGTTTGAAATCTGTT  
GATGCTTTGGTTCCAATTGGTAGAGGTCAAAGAGAATTGATCATTGGTGATCGTCAAACCTGGTAAAACC  
GCCGTTGCCTTGATGCCATCTTGAACCAAAAGAGATGGAACAATGGTTCTGACGAAAAGAAGAAATTG  
TACTGTGTTTTACGTTGCCGTTGGTCAAAGAGATCCACTGTTGCTCAATTGGTCCAACTTTGGAACAA  
CACGACGCTCTTAAATACTCTGTTATTGTTGCTGCTACTGCTTCTGAAGCTGCTCCATTGCAATACATT  
GCTCCATTCACTGCTTGTGCTATTGGTGAATGGTTCAGAGACAATGGTAGACACGCCTTGATTGTCTAC  
GATGATTTGTCAAACAAGCTGTTGCTTACCGTCAATTGTCAATTATTGTTGAGAAGACCACCAGGTAGA  
GAAGCTTACCCTGGTGATGTTTTCTACTTACATTCCAGATTATTGGAAAGAGCTGCTAAGATGTCTGAT  
GCTTACGGTGGTGGTTCTTTGACTGCTTTGCCAGTTATTGAAACCAAGGTGGTGATGTCTCTGCTTAT  
ATTCCAACCTAACGTTATTTCCATTACTGATGGTCAAATTTCTTGGAAGCTGAATTATTCTACAAAGGT  
ATCAGACCAGCTATTAACGTCGGTTTGTCCGCTCTCCCGTGTCCGTTCTGCTGCTCAAGTTAAAGCTATG  
AAACAAGTTGCCGGTTCCTTGAAATTGTTCTTGGCCCAATACAGAGAAGTTGCTGCTTTCGCTCAATTT  
GGTTCTGATTTGGATGCTTCTACCAAAACAACTTGAACAGAGGTGAAAGATTGACCAATTATTGAAA  
CAAAAACAATACAAACCATTTGGCTGCCGAAGAACAAGTTCCATTGATTTTTCGCTGGTGTAAACGGTTTC  
TTGGACAATGTTGCTCTTGACAGAATTGGTGAATTCGAAGAAGCTTTCTTGGGTCACCTTGAAATCTAAC  
GAAACTGGTATCTTGGATGCTATTAAGACCAAGGGTGAATTATCTAAAGATGAATTAGAAAAATTGAGA  
AAAGTCACCGAAGAATTCGTTGCTTCTTTCTAA

YBL099W\_homolog 447aa public: 1..447 (SEQ ID NO 718)

MALNLEADQVGVLFGSDRLVKEGETVKRTGQIVSVPIGPELLGRVVDGLGNPIDKGPIKAAAYSRAQ  
VKAPGILPRRSVHEPMQTGLKSVDALVPIGRGQRELIIGDRQTGKTAVALDAILNQKRWNNGSDEKKKL  
YCVYVAVGQKRSTVAQLVQTLQHDALKYSVIVAATASEAAPLQYIAPFTACAIGEWFRDNGRHALIVY  
DDLKQAVAYRQLSLLLRPPGREAYPGDVFLHSRLLERAAKMSDAYGGGSLTALPVIETQGGDVSA  
IPTNVISITDQIFLEAELFYKGRPAINVGLSVSRVGSAAQVKAMQVAGSLKFLAQYREVAFAQF  
GSDLDASTKQTLNRGERLTQLLKQKQYNPLAAEEQVPLIFAGVNGFLDNVALDRIGEFEEAFLGHLKSN  
ETGILDAIKTKGELSKDELEKLRKVTEEFVASF

232/251

YEL032W\_homolog 2637 bp public: 1..2637 (SEQ ID NO 719)

ATGGATGAACGATTTTTGAATCCACCACCTACAGCTGATCAAGATGATACTAATCAGCCACTTGATGCC  
ATCTTTGGTGATAGAGTCAGAAGATTTCAAGAGTTTTTAGATAGAATTGATTCTAATACAGGTATAGAT  
TACAGATCTATTATCAAAGATATGTTGATCAAGAGTAAGTTTAGATTGAGTGTTTTCAATTGATGAAATA  
AGAGAGTTTGACAGAGAATTTTGGTTGGGGTTGCTCAACCAGCCAGCTGACTATTTACCAGCTTGTGAA  
AGAGCTTTGAGAGACACAGTTTTAGCTATTTACGACCCACAGGATCCAAGTTTCCACATGACAGTTAT  
GACCCTAACCCAGCAATACTATTTATCATTCAAGGGAGCATTGTTGGGGGACATTCGCTCACTCCTAGATCG  
ATTGATTCAGCTATCTTTCCAAAATGGTTTCTATTGAAGGTATTGTGACTAGAGCTTCATTAGTTAGA  
CCAAAGGTTATTAGATCGGTTTATTATGCTGAAAAAACTGGTAGATTTTATGCACGTGAATACCGAGAC  
CAAACAACATCCTTTGATGCAATTGCTACTCCGGCTATATATCCAACCTGAAGATATGGAAGGTAATAAAA  
TTAACCACAGAGTATGGTTATTTCGACATACAGAGATTACCAGAAGATCTCTGTACAAGAAATGCCTGAA  
ACAGCTCCTCCAGGTCAATTGCCAAGATCGGTTGACGTTATTTTGGATGATGATTTGGTGGATTTGACA  
AAACCCGGTGATCGTGTACAAATTGTTGGTGTATTATCGTGCCCTTAGGAGGTGCTGCAACAATAGTTCT  
TCTTTCAAAAACGGTTATCTTAAGTAATTCTGTTTACTTGTACATGCCAGATCAACAGGGGTTGCTTCA  
CAAGAAAAGTTAACTGATCAAGATATTAGAAATATAAATAAACTTGCAAAGGATAGAAAGATTTTTGAT  
ATTTTATCCCGTTCTTTGGCCCCCTTCAATTTATGGGTTTGACTATATTAAGAAAGCTGTTTTACTTATG  
ATGATGGGAGGTGTTGAAAAAATTTAGATAATGGTACACATTTGAGAGGTGACATTAACATTTTGATG  
GTGGGTGACCCATCCACTGCCAAATCTCAAGTATTACGGTTTGTGTTGAACACTGCCTCATTAGCTATT  
GCCACTACTGGTAGAGGATCGTCAGGTGTAGGTTTAAACAGCTGCTGTTACTACCGACAAGGAAACAGGA  
GAAAGAAGATTGGAGGCTGGTGCAATGGTATTGGCTGACAGAGGTATTGTTTGTATTGATGAATTTGAT  
AAATGTCAGATATCGACCGAGTGGCCATTACGAAAGTTATGGAACAACAACAACTGTCACATTATGCTAAA  
GCTGGTATTACACCTCATTGAATGCTCGTTGTTCTGTTATTGCTGCCGCAAATCCGGTTTTTGGACAG  
TACGATGTCCATAAAGATCCACATAAAAAATATTGCCTTGCCCGATTCAATTATTGTCTCGTTTTGATTG  
CTCTTTGTTGTTACAGATGATGTCAACCCAACAAGAGACAGGGTTATTTCTGAGCATGTTTTAAGAATG  
CACAGGTTTGTTCCTCGGATTGATGGAGGGAGAGCCAATCAGAGAAAAATCAGCAGTTACATTGGCT  
GTCGGAGATGATGAAACCAATGAACAAGAATTATTAGAACAGCCAATGTTTGAAAAATTTAACACATTA  
TTGCATGCTGGTATTCAAACAACAAAGTCAAATAATATACTTTTCGATTCCATTCTTGAAAAATATGTC  
CAGTACGCCAAGCAAAGAGTGCAACCAGTGTTGACCAAGGGTGCATCCGACTACATTGTTACTACATAT  
TCCTCCTTAAGAAACGATTTGATAGGCAACAACCAAGAAATACAGCTCCAATAACTGCTAGAACTTTA  
GAAACTTTGATTCTGTTTAGCAACAGCTCATGCAAAAGTCCGTTTATCCAAAACCTGTTGATGTGAAAGAT  
GCAAAAGTTGCCGAAGAGCTATTGAGATATGCATTATTCAAGGAAGTAGCCAAAAAGACAAAAAGAGA  
CAAAAACTACAAGTATAGTGGACTCAGAAGAGGAGGAAGAGGATGAGTCTGATGCAGAAATGGAAAAAT  
TCCGATAACGAAATAATGCCCAGAGAAAGTACTAGAAGAACCAGAGCTACAGCACAAACACAGCCTCCA  
CAACAGCAACAAGCATCTCCTTCACTAACACCCGAACCGCCACTTGGACATCGGGACGATGGAGATGAC  
GATGGAGTTGGTGAAGAATTAGAACAATTCATTGTCATCATCTCAGCAACAACAGCAACAACAATAT  
TTGCAACCATTGACTGAGAGATCATCAAGTAACACTGGTGTACGTTCTGACATTATTTGCCAATGATGACAA  
GCTGCGGCAAACTATCATGACGTTACTCGTGCTATCAATGAACAGATGGAACAAGAAGATATTTCTCA  
GAGCAAGAGTTGAGTGCCTGGATTTGAAGTGATGAGTTCTGAAAACAAGTTTTACCTAGAAAGTGATAAG  
ATTTGGAAGATTTAA

YEL032W\_homolog 878 aa public: 1..878 (SEQ ID NO 720)

MDERFLNPPPTADQDDTNQPLDAIFGDRVRRFQEFLLDRIDSNTGIDYRSIIKMDLIKSKFRLSVSIDEI  
REFDREFWLGLLNQPADYLPACERALRDTVLAIYDPQDPSFPHDSYDPNQYYLSFKGAFGGHSLTPRS  
IDSSYLSKMVSIEGIVTRASLVRPKVIRSVHYAEKTGRFYAREYRDQTTSFDAIATPAIYPTEDMEGNK  
LTTEYGYSTYRDYQKISVQEMPETAPPGQLPRSDVILDDDLVDLTKPGDRVQIVGVYRALGGAANNSS  
SFKTVILSNSVYLLHARSTGVASQEKLTDQDIRNINKLAKDRKIFDILSRSLAPSIYGFYIKKAVLLM  
MMGGVEKNLDNGTHLRGDINILMVGDPSTAKSQVLRFLVNTASLAIATTGRGSSGVGLTAAVTTDKETG  
ERLEAGAMVLADRGIVCIDEFDKMSDIDRVAIHEVMEQQTVTIAKAGIHTSLNARCSVIAAANPVFGQ  
YDVHKDPHKNIALPDSLRSRFDLLFVVTDVNPTRDRVISEHVLRMHRFVPPGLMEGEPIREKSAVTLA  
VGDETNEQELLEQPMFEKFNTLLHAGIQNKSNILSIFLKKYVQYAKQRVQPVLTKGASDYIVTTY  
SSLRNDLIGNNQNTAPITARTLETILRLATAHAKVRLSKTVDVKDAKVAEELLRYALFKEVAKKTKKR  
QKTTSIDVEEEEEDESDAEMENSNDNEIMPRESTRRTRATAQTQPPQQQASPSLTPEPPLGHRDDGDD  
DVGVEELEQFHLSSSQQQQQYQLPLTERSSSNIVSSTATNAISVERLNIFKRILAQVSRSAFANDQ  
AAANYHDVTRAINEDMEQEDIFSEQELSAGFEVMSSSENKFYLESCKIWKI

233/251

YHR135C\_homolog 1488 bp public: 1..1488 (SEQ ID NO 721)

ATGACAACAAACCTGCTTTGGCGGCTGCTCAAGCATCTCATAATAATATTCCTACAAAGCAAATGAAT  
CATTCAACTTCATCTTCAAACGGTAACGGTAGCAATAATTCATCCGTGGTTGGACTTCACTACAAGATT  
GGGAAAAAAATTGGTGAAGGTTCTTTTGGTGTCAATTTTGAAGGTACTAATATAATAAATGGAGTACCC  
GTGGCCATAAAATTTGAACCTAGAAAGACTGAAGCTCCTCAATTACGAGATGAATATAGAAGTTATAAA  
CATTTACAAGGATGTGACGGAATTCCTAATGCATATTATTTTGGTCAAGAAGGATTACATAATATTTTA  
GTCATTGATTTATTGGGTCCTTCTTTAGAAGATTTATTTGATTGGTGTGGTAGAAGATTTAGTGTTAAA  
ACCGTGGTACAAGTTGCTATACAAATGTTGACTTTAGTAGAAGAAGTTCATCGTCATGATTTAATCTAT  
AGAGATATCAAACCCGACAATTTTTTAATTGGAAGAAGAGGTGCTACTGATGAAAATAATGTTTCATTTG  
ATTGATTTTGGTATGGCCAAGCAATATCGTGATCCAAGAACAAAGCAACATATTCATATAGAGAGAAG  
AAATCTTTGAGTGGGACAGCTAGATATATGAGTATTAACACTCATTTAGGAAGAGAACAATCAAGAAGA  
GATGATTTAGAAGCATTGGGTCATGTATTTTTTTATTTCTTAGAGGCCAATTACCTTGGCAAGGTTTA  
AAAGCTCCCAACATAAAACAAAAGTATGAGAAAATTGGTGATAAAAAGAGAACTACACCAGCAGTTACA  
TTATGTGATGGCTTACCTCAACAATTTGCTGAATATTTAGATTCAAGTTAGATCATTACCATTTGATGCT  
GAACCTCCATATGAAGAATATAGAATGTTATTATTGTCAAGTGTGGATGATTTGGGTCAAGCTTGTGAT  
GGAGATATGGATTGGATGCATCTTAATGGTGGTAGAGGTTGGGATGCTACAATTAATAAAAAACCCAAC  
TTGCACGGTTATGGACATCCTAATCCACCAAATGAACGTGAAAGAAGACATCGTGATCAAAGAAGAACA  
AGACAACATCAACAAGTGAACAAGTACAACAACAACAATTACAAGCTCAAGCTCAAGCACAACAATTA  
CAACAATTACAACAAGCACAACAGGCACAACAACAACAACAAGTGAACAACATCAACCACTACTGCA  
GCCCAGTTACATCAACAAAATTACAGCATTGGTTAATCGACCATTACCACCAATTAACAACAAGAATCA  
CAATCAGCAATACAAAGTGGTAATGGACATCATGAACCTTTGAATAATAATTTAGGTGATCAGCATGGA  
GGAAAACATGAAGGATACAGTTCACGACCAGATCAATATCAACAACAACAATGGTTGCCGAAGAAGAA  
GAAAACAAAGGGTTCTGGTCTAAATGTGTTGTCATTAG

YHR135C\_homolog 495 aa public: 1..495 (SEQ ID NO 722)

MTTNPALAAAQASHNNIPTKQMNHSTSSSNGNGSNSSSVVLHYKIGKKIGESFGVIFEGTNIINGVP  
VAIKFEPRKTEAPQLRDEYRTYKHLQGCDGIPNAYYFQEGLEHNLVIDLLGPSLEDLFDWCGRRFVSK  
TVVQVAIQMLTLVEEVHRHDLIYRDIKPDNFIIGRRGATDENNVHLIDFGMAKQYRDPRTKQHI PYREK  
KSLSGTARYMSINTHLGREQSRDDLEALGHVFFYFLRGQLPWQGLKAPTNNKQYKIGDKKRTTPAVT  
LCDGLPQQFAEYLDVSRSLPFDAPPEYRMLLLSVLDDLGQACDGDMDWMHLNNGRGWDATINKKPN  
LHGYGHPNPPNERERRHRDQRRTRQHQQSQVQQQQLQAQAQAQQQLQQAQAQQQQSQQHQP LSA  
AQLHQQKLQHLVNRPLPIKQESQSAIQSGNGHHELLNNNLGQHGKHEGYSSRPDQYQQQQMVAAEE  
ENKGFWSKLCCH

YJL060W\_homolog 1362 bp public: 1..1362 (SEQ ID NO 723)

ATGTTAAGACGGCTCTTTCCAATACGACAATTTGTACACAACAACCTAGAGCCATGGCCAGCAAATCAACA  
GACCCAAGTAGTTTGCATAATCCGTATTTTATCAAAAAACCGGGGCAAAAAGATATCTGGTTCGTTAATC  
AACGAAACTGCGGCCAGGCACAACAAGAATCCGGCGAGCCAATTTGTCAATTTGGGACAAGGGTTTTC  
TCCTACAATCCTCTGAGTTTGCATTAACGCTGTTGAGGAAGCATTGACCAAGCCGCAATTCACCCAA  
TATGCACATGCTCGTGGAAACCCAACTTATTGAAACAAGTGGCAGAGCACTATTCGCGATCGTATGGA  
CGTGCTGTGGGGTTGACGAGGTCCAAATCACCACGGGTGCAATGAGGGAATGTTTGCCATTTTCTTT  
GGTTTCTTGACCCCGGGCGATGAAGTCATTGTGTTTGAACCATTTTTTGACCAATACATCCCCAATGTT  
GAAATGACAGGAGCCAAGATCAAGTACGTTGAAATCAAGTATCCCAAGAAATTTGACAACGAGGTTGTC  
ACGGGCCAGGATTGGGAGATTGACTGGGAAGGATTGAATAATGCCATTACCGACAAGACCAAGATCATC  
GTGATAAATACCCACACAACCAATCGGCAAAGTTTTCACCGAGAAGGAGTTGTACAAGATTGGCAAG  
CTTGCCGTGGAACACAATTTAATCCTTGTCAGCGACGAGGTTTACGAGAACTTGATTATACTGACAAG  
TTCCCTCGTCCAGCTGCATTACCACAGTTGCTTGAATTTGGCTGAAAAGGACGTTGACAGTGGGTTCTGCT  
GGGAAATCATTTGCTGCCACTGGTTGGAGAGTAGGGTATATCCAGGGCCCTGCCAATTTGATTAAATTT  
GTAACAGCGGCCACACCAGAATTTGTTTCTCGACCCACAGCACCATTGCAACAGGCAGTATCTCAGGGG  
TTTGAGCAGGCTGAGAAATCAAATATTTTGAACACTCGAAAGGAGTATGAACACAAAATACAAAATA  
TTCACCAAGGTATTTGACGACTTGGGGTTACCCTACACCGTTGCCGAAGGAGGGTACTTTGTGTTGGTG  
AACTTGCTGAAAGTTAAGATACCCGCAGATTATGAGTTTCCCGGAACCATCAGCGATAGAGGCATTTTA  
GATTTCAAATTTGGCGTATTGGTTGATCAAGAAATTTGGGGTTGTGGGAATCCCTCCAACAGAGTTTTTA  
ACCGAATCGAATAGAAAGGGGAACGGCTTAGAAAATTTGTGTCAGATTTGCTGTTTGCAAAGATGATTCT  
GTTTTAGAAGACGCGGTTGAGAGATTGAAAAAATTTAAAAGACTATTTTATAA

234/251

YJL060W\_homolog 453 aa public: 1..453 (SEQ ID NO 724)  
MLRRLLFPPIRQLYTTTRAMASKSTDPTSLHNPYFYQKPGQKDIWSLINETAAQAQQESGEPVNLGQGFF  
SYNPPEFAINAVEEALTKPQFNQYAHARGNPNLLKQVAEHYSRSYGRAVGVDEVQITTGANEGMFAIFF  
GFLTTPGDEVIVFEPFFDQYIPNVENTGAKIKYVEIKYPKKFDNEVVTGQDWEIDWEGLNNAITDKTKII  
VINTPHNPIGKVFTEKELYKIGKLAVEHNLIIVSDEVYENLYYTDKFFRPAALPQLPELAERTLTVGS  
GKSFAATGWRVGYIQGPANLIKFTAAHTRICFSTPAPLQQAVSQGFQAESNRYFENTRKEYEHKYKI  
FTKVFDDLGLPYTVAEGGYFVLVNLKVKIPADYEFPGTISDRGTLDFKLAYWLIKEIGVVGIPPTFL  
TESNRKNGLENVRFVAVCKDDSVLEDAVERLKKLKDYL

YML028W\_homolog 591 bp public: 1..591 (SEQ ID NO 725)  
ATGGCTCCAGTCGTTCAACAACCAGCTCCAAGTTTCAAGAAAACCGCCGTCGTTGATGGTGTCTTTGAA  
GAAGTCACTTTAGAACAAATACAAAGGTAAATGGGTCTTGTGGCCTTTATTTCCATTGGCCTTCACATTC  
GTCTGCCCCATCAGAAATTATTGCTTATTTCCGAAGCTGTAAAGAAATTTGCCGAAAAGGATGCTCAAGTT  
TTGTTTGCCCTCTACTGACTCCGAATACACCTGGTTGGCTTGGACCAATGTCCGCCAGAAAAGACGGTGGT  
ATTGGCAAAGTCGACTTCCCAGTCTTGGCTGACACCAACCACTCCTTGTCAGAGACTACGGTGTCTTA  
ATTGAAGAAGAAGGTGTTGCCTTGAGAGGTATTTCTTGATTGATCCAAAGGTGTCTTGAGACAAATC  
ACCATCAATGACTTGCCAGTCGGTAGATCTGTTGAAGAATCCTTGAGATTGTTGGAGGCTTTCCAATTC  
ACTGAAAAATACGGTGAAGTTTGTCAGCTAACTGGCACCAGGTGATGAAACCATCAAGCCAAGCCCA  
GAAGCATCCAAGGAATACTTCAACAAAGTCAACAAATAA

YML028W\_homolog 196 aa public: 1..196 (SEQ ID NO 726)  
MAPVVQQPAPSFKKTAVIDGVFEEVTLQYKQKWLAFIPLAFTFVCPSEIIAYSEAVKKFAEKDAQV  
LFASTDSEYTWLAWTNVARKDGGIGKVDLPVLADTNHSLSRDYGVLIEEGVALRGIFLIDPKGVLRQI  
TINDLPVGRSVEESLRLLLEAFQFTEKYGEVCPANWHPGDETIKPSPEASKEYFNKVNK

YOL100W\_homolog 2835 bp public: 1..2835 (SEQ ID NO 727)  
ATGCATAAATTTAGATATTCCTTGCACCAACACTATAGCAAACGCAATTCAGTGACAAATCCAAAGAC  
AGTCCAATTAGCCAAAACAGCAATGAAGAAAATGATTCGACTAAATTAAGTTCAAGTAGTCTTCAAGAC  
TTACATGATGATCTCGATGATATTTATAACAACCTATACTTTAGCACAGGGTACCAATAACAACAGTGTA  
GATACATTGGATTCTGAAAATAATCAAGCTATAAATAAGTTTATTGATAAACCTCCAGCAATTCATGGT  
ATGGAACCACAACCTACCGGTGATGCACGTTTCTTCACGATTATCTTCCCTTAGGTAATACCACCAATGAA  
ACCGGTGAAAGCATCGCCAAAAGTGCACCAGGAACCTCCGTATCTTCACATTCATTTGATTTAGACCG  
CATCATCTCGTGAGTAACAACTCATCCCTCAATGTATTTGTTAGACACCCCTAATGTCAGTTCCGAA  
TTCAATCATTTAGTGGATCAAAACACCACCAATGAGTCGGTAGAAAAGGTTTGACGACAGTAATAATACT  
GTGGACAATACAGAAGAGGAAGAAAATAATGATGATACAGACGAAATACCAAAATCCGAAACATTGAAA  
CAAAACGAGGAGAAATTTGGGAAAAAAGGGTGCTGCAGTTAAAACCTATCAAGACTATGGATGGAGAAATG  
AAAACCTATTCGGCGAAATGTTACTGATTTCAAATTTGGTAAAGAATTGGGTGAAGGTTTCATATTCACG  
GTGATTTTAGCCACTGATAAGATTACTGGTAAACAATATGCTGTAAAAGTACTTTGATAAGCGACATATT  
ATAAAAAGAAAAGTCAAGTATGTCAATATAGAAAAACATGCATTGAATCGATTAGTAATAGATTA  
GGGGTTATTTTCAATTATTTTACCTTCCAGGATAAAGATTTCGCTTTATTTTGTTTTGGATTATGCTTCA  
AATGGTGAATTATTGACATTGATCAAGAGATACAATACTTTAAATGAGGAATGTACTAGACATTTTGGT  
GCACAAATATTAGATGCTATTAAATATATGCATGATAATGGTGTATATACATCGAGACCTAAAACAGAG  
AATATATTATTAGATGACAAAATGAGAATTCAAATTACAGATTTTGGTACTGCAAGATTATTAGAGAAA  
AAGAATGATGAAAGTGAAGAATACCCAGTGGATGTAAGAGCAAAATCATTTGTTGGAACCGCTGAATAT  
GTATCCCCTGAAATTATTAGAAAATAAGTATTGTGGTAAACCTGGAGATGTTTGGGCTTTTGGTTGCATC  
ATATATCAAAATGATTGCTGGGAAACCACCAATTAAGGCAACTAATGAATATTTAACGTTTCAAAAAATT  
ACGAAATTGCAATTTGCGTTTAGTGACAGGATTCCTTACAATTATTAGAGATTTAATAAAGAAGATTCTT  
GTGTTGCAACCTTCACGACGTGCCACCAATTCAGAAATACAAAACATTACTTTTTTCCAATCGGTGAC  
TTTAAAGATTTTGTATCTGATTTGGTTGTCTGATCCTCCTGAAATAGGACCTTATAAAATGACAGCAAAA  
TCCATGATGAAAGTACCGGAATTGAATAAGGCACCTATAACCACAGTCATTGAAGAAGATGTGAAGAAA  
TCCACAACTCAAAATCAAAATACCAACAATGTCGCCACTGCTGTTGGTGGTAGTAGTAGTAACGGACAT  
AAAGGGTCACTACCGACTCCTGAGAAAGAGCCGACCCAGCTACTATTAATAACAAGTCCACAGAAAAA  
GTTAGTCCCGCTAGTGTAGCTGCATATGTTTTAAACAAAACAGCTACAAACCAAAATCCAGTACATCC  
GAGGATTCATCTAAGCGTAGCAGCAACTCCAATGAAACTCGCAAACTTTTCATATTCACAACAGGATTAT  
ATTCCGGGAACAAATATTTTACGTCCACAGATTAGTACTAGACCGTCAGTAGGATCTTATGTGAAAACC  
ACACCATCAAAGGATAGAAAAACATTAACCAAGGTCCCACTGAATATCCATCAACAACAAGAAAAAGTG



## 235/251

AAACCGAAAGTAATGGAAGTGAAGCCAGCAACTACATTGGAAGCAGCATGGGAACCATATTTAACCCAT  
CCAGATGAAAGAATACTTCGTATTGGTCCAGTTATTGCTCATAAAGAACCAACAGAACCATTTGAAAAG  
AAGAATAAAGCATCTTTACATATATCACCTTTGGATATAAATAAAGAACAAAGAAGTAGATCCAATACT  
AGTTTACTTACACAAATTGTAAATGAAGTAAACAATAACACCAGCGAATTGAAAAAAGTGGAAAATGCT  
GATGAATCACTTGCCATTATTGAACCACAATATAATATGAAGAGAAGTCCAACCTTCTGATAGTAAGAAA  
AGTATGGATATTGAAAGATCTGCATCTACTTCTGGAAGTAGAATTAGTAAGAAGGCAATTTTCAAAAAA  
TTGGGGTTTTAGTCATTTAGAAAAAATGATAGTGAAGAATCAAATGGTCCTAGTTTAAACGGAAAAACCA  
CAAACCTGTACATTGGTTGTTACAACCTCATGGTCGAGCATTACTTTTCATTAGAAATGATATAGAATCC  
AATTATCTTTTAATTGCTGAAATCAAATTGAAATATCCATTTATTCAATTTCCAAGAATTAGTTATATCA  
CAAATAAATTTTCTAAATTAGTACCATCAGTCGGAGTATTTGTCATTAGTTCAATTGATAATTCATTA  
ATTTTTGAAGTAGAAAAATTTGAAGTGAATCAATGGACTGAAGCATTAGCTAAATCTAAATATAATGAA  
ATATAA

YOL100W\_homolog 944 aa public: 1..944 (SEQ ID NO 728)

MHKFRYSLHQHYSKRNSSDKSKDSPISQNSNEENDSTKLSSSSLQDLHDDLDDIYNNYTLAQGTNNNSV  
DTLDSENNQAINKFIDKPPAIHGMEPQLPVMHVSSRLSSLGNTTNETGESIAKSAPGTPLSHSHSDFRPF  
HHPRAVTNSSLNVLLDTPNVSSSEFNHLVDQTPPNESVERFDDSNNTVDNTEEEENDDTDEIPKSETLK  
QNEENWEKKGAAVKTIKTMGDGEMKTIIRNVTFDFKFGKELGEGSYSTVILATDKITGKQYAVKVLDRHI  
IKEKKVKYVNIIEKHALNRLSNRLGVISLYFTFQDKDSLIFYVLDYASNGELLTLIKRYNTLNEECTRHFG  
AQILDAIKYMHNDNGVIHRDLKPENILLDDKMRIQITDFGTARLLEKKNDESEYFPVDVRAKSFVGTAEY  
VSPellenKYCGKPGDVWAFGCIYQMIAGKPPFKATNEYLTFOKITKLQFAFSAGFPTIIRDLIKIL  
VLQPSRRATIEIQKHFFQSVDFKDFDSIWLSDPPEIGPYKMTAKSMMKVPELNKAPITTVIKKNVKK  
STNSNSNTNNVATAVGGSSSNHGKSSPTPEKEPSPATINNKSSTEKVSAASVAAYVLNKPATNQNSSTS  
EDSSKRSSNSNETRKLSSYSQQDYIPGTNLRPQISTRPSVGSYVKTPSKDRKTLTKVPSNIHQQKEV  
KPKVMEVKPATTLEAAWEPYLTHPDERILRIGPVIAHKEPTEPFKKNKASLHISPLDINKEQRSRSNT  
SLLTQIVNEVNNNTSELKKVENADESLAIIEPQYNMKRSPTSDSKKSMDIERSASTSGSRISKKAIFKK  
LGFHLEKNDSEESNGPSLTEKPQTCTLVVTTTHRALLFIRNDIESNYLLIAEIKLYPFIHFQELVIS  
QTKFSKLVPSVGVFVISSIDNSLIFEVEKFEVNWTEALAKSKYNEI

YJL166W\_homolog 288bp Pathoseq: 1..288 (SEQ ID NO 729)

ATGGCAGGTGCACCACATCCACATACTTATATGGGCTGGTGGGGTAGTTTAGGCTCCCCAAAGCAAAAA  
TATATTACTCAATATACTATTTCTCCATATGCTGCTAAACCATTAAAGGGGGCTGCTTATAATGCTGTT  
TTCAATACTTTTAGAAGAACCAAGAATCAATTTCTTTATGTTGCCATTCCATTTGTTGTTGTTGGAGT  
ATTTGGACTAGAGCTAGAGATTATAATGAATACTTGTACACTAAAGAAGGTAGAGAAGAATTGGAAAGA  
GTTAATGTTTAA

YJL166W\_homolog 95aa PathoSeq: 1..95 (SEQ ID NO 730)

MAGAPHPTYMGWWSLGSPPKQKYITQYTISPAAKPLKGAAYNAVFNTRRTKNQFLYVAIPFVVVWS  
IWTRARDYNEYLYTKEGREELERVNV

YLR038C\_homolog 252bp PathoSeq: 1..252 (SEQ ID NO 731)

ATGCCAGTCGATCCAGCTACTTTTAAATTCGAACTCCACAATTTGACCCAAGATTCCCAAAACCAAAAC  
CAATCCAAACATTGTGCTCAAGCCTACGTTGATTACCACAAATGTGTCAATGTGAAAGGTGAAGAATTT  
GAACCATGCAAAATCTTTTCAAACTTTCACTTCATTATGTCTTTGGATTGGGTCGAAAAATGGGAT  
GATCAAAGAGCTGCTGGTAAATTTCCAGTCAACATGGACGCTTAG

YLR038C\_homolog 83aa PathoSeq: 1..83 (SEQ ID NO 732)

MPVDPATFKFETPQFDPRFPNQNSKHCAQAYVDYHKCVNVKGEEFEPCKIFFKTFSTSLCPLDWVEKWD  
DQRAAGKFPVNMDA



236/251

**Human homologues**

&gt;YGL080W\_homolog, CDS: 1-330 bp (SEQ ID NO 675)

ATGGCGGGCGGTTGGTGCGGAAAGCGGCGGACTATGTCCGAAGCAAGGATTTCCGGGACTACCTCATG  
AGTACGCACTTCTGGGGCCCAGTAGCCAAC TGGGGTCTTCCCATTGCTGCCATCAATGATATGAAAAAG  
TCTCCAGAGATTATCAGTGGGCGGATGACATTTGCCCTCTGTTGCTATTCTTTGACATTCATGAGATTT  
GCCTACAAGGTACAGCCTCGGAAC TGGCTTCTGTTTGCATGCCACGCAACAAATGAAGTAGCCCAGCTC  
ATCCAGGGAGGGCGGCTTATCAAACACGAGATGACTAAAACGGCATCTGCATAA

&gt;YGL080W\_homolog, 109 aa (SEQ ID NO 676)

MAGALVRKAADYVRSKDFRDYLMSTHFVGPVNWGLPIAAINDMKKSPEIISGRMTFALCCYSLTFMRP  
AYKVQPRNWLLFACHATNEVAQLIQGGRLIKHEMTKTAASA

&gt;YGR243W\_homolog, CDS: 1-384 bp (SEQ ID NO 677)

ATGTCGGCCGCCGGTGCCCGAGGCCGTGCGGGCCACCTACCACCGGCTCCTCGATAAAGTGGAGCTGATG  
CTGCCCGAGAAATTGAGGCCGTTGTACAACCATCCAGCAGGTCCAGAACAGTTTCTTCTGGGCTCCA  
ATTATGAAATGGGGGTTGGTGTGTGCTGGATTGGCTGATATGGCCAGACCTGCAGAAAACTTAGCACA  
GCTCAATCTGCTGTTTTGATGGCTACAGGGTTTATTTGGTCAAGATACTCACTTGTAAATTATTTCCAAAA  
AATTGGAGTCTGTTTGTGTTAATTTCTTTGTGGGGGCAGCAGGAGCCTCTCAGCTTTTTCGTATTTGG  
AGATATAACCAAGAACTAAAAGCTAAAGCACACAAATAA

&gt;YGR243W\_homolog, 127 aa (SEQ ID NO 678)

MSAAGARGLRATYHRLLDKVELMLPEKLRPLYNHPAGPRTVFFWAPIMKWGLVCAGLADMARPAEKLST  
AQSAVLMATGFIWSRYSLVII PKNWSLFAVNFFVGAAGASQLFRIWRYNQELKAKAHK

&gt;YGR183C\_homolog, CDS: 1-399 bp (SEQ ID NO 679)

ATGGCGGCCGCGACGTTGACTTCGAAATTGTACTCCCTGCTGTTCCGCGAGACCTCCACCTTCGCCCTCA  
CCATCATCTTTGGGCGTCATGTTCTTTCGAGCGCGCCTTCCTCAAGGCGCGGACGCTATCTACGACCACA  
TCAACGAGGCTAAGCTGTGGAAACACATCAAGCACAAAGCTATGAGAACAAGTAGTTCCCTGGAGGCCCCC  
ATCCAGGCCAGAAGGACCAGGTCCACCCAGCAGCTGTTTGGCCAGAGCTGGAGCCTCAGCTTGAAGATG  
ATGCTCAAGGTACTCTTCATGGACCACCATTCGCTGTTGGCAAGAAACGGCTTTACTTACAAAACAGAC  
TCTTTACCTTCTGCTGTGTTTGAAGTATGTTTAGTCAGCATGCTCAGGAAATAA

&gt;YGR183C\_homolog, 132 aa (SEQ ID NO 680)

MAAATLTSKLYSLLFRRPPSPSPSSWASCSSSAPSIKARTLSTTTSTRGSCGNTSSSTSMRTSSSLEAP  
IQARRTRSTQQLFAQSWSLSKMMLKVLFMDHHSLLARNGFTYKTDLSLPSAVFEVCLVSMRLK

&gt;YBR009C\_homolog, CDS: 1-312 bp (SEQ ID NO 681)

ATGTCTGCGCCGCGCAAAGCGGGGAAGGGTCTTGGCAAAGGCGGCGCTAAGCGCCACCGTAAAGTACTG  
CGCGACAATATCCAGGGCATACCAAGCCGGCCATCCGGCGCCTTGCTCGCCGCGGCGGCGTGAAGCGC  
ATCTCCGGCCTCATCTACGAGGAGACTCGCGGGGTGCTGAAGGTGTTCCCTGGAGAACGTGATCCGGGAC  
GCCGTGACCTATACAGAGCACGCCAAGCGCAAGACGGTCACCGCCATGGATGTGGTCTACGCGCTCAAG  
CGCCAGGGCCGCACCCCTACGGTTTCGGTGGTTGA

&gt;YBR009C\_homolog, 103 aa (SEQ ID NO 682)

MSGRGKGKGLGKGGAKRHRKVL RDNIQGITKPAIRRLARRGGVKRISGLIYEETRGVLKVFLENVIRD  
AVTYTEHAKRKTVTAMDVVYALKRQGR TLYFGG

237/251

&gt;YGR209C\_homolog, CDS: 1-318 bp (SEQ ID NO 683)

ATGGTGAAGCAGATCGAGAGCAAGACTGCTTTTCAGGAAGCCTTGGACGCTGCAGGTGATAAACTTGT  
GTAGTTGACTTCTCAGCCACGTGGTGTGGGCCTTGCAAAATGATCAACCCTTTCATTCCTCTCT  
GAAAAGTATTCCAACGTGATATTCCTTGAAGTAGATGTGGATGACTGTCAGGATGTTGCTTCAGAGTGT  
GAAGTCAAATGCACGCCAACATTCAGTTTTTTAAGAAGGGACAAAAGGTGGGTGAATTTTCTGGAGCC  
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&gt;YGR209C\_homolog, 105 aa (SEQ ID NO 684)

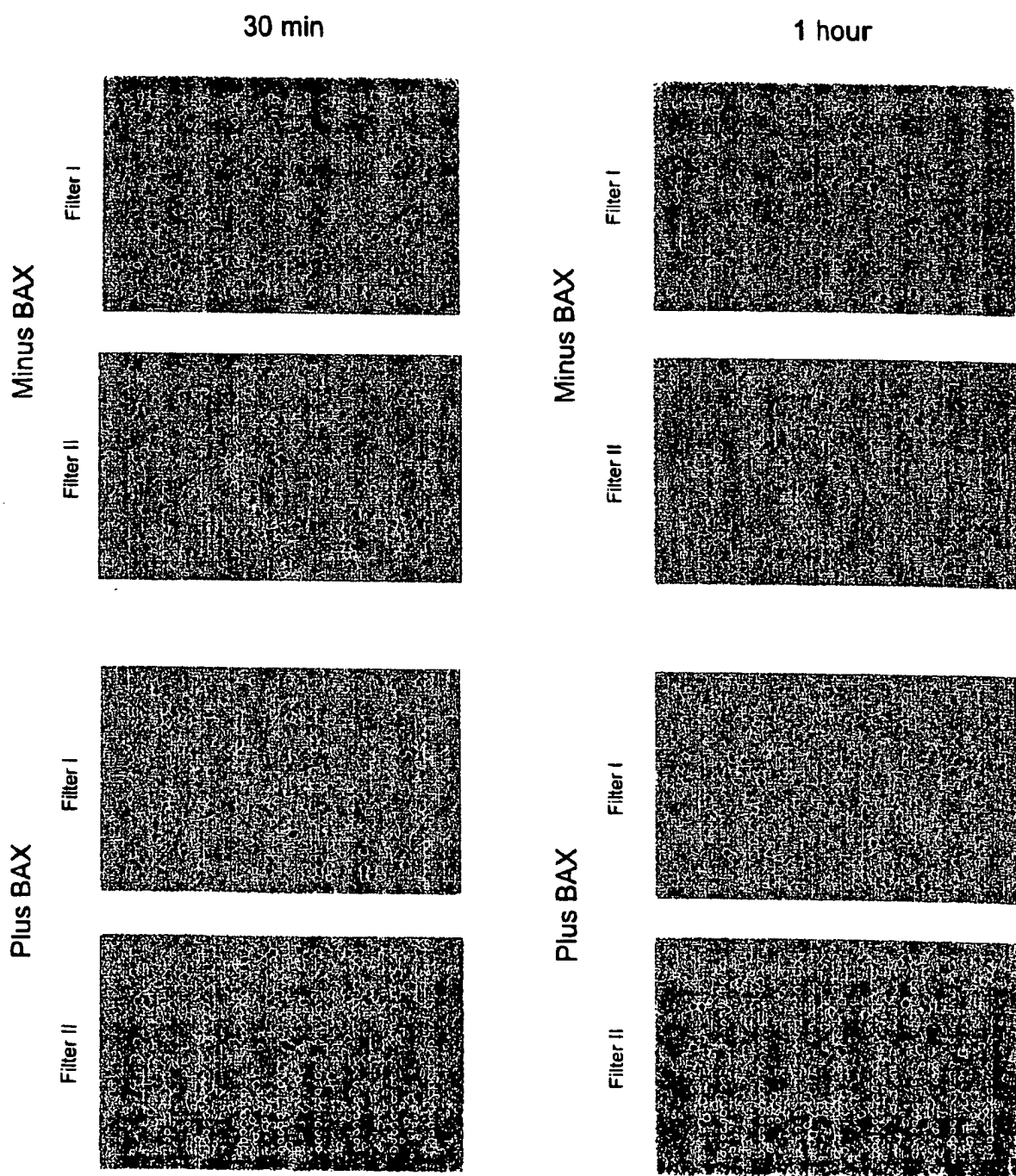
MVKQIESKTAFAQEALDAAGDKLVVDFSATWCGPCKMINPFFHSLSEKYSNVIFLEVDVDDCQDVASEC  
EVKCTPTTFQFFKKGQKVGEFSGANKEKLEATINELV

&gt;YPR028W\_homolog, CDS: 1-594 bp (SEQ ID NO 685)

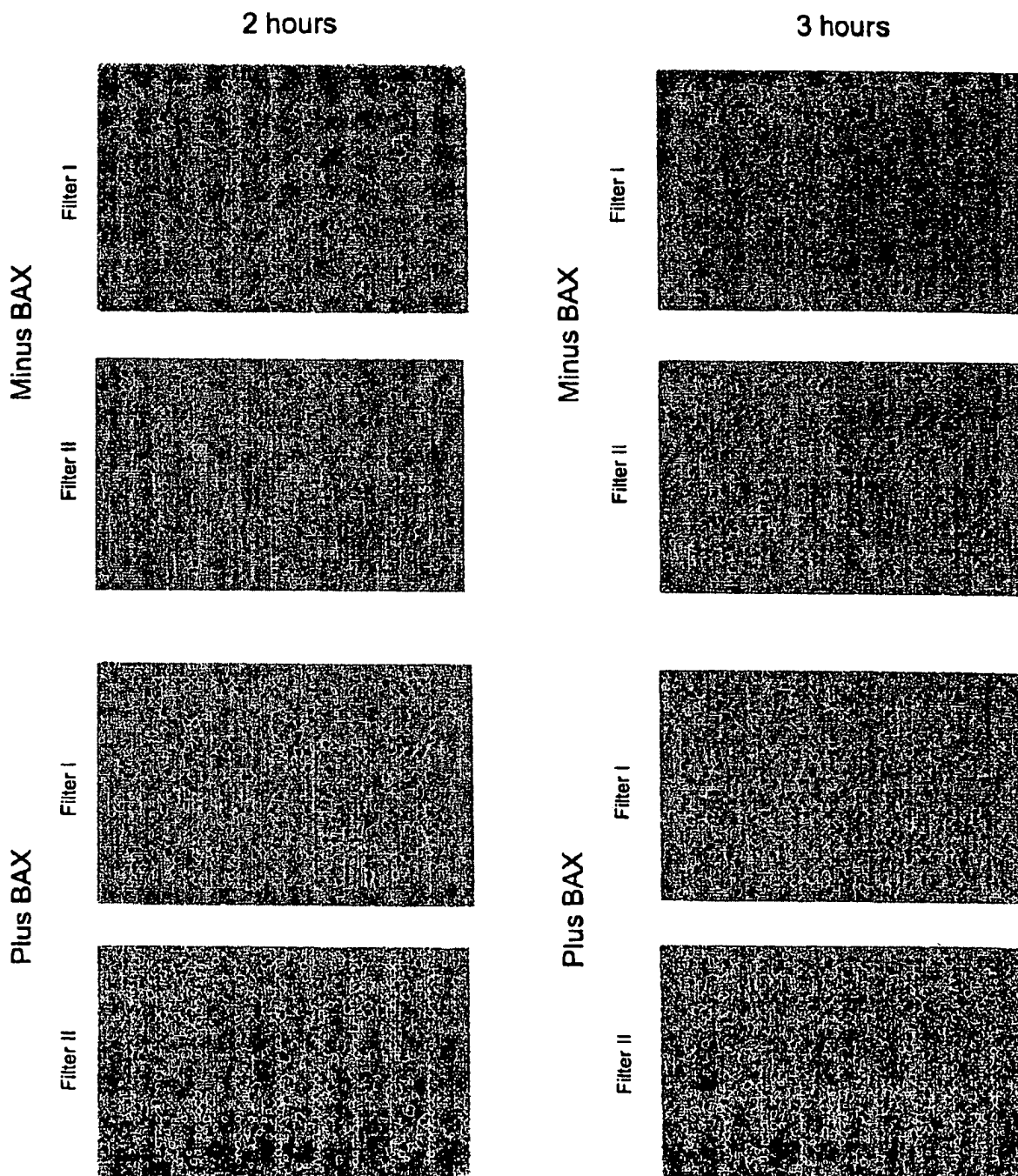
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ATAGGATTTGGCTACCCAGCCTACATCTCAATTAAAGCTATAGAGAGTCCCAACAAAGAAGATGATACC  
CAGTGGCTGACCTACTGGGTAGTGTATGGTGTGTTTTCAGCATTGCTGAATTCTTCTCTGATATCTTCTG  
TCATGGTTCCCTTCTACTACATACTGAAGTGTGGCTTCCTGTTGTGGTGCATGGCCCCGAGCCCTTCT  
AATGGGGCTGAACTGCTCTACAAGCGCATCATCCGTCCTTTCTTCTTCTGAGCAGAGTCCCAGATGGAC  
AGTGTGGTCAAGGACCTTAAAGACAAGGCCAAAGAGACTGCAGATGCCATCACTAAAGAAGCGAAGAAA  
GCTACCGTGAATTTACTGGGTGAAGAAAAGAAGAGCACCTAA

&gt;YPR028W\_homolog, 197 aa (SEQ ID NO 686)

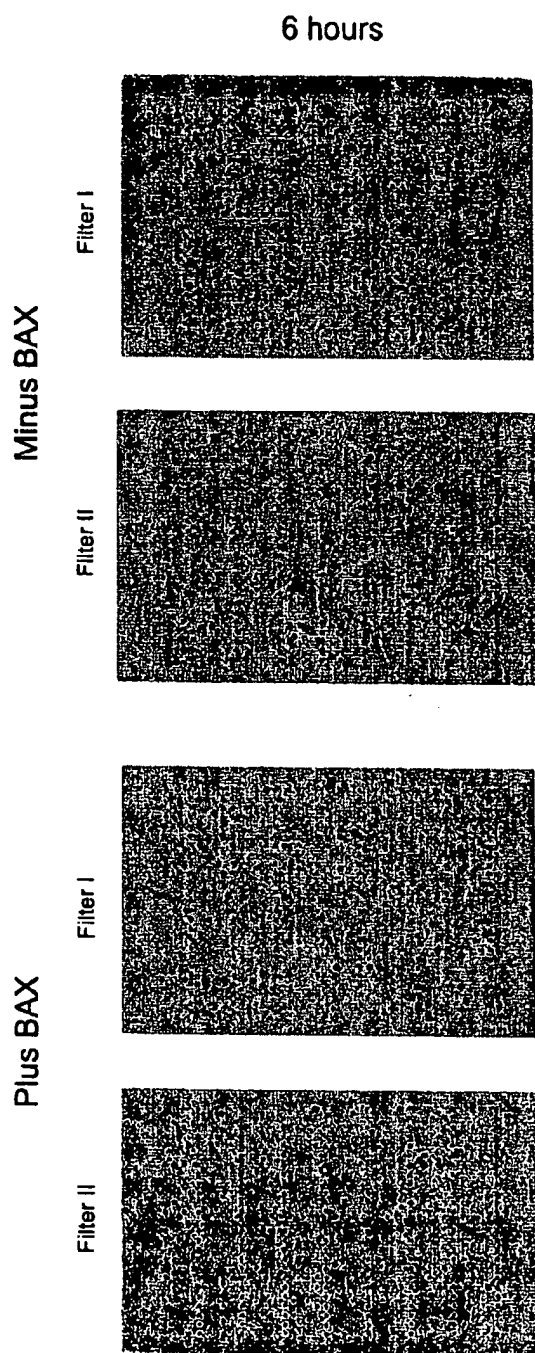
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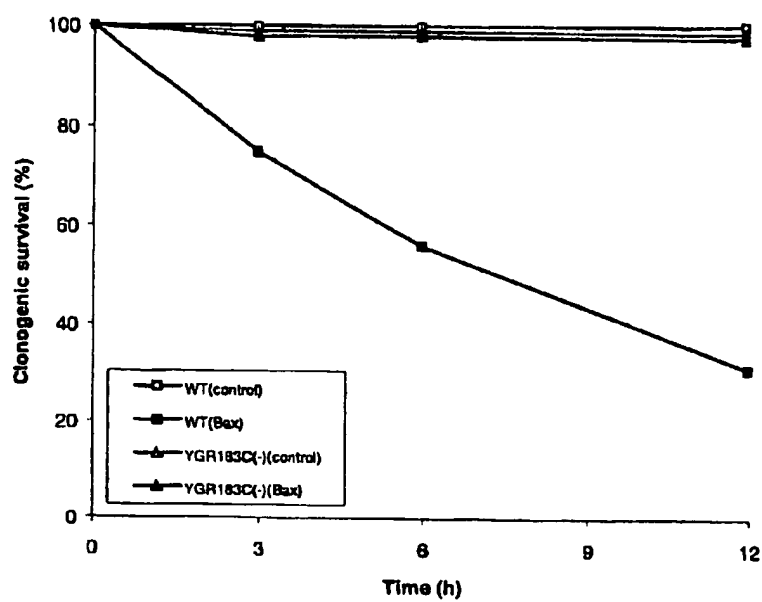
Figuur 3 - 1



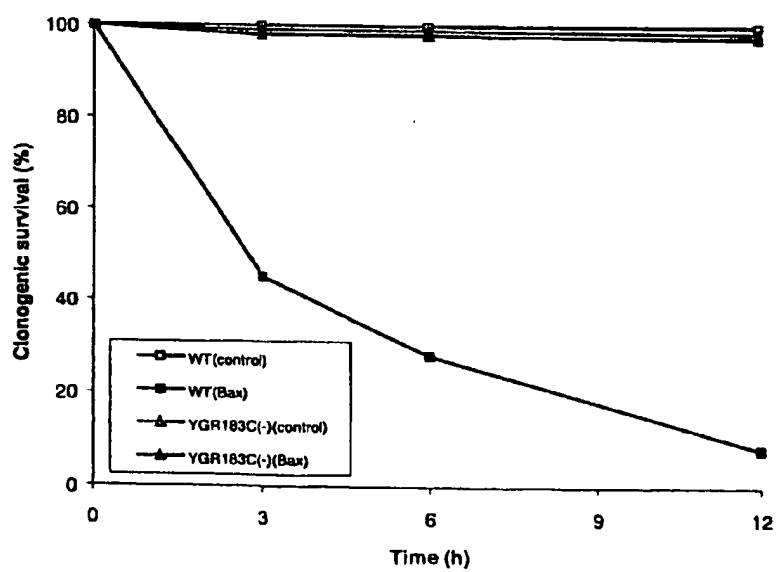
Figuur 3 - 2



Figuur 3 - 3



(A)



(B)

Figure 4

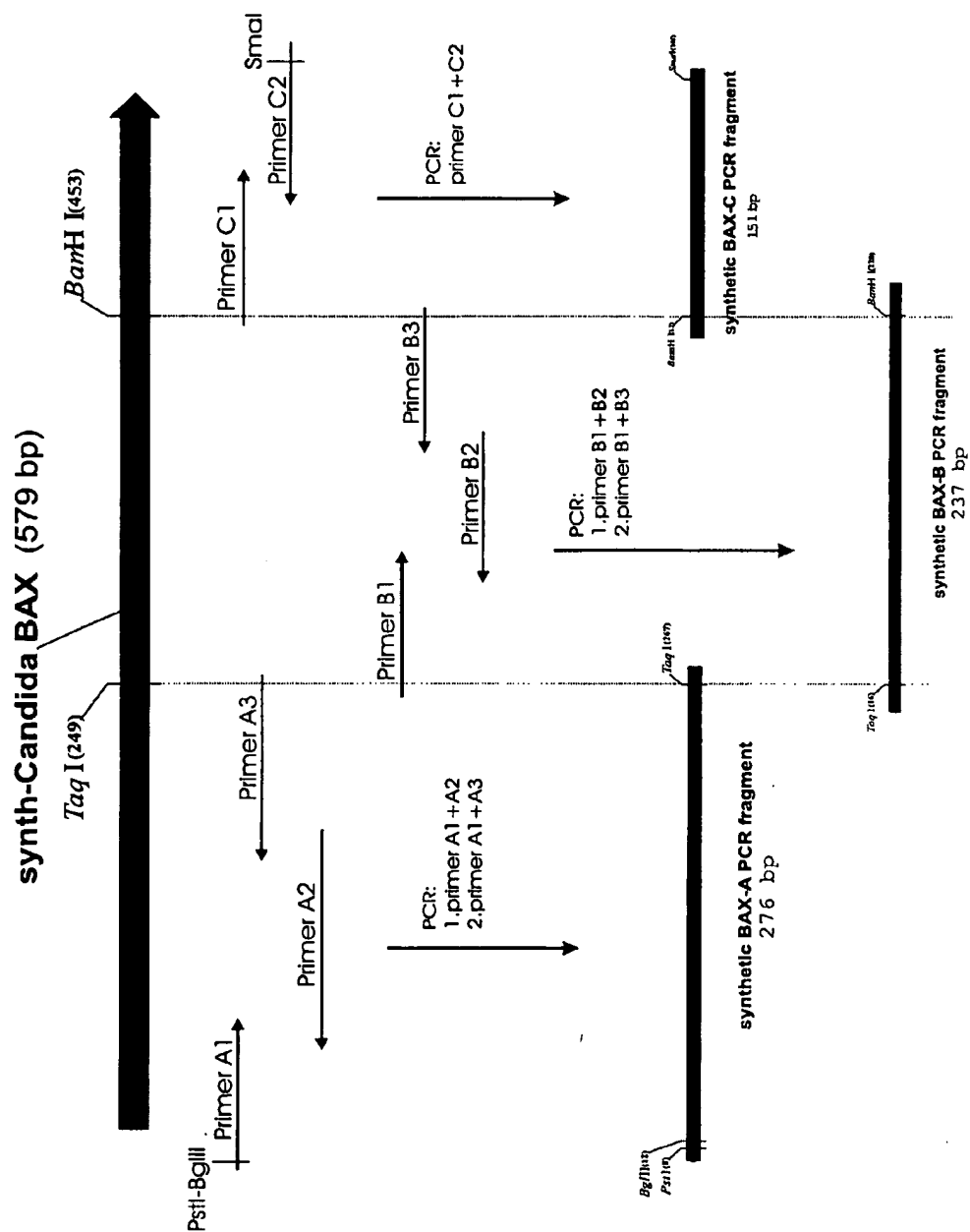


Fig. 5

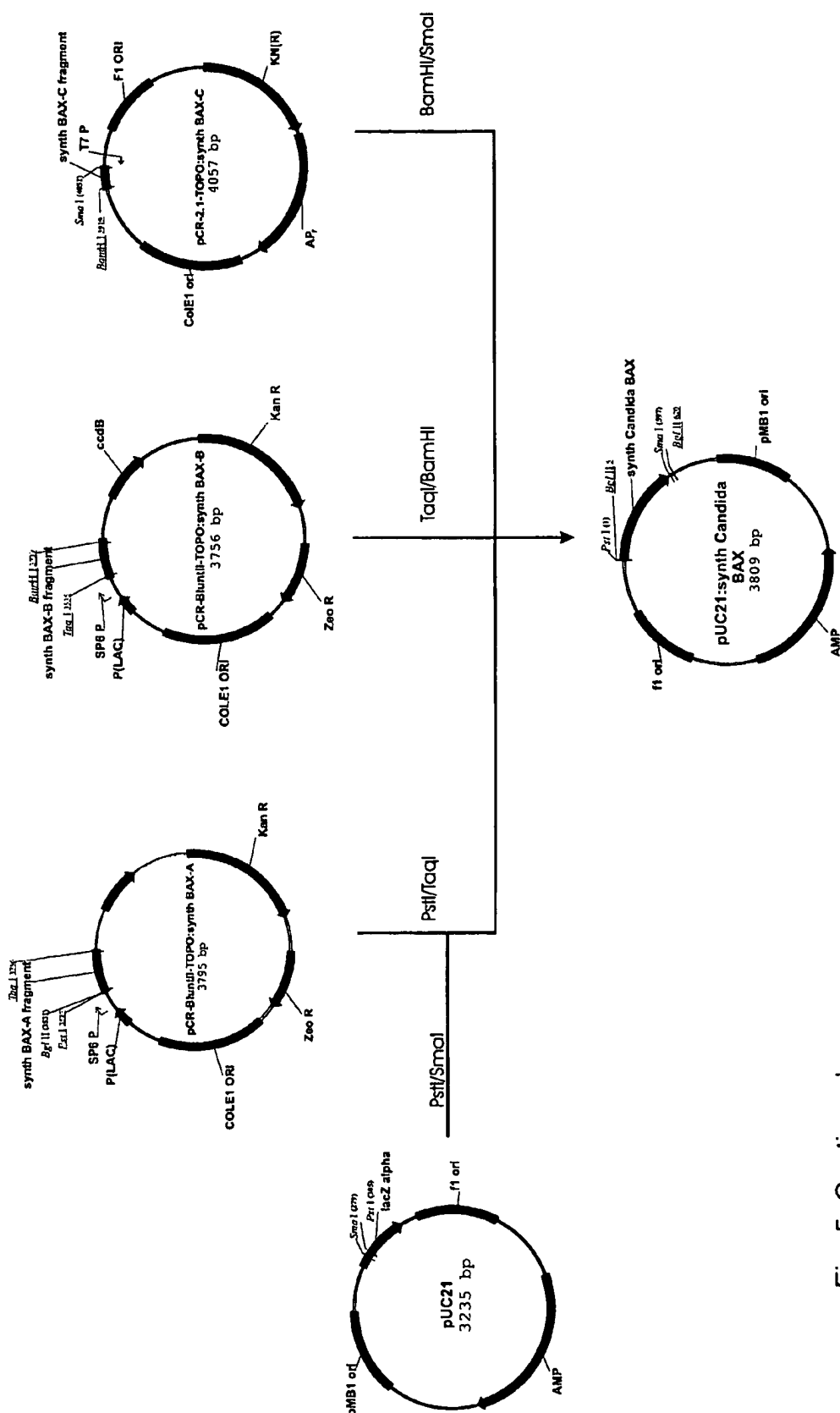


Fig. 5. Continued



Met Asp Gly Ser Gly Glu Gln Leu Gly Ser Gly Gly Pro Thr Ser Ser Glu Gln Ile Met  
1 ATG GAT GGT TCT GGT GAA CAA TTG GGT TCT GGT GGT CCA ACC TCT TCT GAA CAA ATC ATG

Lys Thr Gly Ala Phe Leu Leu Gln Gly Phe Ile Gln Asp Arg Ala Gly Arg Met Ala Gly  
61 AAA ACC GGT GCT TTC TTG TTG CAA GGT TTC ATC CAA GAT AGA GCT GGT AGA ATG GCT GGT

Glu Thr Pro Glu Leu Thr Leu Glu Gln Pro Pro Gln Asp Ala Ser Thr Lys Lys Leu Ser  
121 GAA ACC CCA GAA TTG ACC TTG GAA CAA CCA CCA CAA GAT GCT TCT ACC AAA AAA TTG TCT

Glu Cys Leu Arg Arg Ile Gly Asp Glu Leu Asp Ser Asn Met Glu Leu Gln Arg Met Ile  
181 GAA TGT TTG AGA AGA ATC GGT GAT GAA TTG GAT TCT AAC ATG GAA TTG CAA AGA ATG ATC

Ala Asp Val Asp Thr Asp Ser Pro Arg Glu Val Phe Phe Arg Val Ala Ala Asp Met Phe  
241 GCT GAT GTC GAT ACC GAT TCT CCA AGA GAA GTC TTC TTC AGA GTC GCT GCT GAT ATG TTC

Ala Asp Gly Asn Phe Asn Trp Gly Arg Val Val Ala Leu Phe Tyr Phe Ala Ser Lys Leu  
301 GCT GAT GGT AAC TTC AAC TGG GGT AGA GTC GTC GCT TTG TTC TAC TTC GCT TCT AAA TTG

Val Leu Lys Ala Leu Cys Thr Lys Val Pro Glu Leu Ile Arg Thr Ile Met Gly Trp Thr  
361 GTC TTG AAA GCT TTG TGT ACC AAA GTC CCA GAA TTG ATC AGA ACC ATC ATG GGT TGG ACC

Leu Asp Phe Leu Arg Glu Arg Leu Leu Val Trp Ile Gln Asp Gln Gly Gly Trp Glu Gly  
421 TTG GAT TTC TTG AGA GAA AGA TTG TTG GTC TGG ATC CAA GAT CAA GGT GGT TGG GAA GGT

Leu Leu Ser Tyr Phe Gly Thr Pro Thr Trp Gln Thr Val Thr Ile Phe Val Ala Gly Val  
481 TTG TTG TCT TAC TTC GGT ACC CCA ACC TGG CAA ACC GTC ACC ATC TTC GTC GCT GGT GTC

Leu Thr Ala Ser Leu Thr Ile Trp Lys Lys Met Gly (SEQ ID NO 2)  
541 TTG ACC GCT TCT TTG ACC ATC TGG AAA AAA ATG GGT TAA (SEQ ID NO 1)

Fig. 6

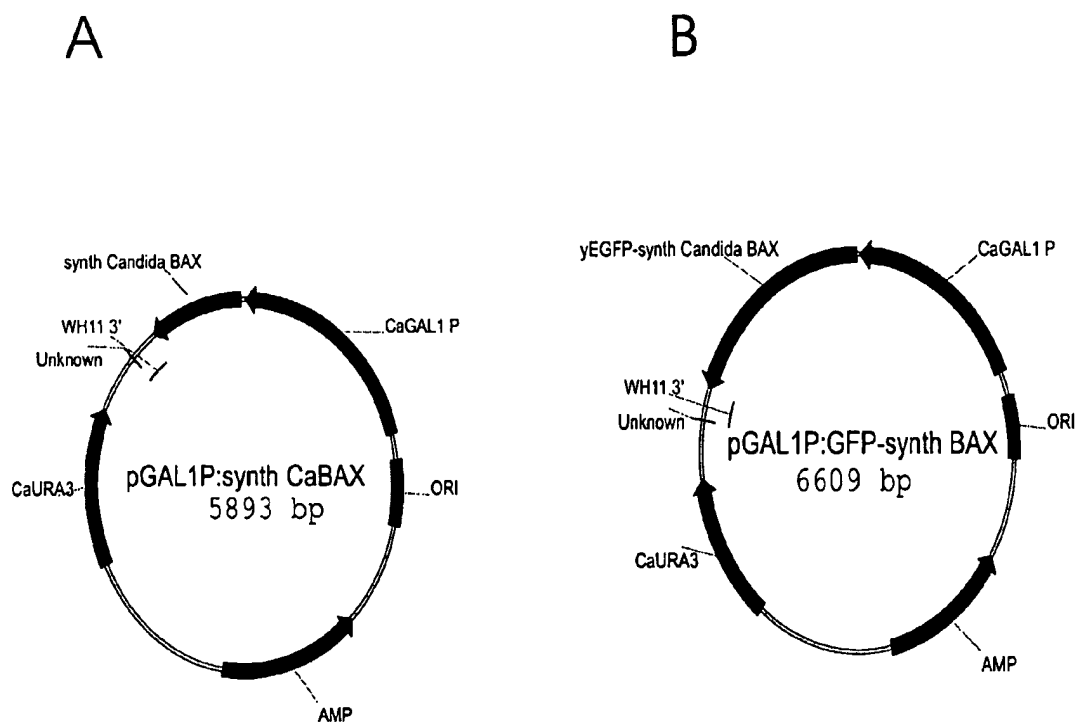


Fig. 7.

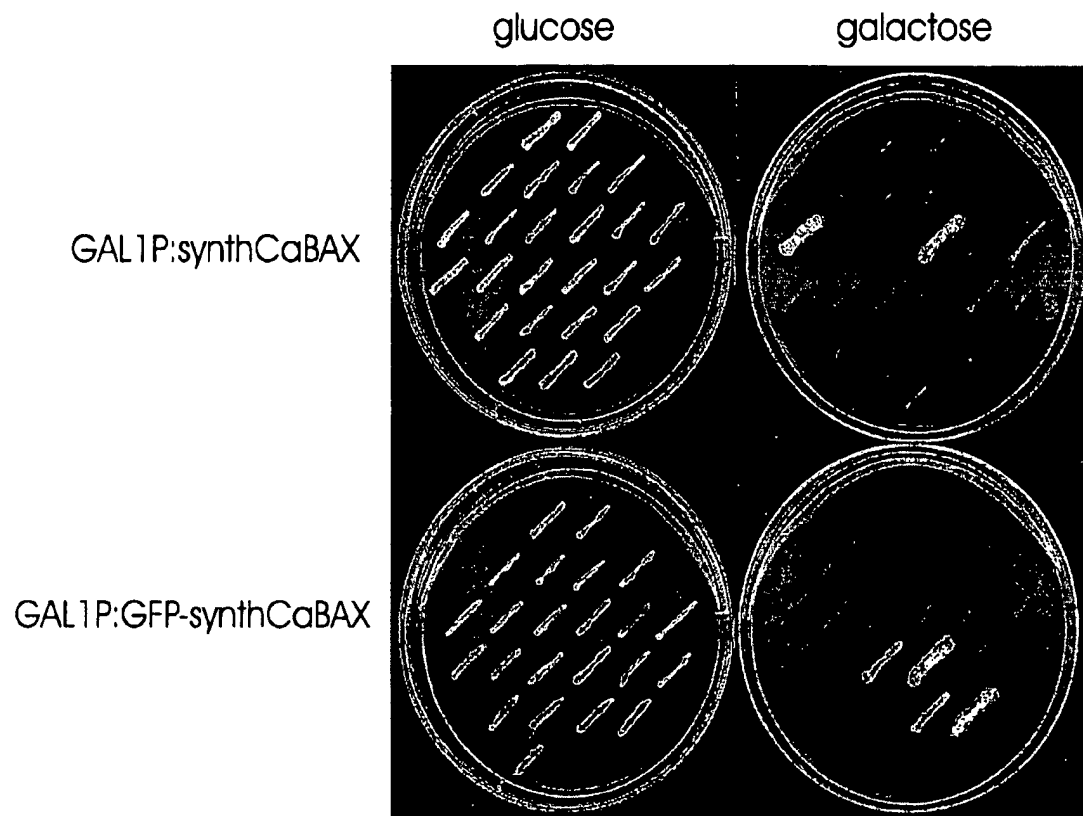


Fig. 8.

247/251

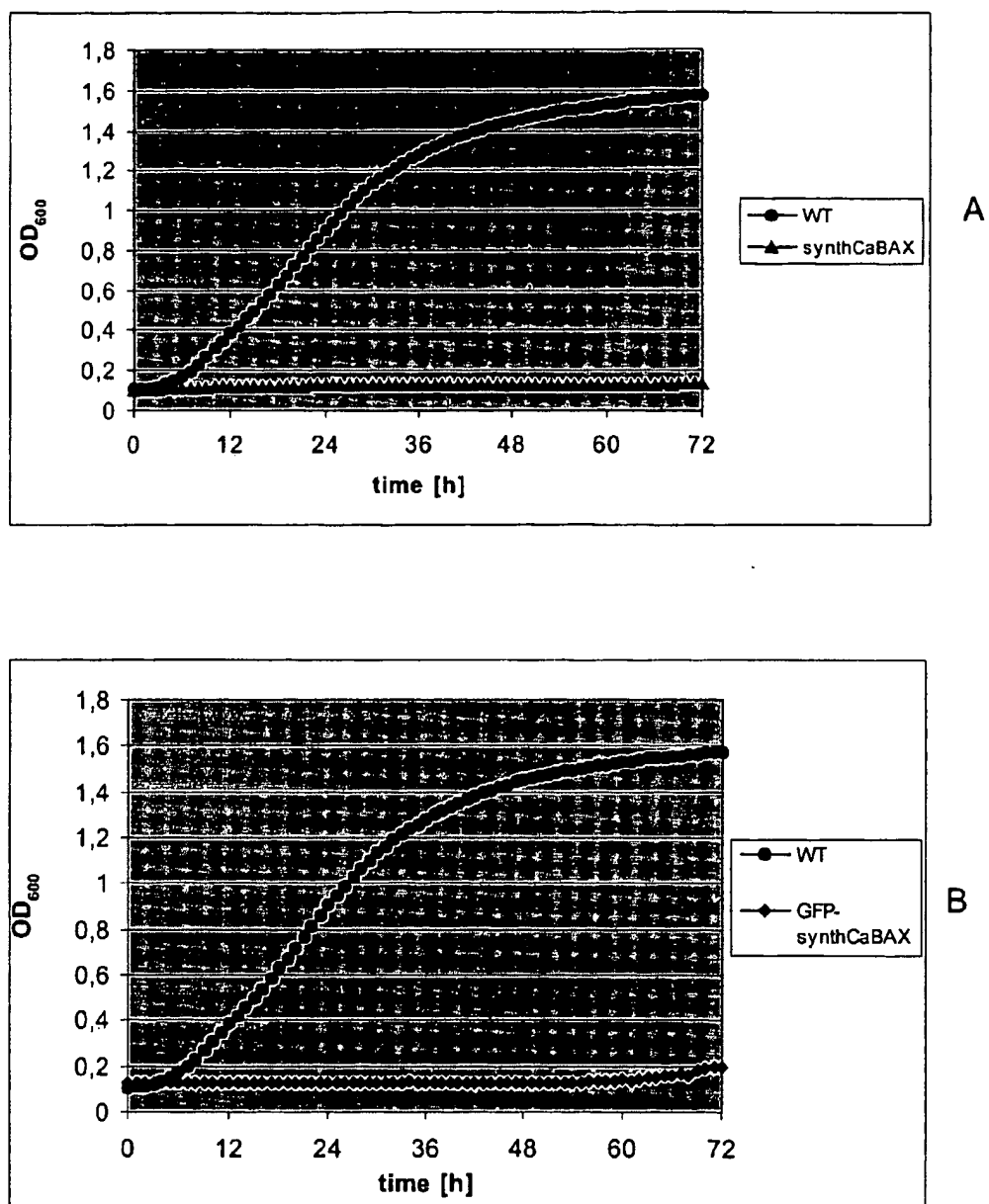


Fig. 9.

248/251

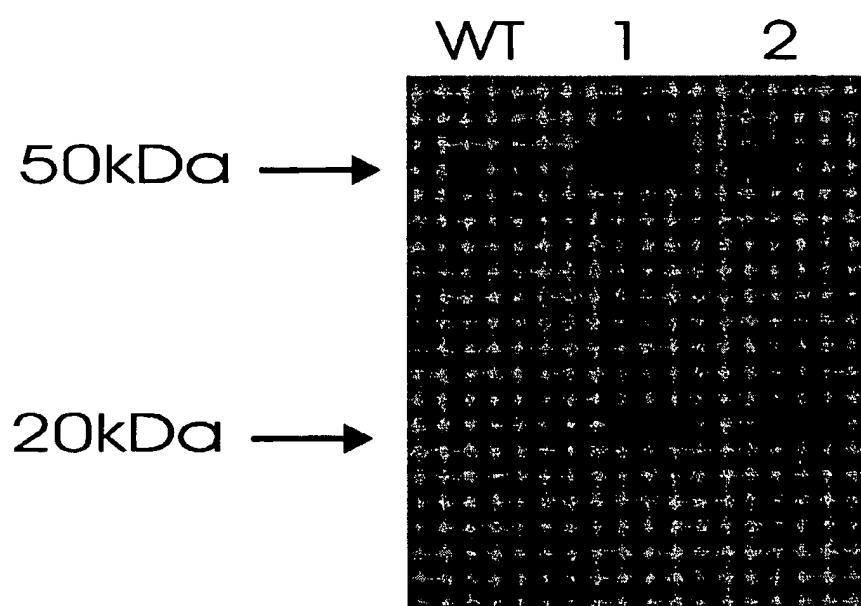


Fig. 10.

249/251

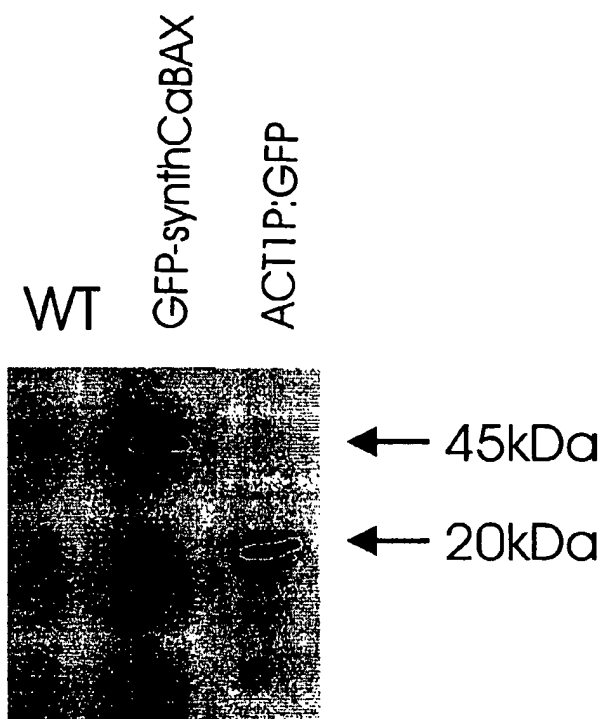


Fig. 11.

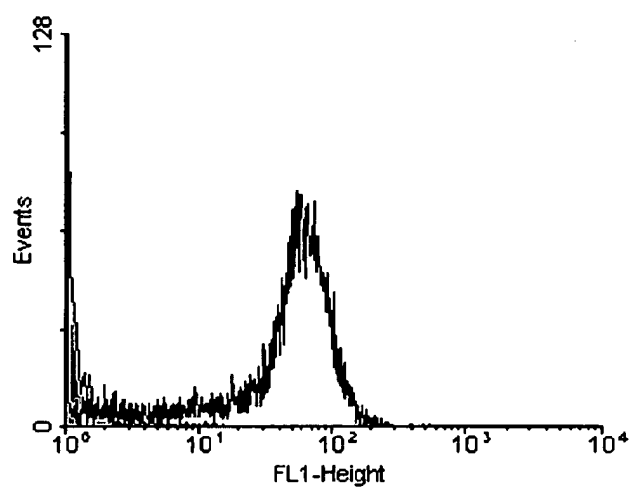
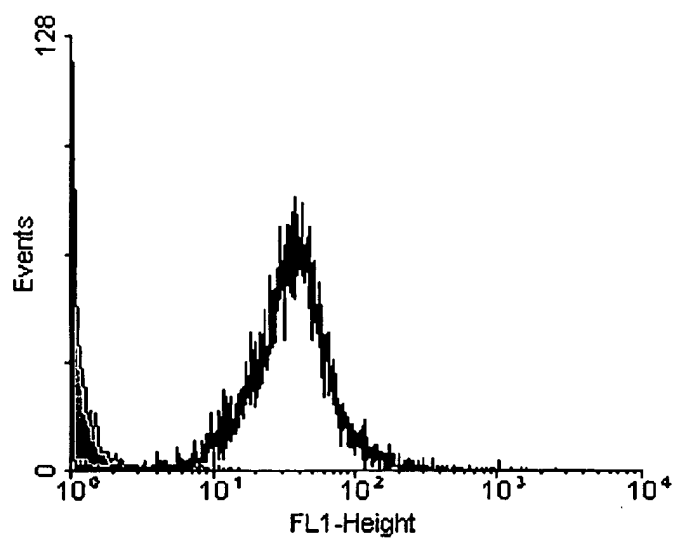


Fig.12.

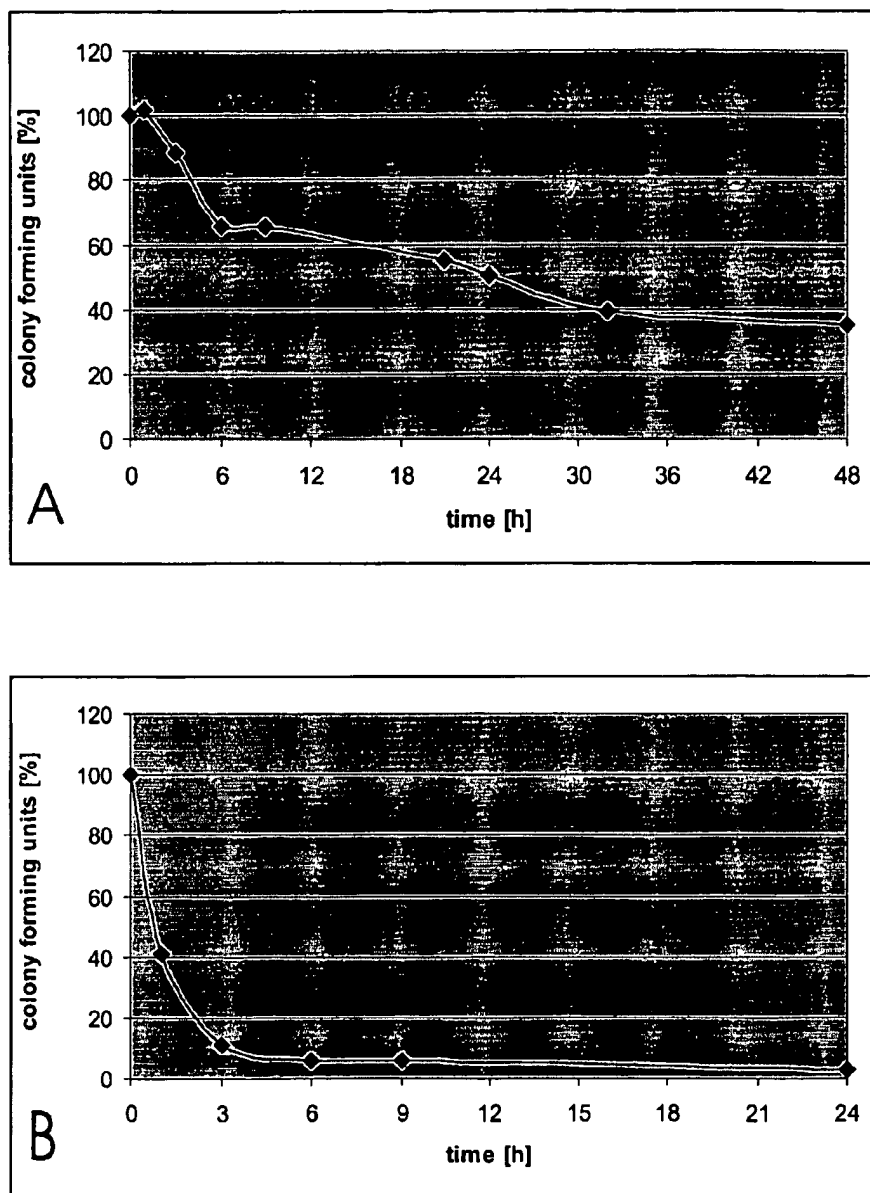


Fig. 13.